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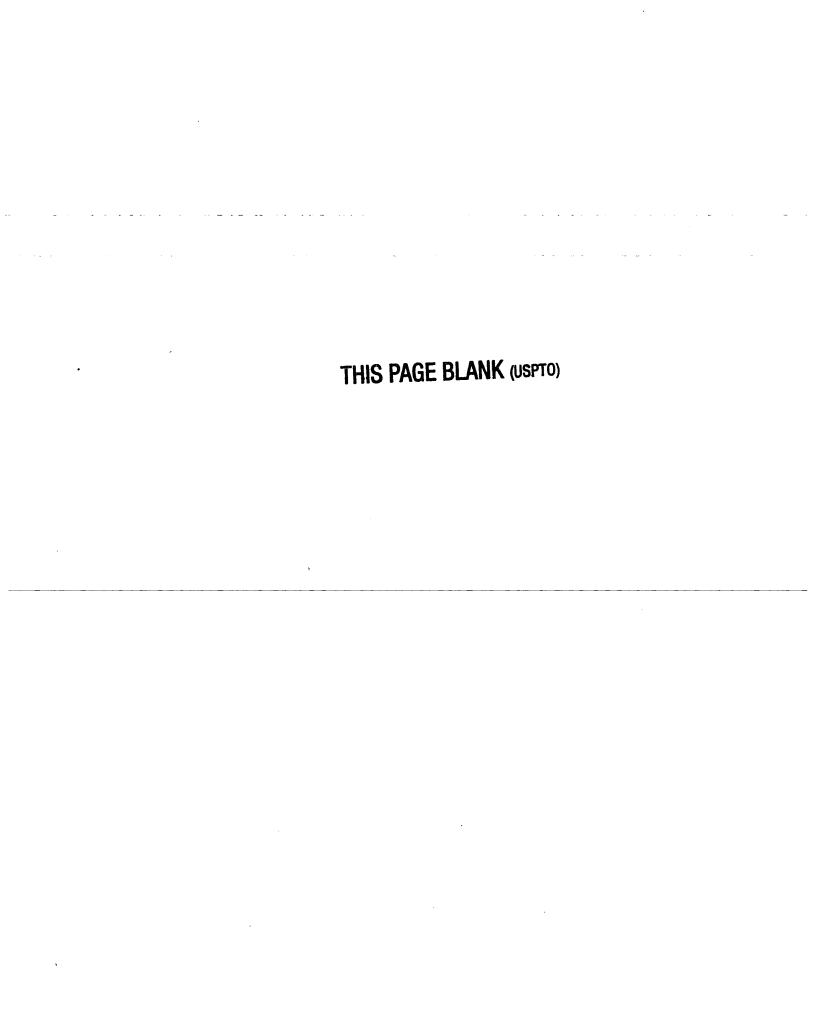
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PTO-1590 (1-2000)

# 43504 SEARCH REQUEST FORM

Access DB#\_

Scientific and Technical Information Center

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Title of Invention:		·	
Inventors (please provide full names):			
Earliest Priority Filing Date: 9-2-5			
*For Sequence Searches Only* Please include appropriate serial number.	all pertinent information (p	arent, child, divisional, or issued patent numbers) along with th	ie .
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FILE 'REGISTRY' ENTERED AT 11:09:26 ON 11 JUN 2001 E CONDUCTINE/CN

FILE 'CAPLUS' ENTERED AT 11:09:46 ON 11 JUN 2001 L1 0 S CONDUCTINE

FILE 'MEDLINE, BIOSIS, EMBASE, WPIDS, CONFSCI, SCISEARCH,
JICST-EPLUS, JAPIO, CANCERLIT' ENTERED AT 11:10:14 ON 11 JUN 2001

L2 . 6 S L1

L3 6 DUP REM L2 (0 DUPLICATES REMOVED)

L3 ANSWER 1 OF 6 JAPIO COPYRIGHT 2001 JPO

ACCESSION NUMBER:

1996-024402 JAPIO

TITLE:

GAME BALL PASSING SENSOR

INVENTOR:

YOSHIKAWA TOSHISUKE

PATENT ASSIGNEE(S):

KYOWA GIKEN KK, JP (CO)

PATENT INFORMATION:

JP

APPLICATION INFORMATION

ST19N FORMAT:

JP1994-169178

19940721

ORIGINAL:

JP06169178

Heisei

SOURCE:

PATENT ABSTRACTS OF JAPAN (CD-ROM), Unexamined

Applications, Vol. 96, No. 1

AN 1996-024402 JAPIO

AB PURPOSE: To prevent an erroneous operation by electromagnetic wave or exter nal light, and precisely detect the passing of game ball by making an operating piece pushed into a switch housing part when the ball passes the through-hole of a switch case, thereby a switch is brought into non-conductine stake and the passing of the ball is detected.

CONSTITUTION: When no game ball passes a through-hole 30, one end of an operating piece 70 supported in the inner part of a switch housing part 40 is in the state capable of protruding into the through-hole 30, and the energizing force of a torsion spring 60 acts on the free end part on the other end to energize the operating piece 70 in the protruding direction. Both ends of the torsion spring 60 come into contact with a fixed pin 54 and a contact pin 53 in this state to hold the conductive state between the connecting terminals 51, 52 of a base 50. When a game ball passes the through-hole 30, the operating piece 70 is pushed against the energizing force of the torsion spring 60. Thus, one end of the torsion spring 60 is pushed in and separated from the contact pin 53 to bring the connecting terminals 51, 52 into the non-conductive

state, thereby the passing of the game ball can be detected.

ANSWER 2 OF 6 MEDLINE

ACCESSION NUMBER: 90181913 MEDLINE

DOCUMENT NUMBER: 90181913

PubMed ID: 2560672 TITLE:

[Sodium conductin of the human brain: purification

and functional characterization].

La conductine au sodium du cerveau humain: purification et caracterisation fonctionnelle.

AUTHOR: Materne-De Rycker C

SOURCE: BULLETIN ET MEMOIRES DE L ACADEMIE ROYALE DE MEDECINE

DE BELGIQUE, (1989) 144 (8-9) 426-33.

Journal code: BOX; 7608462. ISSN: 0377-8231.

PUB. COUNTRY: Belgium

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: French

FILE SEGMENT: Priority Journals

ENTRY MONTH: 199004

ENTRY DATE: Entered STN: 19900601

> Last Updated on STN: 19900601 Entered Medline: 19900426

A sodium channel enriched preparation was obtained from human brain. AB Human sodium channel appeared as a heterocomplex peptide alpha beta 1 beta 2. Functional properties of the protein were maintained since, after reconstitution into liposomes, ion fluxes were sensitive to sodium channel specific toxins and to membrane potential. Moreover, the reconstituted protein showed a well defined ionic selectivity.

ANSWER 3 OF 6 WPIDS COPYRIGHT 2001 DERWENT INFORMATION LTD

ACCESSION NUMBER: 1988-347509 [49]

DOC. NO. NON-CPI: N1988-263366

TITLE: Semiconductor shift register in memory output state

- has two conductive type transistor connected in series between power supply terminal and node.

DERWENT CLASS: **U14** 

INVENTOR(S): NAKAGAWA, K; TAKEUCHI, Y (TOKE) TOSHIBA KK

PATENT ASSIGNEE(S): COUNTRY COUNT:

PATENT INFORMATION:

PA'	TENT NO	KIND	DATE	WEEK	LA	PG
EP	293808 R: DE F	A R GB	19881207	(198849)*	EN	15
JP	63304494	Α	19881212	(198904)		
US	4856034	A	19890808	(198939)		14
EP	293808	B1	19930929		EN	16

Searcher

Shears

308-4994

R: DE FR GB

DE 3884460 G 19931104 (199345)

#### APPLICATION DETAILS:

PAT	TENT NO	KIND	APPLICATION	DATE
EP	293808	A	EP 1988-108632	19880530
JP	63304494	A	JP 1987-139405	19870603
US	4856034	A	US 1988-199914	19880527
EP	293808	B1	EP 1988-108632	19880530
DE	3884460	G	DE 1988-3884460	19880530
			EP 1988-108632	19880530

#### FILING DETAILS:

PATENT NO KIND		PATENT NO
DE 3884460	G Based o	n EP 293808

PRIORITY APPLN. INFO: JP 1987-139405 19870603

AN 1988-347509 [49] WPIDS

AB EP 293808 A UPAB: 19930923

The circuit has a logic circuit (12) with two inputs connected to receive a control clock signal (Phi G) and an input signal (Vin) a two conductine type transistors (P11 P12) are connected in series between a power supply terminal and a node. The first transistor (P11) has a gate connected to receive an output signal of the logic circuit. The other transistor (P12) has a gate connected to receive the control clock signal.

A third transistor (N11) of a different conductive type connects the first node and the second power supply terminal together.

The transistor gate is connected to receive the output signal of the logic circuit.

USE/ADVANTAGE - Latch circuit or swift register in the output stage of the memory.

#### ABEQ US 4856034 A UPAB: 19930923

The semiconductor integrated circuit consists of a three-valued logic circuit connected to receive an output signal of a logic circuit to receive at one input a control clock signal and at the other input an input signal. A flip-flop circuit is composed of a clocked inverter to receive the output signal of the three-valued logic circuit, and another inverter.

ABEQ EP 293808 B UPAB: 19931123

A semiconductor integrated circuit, comprising: a logic circuit (12) consisting of a NOR gate (72) or a NAND gate (82) and having a first

and a second input connected to receive a control clock signal (G) and an input signal (Vin), respectively; first and second transistors (P11, P12) of a first conductivity type connected in series between a first power supply terminal (Vcc) and a first node (1), said first transistor (P11) having a gate connected to receive an output signal of said logic circuit, and said second transistor (P12) having a gate connected to receive the control clock signal; a third transistor (N11) of a second conductivity type connected between said first node and a second power supply terminal (Vss) and having a gate connected to receive the output signal of said logic circuit; fourth and fifth transistors (P13, P14) of the first conductivity type connected in series between said first power supply terminal and a second node (2) connected to said first node, said fourth transistor (P14) having a gate connected to receive the output signal of said logic circuit, and said fifth transistor (P13) having a gate connected to a third node (3); sixth and seventh transistors (N14, N13) of the second conductivity type connected in series between said second power supply terminal and said second node, said sixth transistor (N14) having a gate connected to receive the clock signal, and said seventh transistor (N13) having a gate connected to said third node; an eighth transistor (P15) of the first conductivity type connected between said third node and said first power supply terminal and having a gate connected to said second node; and a ninth transistor (N15) of the second conductivity type connected between said third node and said second power supply terminal, and having a gate connected to said second node; an output signal (Vout) of said semiconductor integrated circuit being taken from at least one of said second node and said third node. Dwg.1/10

ANSWER 4 OF 6 WPIDS COPYRIGHT 2001

DERWENT INFORMATION LTD

ACCESSION NUMBER:

1978-A8315A [04] WPIDS

TITLE:

Insulated splice and terminal - is made from crimped composite strip of non-conductive and

electrically conducting materials.

DERWENT CLASS:

V04

INVENTOR(S):

FISCHER, E M; MEISINGER, W R; ZAHN, I

PATENT ASSIGNEE(S):

(GEST-N) GEN STAPLE CO

WEEK

COUNTRY COUNT:

PATENT INFORMATION:

PATENT NO KIND DATE

PG LA

308-4994

US 4067105

A 19780110 (197804) \*

PRIORITY APPLN. INFO: US 1973-335417 19730223; US 1974-537532

> Searcher Shears

19741230; US 1976-711604 19760804

AN . 1978-A8315A [04] WPIDS

US 4067105 A UPAB: 19930901 AB

> An elongated layer of non-conductive materials is adhered to an elongated layer of electrically conductive material so as to form a composite supply strip. A predetermined length is severed and crimped about the elements to be joined until the electrically conductive material is in electrical contact with the elements and so that the non-conductine material forms an outer insulated layer enclosing the splice or at least a portion of the terminal.

> In a pref. method there is further step of causing the non-conductive material of the splice to "flow" whereby a resultant sealed splice is produced which is impervious to moisture and other contaminants. PRef. the non-conductive material is a thermoplastic resin and the conductive material is brass.

ANSWER 5 OF 6 JAPIO COPYRIGHT 2001 JPO 1.3

ACCESSION NUMBER:

1977-115854 **JAPIO** 

TITLE:

ELECTRICALLY CONDUCTINE RESIN AND

INTERMEDIATES AND ELECTRICALLY CONDUCTIVE COATED

PAPERS

INVENTOR:

JIYOSEFU RII GAANAA

PATENT ASSIGNEE(S):

DOW CHEM CO: THE, US (CO 000723)

PATENT INFORMATION:

PATENT NO KIND DATE ERA MAIN IPC \_\_\_\_\_ JP 52115854 A 19770928 Showa (2) C08L025-06

JP

APPLICATION INFORMATION

ST19N FORMAT: JP1977-29130 19770316 JP52029130 ORIGINAL: Showa PRIORITY APPLN. INFO.: US1976 668335 19760319

AN 1977-115854 JAPIO

ANSWER 6 OF 6 JAPIO COPYRIGHT 2001 JPO

ACCESSION NUMBER: 1977-019984

**JAPIO** 

TO MAKE A SEMICONDUCTOR ELEMENT

INVENTOR:

TITLE:

PATENT ASSIGNEE(S):

KOMATSU RYOSAKU; HARUHARA YOSHIO NIPPON TELEGR & TELEPH CORP <NTT>, JP (CO

MANUFACTURE PROCESS FOR A ISOLATION LAYER USED

000422)

PATENT INFORMATION:

PATENT NO KIND DATE ERA MAIN IPC

JP 52019984 A 19770215 Showa (2) H01L021-76

JΡ

APPLICATION INFORMATION

ST19N FORMAT:

JP1975-96053

19750807

ORIGINAL:

JP50096053

Showa

SOURCE:

PATENT ABSTRACTS OF JAPAN, Unexamined

Applications, Section: E, Sect. No. 34, Vol. 1,

No. 851, P. 1733 (19770809)

AN 1977-019984 **JAPIO** 

PURPOSE: To pour p type ion to the N type semiconductor substrate an AB order to make a p type conductine area as a isolation layer. In this way, we make plural isolation layers at the same time with a desired size and high precision, saving the manufacture work.

FILE 'REGISTRY' ENTERED AT 11:14:12 ON 11 JUN 2001

E CONDUCTIN/CN L4

2 SEA ABB=ON PLU=ON ("CONDUCTIN (HUMAN FETAL BRAIN REDUCED) "/CN OR "CONDUCTIN (HUMAN) "/CN)

FILE 'CAPLUS' ENTERED AT 11:14:41 ON 11 JUN 2001

L5 25 SEA ABB=ON PLU=ON L4 OR CONDUCTIN

15 SEA ABB=ON PLU=ON L5 AND (TUMOUR OR TUMOR OR NEOPLAS? L6

OR CANCER? OR CARCIN?)

ANSWER 1 OF 15 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER:

2001:208094 CAPLUS

DOCUMENT NUMBER:

134:247261

TITLE:

Agents for treating human diseases, especially

for treating tumors such as colon

cancers and melanomas or for

regenerating tissue and promoting hair growth

INVENTOR (S): Birchmeier, Walter; Von Kries, Jens-peter PATENT ASSIGNEE(S):

Max-Delbruck-Centrum fur Molekulare Medizin,

Germany

SOURCE:

PCT Int. Appl., 28 pp.

CODEN: PIXXD2

DOCUMENT TYPE:

Patent German

LANGUAGE:

\_ \_ \_ \_

FAMILY ACC. NUM. COUNT:

PATENT INFORMATION:

PATENT NO. KIND DATE APPLICATION NO. DATE

WO 2001019353 A2 20010322 WO 2000-DE3104 20000907

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH,

CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK,

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LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ. TM
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RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

DE 19944404 A1 20010322 DE 1999-19944404 19990916

PRIORITY APPLN. INFO.:

DE 1999-19944404 A 19990916

The invention relates to agents for treating human diseases which are based on substances that specifically influence the binding of .beta.-catenin with LEF-1/TCF transcription factors, APC or conductin/axin. The invention particularly relates to the identification and use of hydrophobic pockets on the mol. surface in the proximity of the essential binding points for the binding partners of .beta.-catenin with the aim of optimizing these substances. The invention also relates to the use of the substances, preferably for treating tumors, e.g. colon cancers and melanomas, or for regenerating tissue and promoting hair growth.

L6 ANSWER 2 OF 15 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER:

2000:735507 CAPLUS

DOCUMENT NUMBER:

134:28066

TITLE:

Mutations in AXIN2 cause colorectal

cancer with defective mismatch repair by
activating .beta.-catenin/TCF signaling

AUTHOR (S):

Liu, Wanguo; Dong, Xiangyang; Mai, Ming; Seelan, Ratnam S.; Taniguchi, Ken; Krishnadath, Kausilia K.; Halling, Kevin C.; Cunningham, Julie M.;

Qian, Chiping; Christensen, Eric; Roche, Patrick

C.; Smith, David I.; Thibodeau, Stephen N.

CORPORATE SOURCE:

Div. of Experimental Pathol., Dep. of Lab. Med.

and Pathol., Mayo Clinic and Mayo Med. Sch.,

Rochester, MN, USA

SOURCE:

Nat. Genet. (2000), 26(2), 146-147

CODEN: NGENEC; ISSN: 1061-4036

PUBLISHER:

Nature America Inc.

DOCUMENT TYPE:

Journal; General Review

LANGUAGE:

English

AB Colorectal cancer (CRC) with defective DNA mismatch repair (MMR) is assocd. with alterations one of several DNA MMR genes. Here we show that AXIN2 encoding a Wnt signaling component, is mutated in 11 of 45 CRC with defective MMR. We tested the functional importance of AXIN2 mutations in the development of CRCwith defective MMR in a TCF reporter assay. Our findings now provide a link between defective MMR and the activation of TCF-dependent transcription, as mutations in AXIN2 alter the APC

pathway.

REFERENCE COUNT:

REFERENCE(S):

14

- (1) Behrens, J; Science 1998, V280, P596 CAPLUS
- (2) Boland, C; Cancer Res 1998, V58, P5248 CAPLUS
- (3) Chan, E; Nature Genet 1999, V21, P410 CAPLUS
- (4) Ganguly, A; Proc Natl Acad Sci USA 1993, V90, P10325 CAPLUS
- (5) Ishitani, T; Nature 1999, V399, P798 CAPLUS
- ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 3 OF 15 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER:

2000:651706 CAPLUS

DOCUMENT NUMBER:

134:1816

TITLE:

Hot spots in .beta.-catenin for interactions

with LEF-1, conductin and APC

AUTHOR (S):

Von Kries, Jens Peter; Winbeck, Georgia; Asbrand, Christian; Schwarz-Romond, Thomas; Sochnikova, Natalia; Dell'Oro, Andrea; Behrens,

Jurgen; Birchmeier, Walter

CORPORATE SOURCE:

Max-Delbruck-Center for Molecular Medicine,

Berlin, 13093, Germany

SOURCE:

Nat. Struct. Biol. (2000), 7(9), 800-807

CODEN: NSBIEW; ISSN: 1072-8368

PUBLISHER:

Nature America Inc.

DOCUMENT TYPE:

Journal

LANGUAGE:

English

Interactions between .beta.-catenin and LEF-1/TCF, APC and conductin/axin are essential for wnt-controlled stabilization of .beta.-catenin and transcriptional activation. wnt signal transduction pathway is important in both embryonic development and tumor progression. We identify here amino acid residues in .beta.-catenin that distinctly affect its binding to LEF-1/TCF, APC and conductin. These residues form sep. surface clusters, termed hot spots, along the armadillo superhelix of .beta.-catenin. We also show that complementary charged and hydrophobic amino acids are required for formation of the bipartite .beta.-catenin-LEF-1 transcription factor. Moreover, we demonstrate that conductin/axin binding to .beta.-catenin is essential for .beta.-catenin degrdn., and that APC acts as a cofactor of conductin/axin in this process. Binding of APC to conductin/axin activates the latter and occurs between their SAMP and RGS domains, resp.

REFERENCE COUNT:

50

REFERENCE(S):

- (1) Aberle, H; EMBO J 1997, V16, P3797 CAPLUS
- (2) Aberle, H; J Cell Sci 1994, V107, P3655 CAPLUS
- (3) Behrens, J; Nature 1996, V382, P638 CAPLUS

(4) Behrens, J; Science 1998, V280, P596 CAPLUS(5) Brunner, E; Nature 1997, V385, P829 CAPLUS

ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 4 OF 15 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER:

2000:547045 CAPLUS

DOCUMENT NUMBER:

134:27977

TITLE:

Control of .beta.-catenin signaling in

tumor development -

AUTHOR (S):

Behrens, Jurgen

CORPORATE SOURCE:

Max-Delbruck-Center for Molecular Medicine,

Berlin, 13122, Germany

SOURCE:

Ann. N. Y. Acad. Sci. (2000), 910 (Colorectal

Cancer), 21-35

CODEN: ANYAA9; ISSN: 0077-8923 New York Academy of Sciences

DOCUMENT TYPE:

Journal; General Review

LANGUAGE:

PUBLISHER:

English

The wnt signal transduction pathway is A review, with 72 refs. AB involved in various differentiation events during embryonic development and leads to tumor formation when aberrantly activated. The wnt signal is transmitted to the nucleus by the cytoplasmic component .beta.-catenin: in the absence of wnts, .beta.-catenin is constitutively degraded in proteasomes, whereas in the presence of wnts .beta.-catenin is stabilized and can assoc. with HMG box transcription factors of the LEF/TCF family. The LEF/TCF/.beta.-catenin complexes activate specific wnt target genes. In tumors, .beta.-catenin degrdn. is blocked by mutations of .beta.-catenin or of the tumor suppressor gene product APC. As a consequence, .beta.-catenin is stabilized, constitutive complexes with LEF/TCF factors are formed, and oncogenic target genes, such as c-myc, cyclin D1, and c-jun, are activated. control of .beta.-catenin is a major regulatory event in normal wnt signaling and during tumor formation. It has been found that a multiprotein complex assembled by the cytoplasmic component conductin induces degrdn. of cytoplasmic .beta.-catenin. The complex includes APC, the serine/threonine kinase GSK3.beta., and .beta.-catenin, which bind to conductin at distinct domains. In colon carcinoma cells, forced expression of conductin down-regulates .beta.-catenin, whereas in normal cells mutants of conductin that are deficient in complex formation stabilize .beta.-catenin. Fragments of APC that contain a c nductin-binding domain also block .beta.-catenin degrdn. In Xenopus embryos, conductin inhibits the wnt pathway. In situ hybridization anal. shows that conductin is expressed in various embryonal tissues known to be regulated by wnts, such as the developing brain, mesenchyme below the epidermis, lung mesenchyme, and kidney. It is suggested that conductin

controls wnt signaling by assembling the essential components of the .beta.-catenin degrdn. pathway. Alterations of conductin function may lead to tumor formation.

REFERENCE COUNT:

REFERENCE(S):

- (1) Aberle, H; EMBO J 1997, V16, P3797 CAPLUS
- (2) Ahmed, Y; Cell 1998, V93, P1171 CAPLUS
- (3) Aoki, M; Proc Natl Acad Sci 1999, V96, P139 CAPLUS
- (4) Bauer, A; Proc Natl Acad Sci 1998, V95, P14787 CAPLUS
- (5) Behrens, J; Cancer Metastasis Rev 1999, V18, P15 CAPLUS

ALL CITATIONS AVAILABLE IN THE RE FORMAT

ANSWER 5 OF 15 CAPLUS COPYRIGHT 2001 ACS ACCESSION NUMBER:

DOCUMENT NUMBER:

2000:275313 CAPLUS 132:313670

TITLE:

Coated substrates for blood, plasma, or tissue

DE 1998-19845286

washing and columns equipped with these

substrates

INVENTOR(S):

Dunzendorfer, Udo; Will, Gottfried

PATENT ASSIGNEE(S):

Germany

SOURCE:

Ger. Offen., 30 pp.

CODEN: GWXXBX

DOCUMENT TYPE:

Patent

LANGUAGE:

German

FAMILY ACC. NUM. COUNT:

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO. DATE
DE 19845286	A1	20000427	DE 1998-19845286 19981001
EP 1004598	A2	20000531	EP 1999-118541 19990918
EP 1004598	<b>A</b> 3	20000607	100000000000000000000000000000000000000

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO

PRIORITY APPLN. INFO.:

Columns, filters, cannulas, etc. contg. substrates coated with specific antibodies can be used during plasmapheresis to remove pathogenic cytokines such as tumor necrosis factor (TNF), anti-TNF, fragments of TNF or anti-TNF, or TNF transport proteins from blood, plasma, or tissues. The substrates may addnl. be coated with antibodies to microbial or viral pathogens or mixts. of pathogens as well as to polysaccharide antigens, viral capsids, microbial antigens, reverse transcriptase, endothelin, protein A, etc. Selective removal of these pathogens, antigens, proteins, etc. leaves all normal plasma components unchanged and obviates the need

for supplementation of the plasma with these components. Suitable

substrates include polymers, polymer-coated metals, cellulose derivs., starch, and Sepharose; these may be derivatized for covalent binding of the pathogens or pathogenic mols. Thus, Escherichia coli pyelonephritis was successfully treated by plasmapheresis coupled with columns loaded with anti-TNF-.alpha. for 14 days, 4 h/day, as detd. by decreases in plasma TNF-.alpha. levels and colony counts in urine cultures.

L6 ANSWER 6 OF 15 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER: 2000:94336 CAPLUS

DOCUMENT NUMBER: 133:56735

TITLE: The regulation of .beta.-catenin degradation and

cancer

AUTHOR(S): Kishida, Shosei; Kikuchi, Akira

CORPORATE SOURCE: Sch. Med., Hiroshima Univ., Hiroshima, 734-8551,

Japan

SOURCE: Mol. Med. (Tokyo) (2000), 37(2), 166-175

CODEN: MOLMEL; ISSN: 0918-6557

PUBLISHER: Nakayama Shoten

DOCUMENT TYPE: Journal; General Review

LANGUAGE: Japanese

AB A review with 37 refs. The structure of .beta.-catenin is described. .beta.-Catenin accumulates in colon cancer and malignant melanoma. .beta.-Catenin is degraded by the ubiquitin/proteasome system. Axin (conductin) possesses regulators of G protein signaling (RGS) for binding APC at N-terminus, GSK-3.beta. and .beta.-catenin binding domains at central region, and DIX region at C-terminus. Wnt protein releases .beta.-catenin from the Axin complex.

L6 ANSWER 7 OF 15 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER: 2000:53973 CAPLUS

DOCUMENT NUMBER: 132:303902

TITLE: The yin-yang of TCF/.beta.-catenin signaling
AUTHOR(S): Barker, Nick; Morin, Patrice J.; Clevers, Hans
CORPORATE SOURCE: Department of Immunology, University Hospital,

Utrecht, 85500, Neth.

SOURCE: Adv. Cancer Res. (2000), 77, 1-24

CODEN: ACRSAJ; ISSN: 0065-230X

PUBLISHER: Academic Press

DOCUMENT TYPE: Journal; General Review

LANGUAGE: English

AB A review with 90 refs. Wingless/Wnt signaling directs cell-fate choices during embryonic development. In Drosophila, Wingless signaling mediates endoderm induction and the establishment of segment polarity in the developing embryo. The fly Wingless cascade is strikingly similar to the vertebrate Wnt signaling pathway, which controls a no. of key developmental decisions such as dorsal-ventral

patterning in Xenopus. Factors of the TCF/LEF HMG domain family (Tcfs) have recently been established as the downstream effectors of the Wingless/Wnt signal transduction pathways. Upon Wingless/Wnt signaling, a cascade is initiated that results in the accumulation of cytoplasmic .beta.-catenin (or its fly homolog, Armadillo). There is also a concomitant translocation of .beta.catenin/Armadillo to the nucleus, where it interacts with a specific sequence motif at the N terminus of Tcfs to generate a transcriptionally active complex. This bipartite transcription factor is targeted to the upstream regulatory regions of Tcf target genes including Siamois and Nodal related gene-3 in Xenopus, engrailed and Ultrabithorax in Drosophila via the sequence-specific HMG box, and mediates their transcriptional activation by virtue of transactivation domains contributed by .beta.-catenin/Armadillo. the absence of Wingless/Wnt signals, a key neg. regulator of the pathway, GSK3.beta., is activated, which mediates the downregulation of cytoplasmic .beta.-catenin/Armadillo via the ubiquitin-proteasome pathway. In the absence of nuclear .beta.-catenin, the Tcfs recruit the corepressor protein Groucho to the target gene enhancers and actively repress their transcription. An addnl. corepressor protein, CREB-binding protein (CBP), may also be involved in this repression of Tcf target gene activity. Several other proteins, including adenomatous polyposis coli (APC), GSK3.beta., and Axin/ Conductin, are instrumental in the regulation of .beta.-catenin/Armadillo. In APC-deficient colon carcinoma cell lines, .beta.-catenin accumulates and is constitutively complexed with nuclear Tcf-4. A proportion of APC wild-type colon carcinomas and melanomas also contains constitutive nuclear Tcf-4/.beta.-catenin complexes as a result of dominant mutations in the N terminus of .beta.-catenin that render it insensitive to downregulation by APC, GSK3.beta., and Axin/Conductin. This results in the unregulated expression of Tcf-4 target genes such as c-myc. Based on the established role for Tcf-4 in maintaining intestinal stem cells it is likely that deregulation of c-myc expression as a result of constitutive Tcf-4/.beta.-catenin activity promotes uncontrolled intestinal cell proliferation. This would readily explain the formation of intestinal polyps during colon carcinogenesis. Similar mechanisms leading to deregulation of Tcf target gene activity are likely to be involved in melanoma and other forms of cancer. (c) 2000 Academic Press.

REFERENCE COUNT:

REFERENCE(S):

90

- (2) Barker, N; Am J Pathol 1999, V154, P29 **CAPLUS**
- (3) Behrens, J; Nature (London) 1996, V382, P638 **CAPLUS**
- (4) Behrens, J; Science 1998, V280, P596 CAPLUS
- (5) Bhanot, P; Nature (London) 1996, V382, P225

CAPLUS

(6) Bienz, M; Trends Genet 1994, V10, P22 CAPLUS ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 8 OF 15 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER:

1999:737696 CAPLUS

DOCUMENT NUMBER:

132:90977

TITLE:

Identification and characterization of E-APC, a

novel Drosophila homolog of the tumor

suppressor APC

AUTHOR (S):

Hamada, Fumihiko; Murata, Yoji; Nishida, Ayumu; Fujita, Fumitaka; Tomoyasu, Yoshinori; Nakamura, Makoto; Toyoshima, Kumao; Tabata, Tetsuya; Ueno,

Naoto; Akiyama, Tetsu

CORPORATE SOURCE:

Department of Oncogene Research, Research

Institute for Microbial Diseases, Osaka

University, Suita, 565-0871, Japan

SOURCE: Genes Cells (1999), 4(8), 465-474

CODEN: GECEFL; ISSN: 1356-9597

PUBLISHER:

Blackwell Science Ltd.

DOCUMENT TYPE:

Journal English

LANGUAGE:

AB

We have identified a novel Drosophila homolog of APC, E-APC, which is similar to but differs in several respects from D-APC. The E-APC cDNA encodes a protein of predicted 1067 amino acids, with 7 armadillo repeats, 2 copies of the 15-amino acid repeat, 5 copies of the 20-amino acid repeat, and 1 Axin/conductin binding site. E-APC directly interacts with D-Axin and Armadillo (Arm, the Drosophila homolog of .beta.-catenin) in vitro, destabilizes

intracellular .beta.-catenin, and suppresses .beta.-catenin/TCF-regulated transcription in APC-/- colon cancer cells. The E-APC mRNA is ubiquitously expressed throughout all developmental stages in Drosophila. Our findings suggest that E-APC may be universally involved in the regulation of the Wingless signaling pathway by down-regulating the level of Arm in Drosophila.

REFERENCE COUNT:

35

REFERENCE(S):

- (1) Ahmed, Y; Cell 1998, V93, P1171 CAPLUS
- (2) Baeg, G; EMBO J 1995, V14, P5618 CAPLUS
- (3) Behrens, J; Science 1998, V280, P596 CAPLUS
- (4) Cadigan, K; Genes Dev 1997, V11, P3286 CAPLUS
- (5) Hamada, F; Science 1999, V283, P1739 CAPLUS

ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 9 OF 15 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER:

1999:733931 CAPLUS

DOCUMENT NUMBER:

131:333485

TITLE:

Signaling through .beta.-catenin and Lef/Tcf

AUTHOR (S):

CORPORATE SOURCE:

Novak, A.; Dedhar, S.

Sunnybrook Health Science Center, Toronto, ON,

M4N 3M5, Can.

SOURCE:

Cell. Mol. Life Sci. (1999), 56(5/6), 523-537

CODEN: CMLSFI; ISSN: 1420-682X

PUBLISHER:

Birkhaeuser Verlag

DOCUMENT TYPE:

Journal; General Review

LANGUAGE:

English

A review with 167 refs. is given. .beta.-Catenin plays a structural role in cell adhesion by binding to cadherins at the intracellular surface of the plasma membrane and a signaling role in the cytoplasm as the penultimate downstream mediator of the wnt signaling pathway. The ultimate mediator of this pathway is a nuclear complex of .beta.-catenin acting as a coactivator with lymphoid enhancer factor/T cell factor (Lef/Tcf) transcription factors to stimulate transcription of a variety of target genes. Signaling through .beta.-catenin is regulated by modulating its degrdn. and nuclear translocation. In the absence of an activating signal, phosphorylation of .beta.-catenin by glycogen synthase kinase 3 (GSK3) acting in conjunction with adenomatous polyposis coli and axin/ conductin causes .beta.-catenin to interact with the .beta.-transducin repeat-contg. protein which results in its ubiquitination and degrdn. Signaling from the wnt pathway activates dishevelled which, in an as yet undefined manner, inhibits the activity of GSK3 resulting in an increase in the cytoplasmic free pool of .beta.-catenin, and translocation into the nucleus. The integrin-linked kinase (ILK) pathway also activates .beta.-catenin-Lef/Tcf signaling. ILK phosphorylates CiSK3 to inhibit its activity and translocates .beta.-catenin into the In addn., ILK downregulates the expression of E-cadherin and upregulates Lef-1 expression. In the final step of the .beta.-catenin-Lef/Tcf signaling pathway, nuclear .beta.-catenin binds pontin52-TATA binding protein and displaces Groucho-related gene or CREB-binding protein corepressors from Lef/ Tcf resulting in stimulation of transcription. During development, .beta.-catenin-Lef/Tcf signaling is involved in the formation of dorsal mesoderm and dorsal axis. Furthermore, defects in the .beta.-catenin-Lef/Tcf pathway are involved in the development of several types of cancers.

REFERENCE COUNT:

167

REFERENCE(S):

- (1) Aberle, H; EMBO J 1997, V16, P3797 CAPLUS
- (2) Aberle, H; J Cell Biochem 1996, V61, P514 CAPLUS
- (4) Ahmed, Y; Cell 1998, V93, P1171 CAPLUS
- (5) Aoki, M; Proc Natl Acad Sci USA 1999, V96, P139 CAPLUS
- (7) Axelrod, J; Science 1996, V271, P1826 CAPLUS ALL CITATIONS AVAILABLE IN THE RE FORMAT

ANSWER 10 OF 15 CAPLUS COPYRIGHT 2001 ACS L6

1999:549289 CAPLUS ACCESSION NUMBER:

131:194280 DOCUMENT NUMBER:

Agents for treating cancer and other TITLE:

human illnesses based on .beta.-catenin

Birchmeier, Walter; Von Kries, Jens-Peter INVENTOR(S):

Max-Delbrueck-Centrum fuer Molekulare Medizin, PATENT ASSIGNEE(S):

Germany

PCT Int. Appl., 26 pp. SOURCE:

CODEN: PIXXD2

Patent DOCUMENT TYPE: German LANGUAGE:

FAMILY ACC. NUM. COUNT:

PATENT INFORMATION:

P#	ATENT :	NO.		KIND	DATE		A.	PPLI	CATI	ON No	o. :	DATE		
							_							
WC	9942	481		<b>A2</b>	19990826		W	0 19	99-D	E554		1999	0222	
WC	9942	481		A3	20000210									
	W:	CA,	JP,	US										
	RW:	ΑT,	BE,	CH, CY	, DE, DK,	ES,	FI,	FR,	GB,	GR,	ΙE,	IT,	LU,	M
	•			~										

NL, PT, SE

19990826 DE 1999-19909251 19990222 DE 19909251. A1 EP 1999-913097 19990222 EP 1054899 A2 20001129

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, NL, SE, PT, IE, FΙ

PRIORITY APPLN. INFO.:

DE 1998-19807390 A 19980221 WO 1999-DE554

C.beta.-catenin is a central mol. of the Wnt signal path. AB Increasing .beta.-catenin in the cell leads to its translocation into the cell nucleus and to its interaction with transcription factors of the LEF-1/TCF family. This can lead to colonic cancers and melanomas (oncogenic signal path). However, .beta.-catenin also interacts with the tumor-suppressor genes APC, conductin, and E-cadherin, which have a contrary effect on the cell (antioncogenic effect). derived from LEF-1-/TCF-4 transcription factors and analogous mols. can be used in the treatment of tumors, esp. colonic These peptides and analogous mols. cancers and melanomas. influence the interaction between .beta.-catenin and LEF-1/TCF. peptides comprise parts of the LEF-1/TCF-4 transcription factors and variants and mutations thereof, preferably the 10-40 N-terminal amino acids of LEF-1 or TCF-4, as well as peptides derived from the armadillo region of .beta.-catenin which were identified as interaction domains with LEF-1/TCF, APC, conductin, and E-cadherin. The peptides constituting interaction domains with APC or conductin can increase the concn. of .beta.-catenin in

the cell. These last mols. can be used to influence the formation of tissues and organs, e.g. to promote hair growth.

IT 221220-50-4, Conductin (human)

RL: BPR (Biological process); BIOL (Biological study); PROC (Process)

(interaction with .beta.-catenin, modulators of; agents for treating cancer and other human illnesses based on .beta.-catenin)

L6 ANSWER 11 OF 15 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER:

1999:189197 CAPLUS

DOCUMENT NUMBER:

130:232471

TITLE:

The protein conductin and its

application for diagnosis and gene therapy of

colon cancer

INVENTOR (S):

Behrens, Jurgen; Birchmeier, Walter

PATENT ASSIGNEE(S):

Max-Delbruck-Centrum fur Molekulare Medizin,

Germany

SOURCE:

PCT Int. Appl., 22 pp.

CODEN: PIXXD2

DOCUMENT TYPE:

Patent

LANGUAGE:

German

FAMILY ACC. NUM. COUNT:

PATENT INFORMATION:

PATENT NO.	KIND 1	DATE	APPLICATION NO.	DATE
WO 9911780	A2 :	19990311	WO 1998-DE2621	19980901
WO 9911780	A3 :	19990527		
W: CA, JP,	US			
RW: AT, BE,	CH, CY,	DE, DK, ES, FI	FR, GB, GR, IE,	IT, LU. MC.
NL, PT,				,, ,,
DE 19840875	A1 :	19990512 I	DE 1998-19840875	19980901
EP 1029047	A2 2	20000823 I	P 1998-954120	19980901
R: AT, BE,	CH, DE,	DK, FR, GB, IT,	LI, NL, SE, FI	
PRIORITY APPLN. INFO	.:	DE 1	1997-19738205 A	19970902
		WO 1	L998-DE2621 W	19980901
	•			

AB The invention concerns the novel protein conductin that is able to regulate the .beta.-catenin function and interacts with the tumor suppressor adenomatous polyposis coli (APC); and its application in the gene therapy of colon cancer. The 840 amino acid contg. protein contains domains with various activities: 78-200 is the RGS (Regulator of G-Protein Signalling) binding sequence; 343-396 is the GSK 3.beta. (glycogen synthase kinase 3.beta.) binding sequence; 397-465 is the .beta.-catenin binding sequence; 783-833 is the Dishevelled homol. region. Mutations, variants and fragments of conductin with the corresponding coding genes and mRNA sequences are also included. Antibodies and

nucleic acid probes for the detection of c nductin are part of the diagnosis tools. For therapeutic purposes a vector contg. the conductin gene is constructed; substances that activate and reactivate conductin in the body are co-administered, e.g. a substance that activates the c nductin promoter or stabilizes mRNA. The effect of conductin was proved using SW480 cells with APC mutation and thus increased .beta.-catenin level. Introduction of conductin resulted in the decrease of .beta.-catenin to the same concn. as in non APC mutated SW480 cells. In an expt. with Xenopus embryos it was shown that conductin inhibits the Wnt/Wingless signaling pathway via its interaction with .beta.-catenin.

IT 221220-50-4, Conductin (human)

RL: BAC (Biological activity or effector, except adverse); PRP (Properties); BIOL (Biological study)

(amino acid sequence; protein conductin and application for diagnosis and gene therapy of colon cancer)

L6 ANSWER 12 OF 15 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER:

1999:179719 CAPLUS

DOCUMENT NUMBER:

131:16667

TITLE:

APC protein: protein interactions and cellular

functions

AUTHOR (S):

Jais, Philippe; Laurent-Puig, Pierre; Olschwang,

Sylviane

CORPORATE SOURCE:

Unite des Marqueurs Genetiques des Cancers (UMGC), Institut Gustave-Roussy, Villejuif,

94805, Fr.

SOURCE:

Gastroenterol. Clin. Biol. (1998), 22(12),

1071-1080

CODEN: GCBIDC; ISSN: 0399-8320

PUBLISHER:

Masson Editeur

DOCUMENT TYPE:

Journal; General Review

LANGUAGE:

French

AB A review with 112 refs., discussing structures of APC gene and protein; functions of APC protein in epithelial cell homeostasis and cell adhesion; assocn. of APC protein with .beta.-catenin, conductin, and GSK3.beta. in normal and transformed cells and other proteins-assocns.

REFERENCE COUNT:

112

REFERENCE(S):

- (1) Aberle, H; EMBO J 1997, V16, P3797 CAPLUS
- (3) Behrens, J; Nature 1996, V382, P638 CAPLUS
- (4) Behrens, J; Science 1998, V280, P596 CAPLUS
- (5) Beinhauer, J; J Cell Biol 1997, V139, P717 CAPLUS
- (6) Beroud, C; Nucleic Acids Res 1996, V24, P121 CAPLUS

#### ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 13 OF 15 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER:

1999:134134 CAPLUS

DOCUMENT NUMBER:

131:14675

TITLE:

Cloning of the Human Homolog of Conduction

(AXIN2), a Gene Mapping to Chromosome 17q23-q24

AUTHOR (S):

Mai, Ming; Qian, Chiping; Yokomizo, Akira;

Smith, David I.; Liu, Wanguo

CORPORATE SOURCE:

Division of Experimental Pathology, Mayo

Clinic/Foundation, Rochester, MN, 55905, USA

SOURCE:

Genomics (1999), 55(3), 341-344 CODEN: GNMCEP; ISSN: 0888-7543

PUBLISHER:

Academic Press

DOCUMENT TYPE:

Journal

LANGUAGE:

English

Conduction or Axil, an Axin homolog, plays an important role in the regulation of .beta.-catenin stability in the Wnt signaling pathway. To facilitate the mol. anal. of the human gene, we isolated the human homolog, AXIN2. The cDNA contains a 2529-bp open reading frame and encodes a putative protein of 843 amino acids. Compared with rat and mouse homologs, AXIN2 shows an overall 89% amino acid identity. Several functional domains in this protein are highly conserved including the GRS (95.9%), GSK-3.beta. (96.3%), Dsh (98%), and .beta.-catenin (89.9%) domains. Radiation hybrid mapping localized the AXIN2 gene to human chromosome 17q23-q24, a region that shows frequent loss of heterozygosity in breast cancer, neuroblastoma, and other tumors. Human AXIN2 is thus a very strong candidate involved in multiple tumor types. (c) 1999 Academic Press.

IT 226387-63-9, Conduction (human fetal brain reduced)
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(amino acid sequence; cloning of the human homolog of conductin (AXIN2), a gene mapping to chromosome 17q23-q24)

REFERENCE COUNT:

22

REFERENCE (S):

- (1) Aberle, H; EMBO J 1997, V16, P3797 CAPLUS
- (2) Aberle, H; J Cell Sci 1994, V107, P3655 CAPLUS
- (3) Barlund, M; Genes Chromosomes Cancer 1997, V20, P372 CAPLUS
- (4) Behrens, J; Nature 1996, V382, P638 CAPLUS
- (5) Behrens, J; Science 1998, V280, P596 CAPLUS
- ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 14 OF 15 CAPLUS COPYRIGHT 2001 ACS ACCESSION NUMBER: 1999:106086 CAPLUS

Searcher :

Shears 308-4994

DOCUMENT NUMBER:

130:323365

TITLE:

Identification of APC2, a homolog of the

adenomatous polyposis coli tum r

suppressor

AUTHOR (S):

Van Es, J. H.; Kirkpatrick, C.; Van de Wetering,

M.; Molenaar, M.; Miles, A.; Kuipers, J.;

Destree, O.; Peifer, M.; Clevers, H.

CORPORATE SOURCE:

Department of Immunology, University Hospital,

Utrecht, 3508 GA, Neth.

SOURCE:

Curr. Biol. (1999), 9(2), 105-108

CODEN: CUBLE2; ISSN: 0960-9822

PUBLISHER:

Current Biology Publications

DOCUMENT TYPE:

Journal

LANGUAGE: English

We report the identification and genomic structure of APC homologs. Mammalian APC2, which closely resembles APC in overall domain structure, was functionally analyzed and shown to contain 2 SAMP domains, both of which are required for binding to conductin

Like APC, APC2 regulates the formation of active .beta.-catenin-Tcf complexes, as demonstrated using transient transcriptional activation assays in APC-/- colon carcinoma cells. Human APC2 maps to chromosome 19p13.3. APC and APC2 may therefore have comparable functions in development and cancer.

REFERENCE COUNT:

23

REFERENCE(S):

- (1) Aberle, H; EMBO J 1997, V16, P3797 CAPLUS
- (2) Behrens, J; Nature 1996, V382, P638 CAPLUS
- (3) Behrens, J; Science 1998, V280, P596 CAPLUS
- (4) Brunner, E; Nature 1997, V385, P829 CAPLUS
- (5) Cadigan, K; Genes Dev 1997, V11, P3286 CAPLUS

ALL CITATIONS AVAILABLE IN THE RE FORMAT

ANSWER 15 OF 15 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER:

1998:302214 CAPLUS

TITLE:

Functional interaction of an axin homolog, conductin, with .beta.-catenin, APC and

GSK3.beta.

AUTHOR (S):

Behrens, Jurgens; Jerchow, Boris-Alexander; Wurtele, Martin; Grimm, Jan; Asbrand, Christian; Wirtz, Ralph; Kuhl, Michael; Wedlich, Doris;

Birchmeier, Walter

CORPORATE SOURCE:

Max Delbruck Cent. Molecular Med., Berlin,

13122, Germany

SOURCE:

Science (Washington, D. C.) (1998), 280 (5363),

596-599

CODEN: SCIEAS; ISSN: 0036-8075

**PUBLISHER:** 

American Association for the Advancement of

Science

DOCUMENT TYPE:

Journal

LANGUAGE:

English

AB Control of stability of .beta.-catenin is central in the wnt signaling pathway. Here, the protein conductin was found to form a complex with both .beta.-catenin and the tumor suppressor gene product adenomatous polyposis coli (APC). Conductin induced .beta.-catenin degrdn., whereas mutants of conductin that were deficient in complex formation stabilized .beta.-catenin. Fragments of APC that contained a conductin-binding domain also blocked .beta.-catenin degrdn. Thus, conductin is a component of the multiprotein complex that directs .beta.-catenin to degrdn. and is located downstream of APC. In Xenopus embryos, conductin interfered with wnt-induced axis formation.

(FILE 'MEDLINE, BIOSIS, EMBASE, WPIDS, CONFSCI, SCISEARCH, JICST-EPLUS, JAPIO, CANCERLIT' ENTERED AT 11:17:14 ON 11 JUN 2001)

L7

57 S L6

L8

22 DUP REM L7 (35 DUPLICATES REMOVED)

L8 ANSWER 1 OF 22

WPIDS COPYRIGHT 2001 DERWENT INFORMATION LTD

ACCESSION NUMBER:

2001-246094 [26] WPIDS

DOC. NO. CPI:

C2001-074206

TITLE:

Agent for tumor therapy, tissue

regeneration or stimulation of hair growth,

comprising inhibitor of binding of beta-catenin to

LEF-1/TCF-transcription factors, APC or conductin, obtained by specific screening

method.

DERWENT CLASS:

B04 D16

INVENTOR(S):

BIRCHMEIER, W; VON KRIES, J

PATENT ASSIGNEE(S):

(DELB-N) DELBRUECK CENT MOLEKULARE MEDIZIN MAX

COUNTRY COUNT:

94

PATENT INFORMATION:

PATENT	ИО	KIND	DATE	WEEK	LA	PG
			·		- <b></b>	

DE 19944404 A1 20010322 (200126) \* 14
WO 2001019353 A2 20010322 (200126) GE

RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TZ UG ZW

W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CR CU CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW

#### APPLICATION DETAILS:

11112111 110 111	IND		PLICATION	DATE
DE 19944404	A1		1999-19944404	
WO 2001019353	A2	WO	2000-DE3104	20000907

PRIORITY APPLN. INFO: DE 1999-19944404 19990916

AN 2001-246094 [26] WPIDS

AB DE 19944404 A UPAB: 20010515

NOVELTY - An agent (I) for therapy of human disorders, comprising an inhibitor of the binding of beta -catenin to LEF-1/TCF-transcription factors, APC (undefined) or conductin, is new.

DETAILED DESCRIPTION - An INDEPENDENT CLAIM is included for identifying agents (I), comprising identifying hydrophobic pockets in the vicinity of essential binding sites in the beta -catenin molecule, and synthesizing compounds which fit in these pockets.

ACTIVITY - Cytostatic.

No biological data is given.

MECHANISM OF ACTION - Inhibition of binding of beta -catenin to LEF-1/TCF-transcription factors, APC or conductin.

USE - For therapy of tumors (e.g. colon carcinoma or melanoma), for tissue regeneration or for stimulation of hair growth (claimed).

Dwg.0/3

L8 ANSWER 2 OF 22 EMBASE COPYRIGHT 2001 ELSEVIER SCI. B.V.

ACCESSION NUMBER: 2001

2001083138 EMBASE

TITLE:

Oncogenic targets of .beta.-catenin-mediated

transcription in molecular pathogenesis of intestinal

polyposis.

AUTHOR:

Watson S.A.

CORPORATE SOURCE:

S.A. Watson, Academic Unit of Cancer Studies,

University of Nottingham, Nottingham NG7 2UH, United

Kingdom. sue.watson@nottingham.ac.uk

SOURCE:

Lancet, (24 Feb 2001) 357/9256 (572-573).

Refs: 14

ISSN: 0140-6736 CODEN: LANCAO

COUNTRY:

United Kingdom
Journal; Note

DOCUMENT TYPE: FILE SEGMENT:

016 Cancer

022 Human Genetics

029 Clinical Biochemistry

048 Gastroenterology

LANGUAGE:

English

L8 ANSWER 3 OF 22 WPIDS COPYRIGHT 2001 DERWENT INFORMATION LTD

ACCESSION NUMBER:

2000-293152 [25] WPIDS

DOC. NO. NON-CPI:

N2000-219772

DOC. NO. CPI:

C2000-088675

TITLE:

Novel human tumor suppressor gene,

adenomatous polyposis coli (APC)-2, used in the

diagnosis, prevention, and treatment of

cancer.

DERWENT CLASS:

B04 C06 D16 P14 S03

INVENTOR (S):

CLEVERS, J C; PELFER, M A; VAN ES, J H

PATENT ASSIGNEE(S):

(UYUT-N) RIJKSUNIV UTRECHT

COUNTRY COUNT:

89

PATENT INFORMATION:

PATENT NO	KIND DATE	WEEK	LA	PG

WO 2000018913 A1 20000406 (200025) \* EN 42

RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL OA PT SD SE SL SZ TZ UG ZW

W: AE AL AM AT AU AZ BA BB BG BR BY CA CH CN CR CU CZ DE DK DM EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW

AU 9960106 A 20000417 (200035)

#### APPLICATION DETAILS:

	IND 	APPLICATION	DATE
WO 2000018913			19990924
AU 9960106	A	AU 1999-60106	19990924

#### FILING DETAILS:

PATENT NO	KIND	PATENT NO
AU 9960106	A Basec	on wo sonosess

PRIORITY APPLN. INFO: EP 1998-203237 19980925

AN 2000-293152 [25] WPIDS

AB WO 200018913 A UPAB: 20000524

NOVELTY - Isolated and/or recombinant nucleic acid (NA) or a specific fragment, homolog or derivative thereof (I), corresponding to a gene located at position 19p13.3 in humans and comprising the 2397 base pair (bp) sequence given in the specification (adenomatous polyposis coli (APC)-2), is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

an expression vector comprising (I);

- (2) a cell comprising (I) or the expression vector of (1);
- (3) an animal comprising the cell of (2);
- (4) a protein, derivative, or fragment encoded by (I) or produced by the cell of (2);
  - (5) an antibody directed against the protein of (4);
- (6) identifying a candidate drug (especially a drug for use in a cancer patient), by using of the cell of (2), animal of (3), protein of (4), or antibody of (5); and
- (7) diagnosing cancer by using (I), the cell of (2), animal of (3), protein of (4), or antibody of (5).

ACTIVITY - Cytostatic.

MECHANISM OF ACTION - The adenomatous polyposis coli (APC) -2 tumor suppressor gene controls the Wnt pathway by the formation of a complex with GSK-3b, axin/conductin and beta -catenin, inducing the rapid degradation of the latter.

USE - The adenomatous polyposis coli (APC) - 2 polynucleotides are used for the diagnosis (claimed), prevention and treatment of cancer. They are also used for the recombinant production of APC-2 proteins. The methods are used to identify candidate drugs (claimed), especially for use in the treatment of cancers, preferably a fetal cancer, cancers with a stem cell phenotype, brain, lung, kidney or intestinal cancer (all claimed).

ADVANTAGE - None given.

DESCRIPTION OF DRAWING(S) - The figure shows the comparison of adenomatous polyposis coli (APC) and APC-2. Domain structures conserved between these APC relatives are indicated in various boxes.

Dwg. 1A/4

L8 ANSWER 4 OF 22 SCISEARCH COPYRIGHT 2001 ISI (R)

ACCESSION NUMBER: 2000:808103 SCISEARCH

THE GENUINE ARTICLE: 366KD

TITLE: Differential regulation of glycogen synthase kinase

3 beta by insulin and Wnt signaling

AUTHOR: Ding V W; Chen R H; McCormick F (Reprint)

CORPORATE SOURCE: UNIV CALIF SAN FRANCISCO, CANC RES INST, 2340 SUTTER

ST, BOX 0128, SAN FRANCISCO, CA 94115 (Reprint); UNIV CALIF SAN FRANCISCO, CANC RES INST, SAN

FRANCISCO, CA 94143

COUNTRY OF AUTHOR: USA

SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (20 OCT 2000) Vol.

275, No. 42, pp. 32475-32481.

Publisher: AMER SOC BIOCHEMISTRY MOLECULAR BIOLOGY

INC, 9650 ROCKVILLE PIKE, BETHESDA, MD 20814.

ISSN: 0021-9258.

DOCUMENT TYPE: Article; Journal

FILE SEGMENT: LIFE

LANGUAGE:

English

REFERENCE COUNT:

53

\*ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS\*

Glycogen synthase kinase 3 beta (GSK3 beta) is a key component in AB many biological processes including insulin and Wnt signaling. Since the activation of each signaling pathway results in a decrease in GSK3 beta activity, we examined the specificity of their downstream effects in the same cell type. Insulin induces an increased activity of glycogen synthase but has no influence on the protein level of beta -catenin. In contrast, Wnt increases the cytosolic pool of beta -catenin but not glycogen synthase activity. We found that, unlike insulin, neither the phosphorylation status of the serine9 residue of GSK3 beta nor the activity of protein kinase B is regulated by Wnt. Although the decrease in GSK3 beta activity is required, GSK3 beta may not be the limiting component for Wnt signaling in the cells that we examined. Our results suggest that the axinconductin complexed GSK3 beta may be dedicated to Wnt rather than insulin signaling. Insulin and Wnt pathways regulate GSK3 beta through different mechanisms, and therefore lead to distinct downstream events.

L8 ANSWER 5 OF 22 MEDLINE

DUPLICATE 1

ACCESSION NUMBER:

2000455676 MEDLINE

DOCUMENT NUMBER:

20423090 PubMed ID: 10966653

TITLE:

Hot spots in beta-catenin for interactions with

LEF-1, conductin and APC.

**AUTHOR:** 

von Kries J P; Winbeck G; Asbrand C; Schwarz-Romond T; Sochnikova N; Dell'Oro A; Behrens J; Birchmeier W

CORPORATE SOURCE:

Max-Delbruck-Center for Molecular Medicine,

Robert-Rossle-Strasse 10, 13093 Berlin, Germany.

SOURCE:

NATURE STRUCTURAL BIOLOGY, (2000 Sep) 7 (9) 800-7.

Journal code: B98; 9421566. ISSN: 1072-8368.

PUB. COUNTRY:

United States

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE:

English

FILE SEGMENT:

Priority Journals

ENTRY MONTH:

200009

ENTRY DATE:

Entered STN: 20001005

Last Updated on STN: 20001005 Entered Medline: 20000928

AB Interactions between beta-catenin and LEF-1/TCF, APC and conductin/axin are essential for wnt-controlled stabilization of beta-catenin and transcriptional activation. The wnt signal transduction pathway is important in both embryonic development and tumor progression. We identify here amino acid residues in beta-catenin that distinctly affect its binding to LEF-1/TCF, APC and conductin. These residues form separate surface clusters, termed hot spots, along the armadillo superhelix

of beta-catenin. We also show that complementary charged and hydrophobic amino acids are required for formation of the bipartite beta-catenin-LEF-1 transcription factor. Moreover, we demonstrate that conductin/axin binding to beta-catenin is essential for beta-catenin degradation, and that APC acts as a cofactor of conductin/axin in this process. Binding of APC to conductin/axin activates the latter and occurs between their SAMP and RGS domains, respectively.

L8 ANSWER 6 OF 22 BIOSIS COPYRIGHT 2001 BIOSIS

ACCESSION NUMBER: 2000:275471 BIOSIS DOCUMENT NUMBER: PREV200000275471

TITLE: Human conductin (Axin2), like its mouse

Counterpart, binds to APC, GSK3betaand beta-catenin.

AUTHOR(S): Dong, Xiangyang (1); Mai, Ming (1); Seelan, Ratnam

(1); Qian, Chiping (1); Smith, David I. (1); Liu,

Wanguo (1)

CORPORATE SOURCE: (1) Mayo Clin, Rochester, MN USA

SOURCE: Proceedings of the American Association for Cancer

Research Annual Meeting, (March, 2000) No. 41, pp.

745. print..

Meeting Info.: 91st Annual Meeting of the American Association for Cancer Research. San Francisco,

California, USA April 01-05, 2000

ISSN: 0197-016X.

DOCUMENT TYPE: Conference

LANGUAGE: English SUMMARY LANGUAGE: English

L8 ANSWER 7 OF 22 MEDLINE DUPLICATE 2

ACCESSION NUMBER: 2000123741 MEDLINE

DOCUMENT NUMBER: 20123741 PubMed ID: 10656974

TITLE: Biochemical interactions in the wnt pathway.

AUTHOR: Seidensticker M J; Behrens J

CORPORATE SOURCE: Max-Delbruck-Center for Molecular Medicine,

Robert-Rossle-Strasse 10, 13122, Berlin, Germany.

SOURCE: BIOCHIMICA ET BIOPHYSICA ACTA, (2000 Feb 2) 1495 (2)

168-82. Ref: 143

Journal code: AOW; 0217513. ISSN: 0006-3002.

PUB. COUNTRY: Netherlands

Journal; Article; (JOURNAL ARTICLE)

General Review; (REVIEW)

(REVIEW, TUTORIAL)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 200005

ENTRY DATE: Entered STN: 20000512

Last Updated on STN: 20000512

Entered Medline: 20000502

AB The wnt signal transduction pathway is involved in many differentiation events during embryonic development and can lead to tumor formation after aberrant activation of its components. The cytoplasmic component beta-catenin is central to the transmission of wnt signals to the nucleus: in the absence of wnts beta-catenin is constitutively degraded in proteasomes, whereas in the presence of wnts beta-catenin is stabilized and associates with HMG box transcription factors of the LEF/TCF family. In tumors, beta-catenin degradation is blocked by mutations of the tumor suppressor gene APC (adenomatous polyposis coli), or of beta-catenin itself. As a consequence, constitutive TCF/beta-catenin complexes are formed and activate oncogenic target genes. This review discusses the mechanisms that silence the pathway in cells that do not receive a wnt signal and goes on to describe the regulatory steps involved in the activation of the pathway.

L8 ANSWER 8 OF 22 MEDLINE

DUPLICATE 3

ACCESSION NUMBER: DOCUMENT NUMBER:

2001019501

MEDLINE 20472311 PubMed ID: 11017067

TITLE:

Mutations in AXIN2 cause colorectal cancer

with defective mismatch repair by activating

beta-catenin/TCF signalling.

AUTHOR:

Liu W; Dong X; Mai M; Seelan R S; Taniguchi K;

Krishnadath K K; Halling K C; Cunningham J M; Oian C;

Christensen E; Roche P C; Smith D I; Thibodeau S N

CORPORATE SOURCE:

Division of Experimental Pathology, Department of Laboratory Medicine and Pathology, Mayo Clinic and Mayo Medical School, Rochester, Minnesota, USA..

liu.wanguo@mayo.edu

CONTRACT NUMBER:

CA 48031 (NCI)

CA 60117 (NCI)

SOURCE:

NATURE GENETICS, (2000 Oct) 26 (2) 146-7.

Journal code: BRO. ISSN: 1061-4036.

PUB. COUNTRY:

United States

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE:

English

FILE SEGMENT:

Priority Journals

ENTRY MONTH:

200011

ENTRY DATE:

Entered STN: 20010322

Last Updated on STN: 20010322 Entered Medline: 20001108

ANSWER 9 OF 22 MEDLINE

**DUPLICATE 4** 

ACCESSION NUMBER:

2000400028

MEDLINE

DOCUMENT NUMBER: TITLE:

20369556 PubMed ID: 10911903

Control of beta-catenin signaling in tumor

development.

Searcher

Shears

308-4994

AUTHOR: Behrens J

CORPORATE SOURCE: Max-Delbruck-Center for Molecular Medicine, Berlin,

Germany.. jbehren@mdc-berlin.de

SOURCE: ANNALS OF THE NEW YORK ACADEMY OF SCIENCES, (2000

Jun) 910 21-33; discussion 33-5. Ref: 72
Journal code: 5NM; 7506858. ISSN: 0077-8923.

PUB. COUNTRY: United States

Journal; Article; (JOURNAL ARTICLE)

General Review; (REVIEW)

(REVIEW, TUTORIAL)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 200008

ENTRY DATE: Entered STN: 20000824

Last Updated on STN: 20000824 Entered Medline: 20000817

The wnt signal transduction pathway is involved in various AB differentiation events during embryonic development and leads to tumor formation when aberrantly activated. The wnt signal is transmitted to the nucleus by the cytoplasmic component beta-catenin: in the absence of wnts, beta-catenin is constitutively degraded in proteasomes, whereas in the presence of wnts beta-catenin is stabilized and can associate with HMG box transcription factors of the LEF/TCF family. The LEF/TCF/beta-catenin complexes activate specific wnt target genes. In tumors, beta-catenin degradation is blocked by mutations of beta-catenin or of the tumor suppressor gene product APC. As a consequence, beta-catenin is stabilized, constitutive complexes with LEF/TCF factors are formed, and oncogenic target genes, such as c-myc, cyclin D1, and c-jun, are activated. Thus, control of beta-catenin is a major regulatory event in normal wnt signaling and during tumor formation. It has been found that a multiprotein complex assembled by the cytoplasmic component conductin induces degradation of cytoplasmic beta-catenin. The complex includes APC, the serine/threonine kinase GSK3 beta, and beta-catenin, which bind to conductin at distinct domains. In colon carcinoma cells, forced expression of conductin downregulates beta-catenin, whereas in normal cells mutants of conductin that are deficient in complex formation stabilize beta-catenin. Fragments of APC that contain a conductin-binding domain also block beta-catenin degradation. In Xenopus embryos, conductin inhibits the wnt pathway. In situ hybridization analysis shows that conductin is expressed in various embryonal tissues known to be regulated by wnts, such as the developing brain, mesenchyme below the epidermis, lung mesenchyme, and kidney. It is suggested that conductin controls wnt signaling by assembling the essential components of the beta-catenin degradation pathway. Alterations of

#### conductin function may lead to tumor formation.

L8 ANSWER 10 OF 22 MEDLINE

DUPLICATE 5

ACCESSION NUMBER:

2000017120

MEDLINE

DOCUMENT NUMBER:

20017120 PubMed ID: 10549354

TITLE:

The Yin-Yang of TCF/beta-catenin signaling.

AUTHOR:

Barker N; Morin P J; Clevers H

CORPORATE SOURCE:

Department of Immunology, University Hospital,

Utrecht, The Netherlands.

SOURCE:

ADVANCES IN CANCER RESEARCH, (2000) 77 1-24. Ref:

100

Journal code: 2J6; 0370416. ISSN: 0065-230X.

PUB. COUNTRY:

United States

Journal; Article; (JOURNAL ARTICLE)

General Review; (REVIEW)

(REVIEW, ACADEMIC)

LANGUAGE:

English

FILE SEGMENT:

Priority Journals

ENTRY MONTH:

199911

ENTRY DATE:

Entered STN: 20000111

Last Updated on STN: 20000111

Entered Medline: 19991123

Wingless/Wnt signaling directs cell-fate choices during embryonic AB development. In Drosophila, Wingless signaling mediates endoderm induction and the establishment of segment polarity in the developing embryo. The fly Wingless cascade is strikingly similar to the vertebrate Wnt signaling pathway, which controls a number of key developmental decisions such as dorsal-ventral patterning in Xenopus. Factors of the TCF/LEF HMG domain family (Tcfs) have recently been established as the downstream effectors of the Wingless/Wnt signal transduction pathways. Upon Wingless/Wnt signaling, a cascade is initiated that results in the accumulation of cytoplasmic beta-catenin (or its fly homolog, Armadillo). There is also a concomitant translocation of beta-catenin/Armadillo to the nucleus, where it interacts with a specific sequence motif at the  ${\tt N}$ terminus of Tcfs to generate a transcriptionally active complex. This bipartite transcription factor is targeted to the upstream regulatory regions of Tcf target genes including Siamois and Nodal related gene-3 in Xenopus, engrailed and Ultrabithorax in Drosophila via the sequence-specific HMG box, and mediates their transcriptional activation by virtue of transactivation domains contributed by beta-catenin/Armadillo. In the absence of Wingless/Wnt signals, a key negative regulator of the pathway, GSK3 beta, is activated, which mediates the downregulation of cytoplasmic beta-catenin/Armadillo via the ubiquitin-proteasome pathway. In the absence of nuclear beta-catenin, the Tcfs recruit the corepressor protein Groucho to the target gene enhancers and actively repress their transcription. An additional corepressor protein, CREB-binding

protein (CBP), may also be involved in this repression of Tcf target gene activity. Several other proteins, including adenomatous polyposis coli (APC), GSK3 beta, and Axin/Conductin, are instrumental in the regulation of beta-catenin/Armadillo. In APC-deficient colon carcinoma cell lines, beta-catenin accumulates and is constitutively complexed with nuclear Tcf-4. A proportion of APC wild-type colon carcinomas and melanomas also contains constitutive nuclear Tcf-4/beta-catenin complexes as a result of dominant mutations in the N terminus of beta-catenin that render it insensitive to downregulation by APC, GSK3 beta, and Axin/ C nductin. This results in the unregulated expression of Tcf-4 target genes such as c-myc. Based on the established role for Tcf-4 in maintaining intestinal stem cells it is likely that deregulation of c-myc expression as a result of constitutive Tcf-4/beta-catenin activity promotes uncontrolled intestinal cell proliferation. This would readily explain the formation of intestinal polyps during colon carcinogenesis. Similar mechanisms leading to deregulation of Tcf target gene activity are likely to be involved in melanoma and other forms of cancer

ANSWER 11 OF 22 WPIDS COPYRIGHT 2001 DERWENT INFORMATION LTD

1999-214706 [18] ACCESSION NUMBER:

N1999-158020 DOC. NO. NON-CPI: C1999-063258

DOC. NO. CPI:

TITLE: Tumor-suppressing protein

conductin - used for treatment and

WPIDS

diagnosis of tumors.

B04 D16 S03 DERWENT CLASS:

BEHRENS, J; BIRCHMEIER, W INVENTOR(S):

(DELB-N) DELBRUECK CENT MOLEKULARE MEDIZIN MAX PATENT ASSIGNEE(S):

COUNTRY COUNT: 22

PATENT INFORMATION:

WEEK LA PG PATENT NO KIND DATE

A2 19990311 (199918)\* GE WO 9911780

RW: AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE

W: CA JP US

DE 19840875 A1 19990512 (199925)

EP 1029047 A2 20000823 (200041) GE

R: AT BE CH DE DK FI FR GB IT LI NL SE

#### APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 9911780	A2	WO 1998-DE2621	19980901

308-4994 Searcher Shears

DE 19840875 **A1** EP 1029047 **A2** 

DE 1998-19840875 19980901 EP 1998-954120 19980901 WO 1998-DE2621 19980901

FILING DETAILS:

PATENT NO KIND

PATENT NO

EP 1029047

A2 Based on

WO 9911780

PRIORITY APPLN. INFO: DE 1997-19738205 19970902

AN 1999-214706 [18] WPIDS

AΒ 9911780 A UPAB: 19990511

> NOVELTY - The protein conductin (I) and its variants, mutants and fragments are new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following: (1) composition for diagnosing tumors comprising an agent that detects (I), the (I)-encoding gene (II) or derived mRNA; (2) composition for treating tumors containing an agent that activates or reactivates (I) in vivo; (3) cDNA (III) that encodes (I), its variants, mutants or fragments; (4) use of (II) for gene therapy of tumors; and (5) partial sequences of the adenomatosis polyposis coli (APC) protein comprising amino acids (aa) 1464-1604, 1516-1595, 1690-1778 or 1995-2083 as RGS-domain interaction sites (RGS = regulator of G-protein signaling).

USE - Detecting presence or amount of (I), at protein or nucleic acid levels, is used to diagnose tumors, while agents that (re)activate (I) are used for tumor therapy. Antitumor. (I) binds to beta -catenin and induces its cytoplasmic degradation, resulting in blockade of the Wnt/Wingless signaling pathway in vertebrates. (I) also binds to APC fragments and, in conjunction with APC, acts as a tumor suppressor. In SW840 cells APC is mutated, leading to increased levels of beta -catenin in cytoplasm and the nucleus. When (I) was introduced into these cells, beta -catenin was depleted in both cell compartments, with the effect being as strong as that for wild-type APC. Dwg. 0/4

L8

ANSWER 12 OF 22 WPIDS COPYRIGHT 2001 DERWENT INFORMATION LTD

ACCESSION NUMBER:

1999-470389 [40] WPIDS

DOC. NO. CPI:

C1999-138212

TITLE:

Agents for treating human diseases, particularly

cancer, modulate interaction of

beta-catenin with transcription factors or

tumor suppressor gene products.

DERWENT CLASS:

B04 D16

INVENTOR(S):

BIRCHMEIER, W; VON KRIES, J

Searcher

Shears

308-4994

PATENT ASSIGNEE(S):

(DELB-N) DELBRUECK CENT MOLEKULARE MEDIZIN MAX

COUNTRY COUNT:

22

PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
DE 19909251					15

WO 9942481 A2 19990826 (199942) GE

RW: AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE

W: CA JP US

EP 1054899 A2 20001129 (200063) GE

R: AT BE CH DE DK ES FI FR GB GR IE IT LI NL PT SE

#### APPLICATION DETAILS:

	ENT NO	KIND		PLICATION	DATE
	19909251	A1		1999-19909251	
WO	9942481	A2	WO	1999-DE554	19990222
EP	1054899	A2	ЕP	1999-913097	19990222
			WO	1999-DE554	19990222

#### FILING DETAILS:

PATENT NO	KIND	PATENT NO
EP 1054899	A2 Based on	WO 9942481

PRIORITY APPLN. INFO: DE 1998-19807390 19980221

AN 1999-470389 [40] WPIDS

AB DE 19909251 A UPAB: 19991004

NOVELTY - Agent (A) for treating human disease is based on substances (I) that modulate (inhibit or promote) the interaction of beta -catenin (bC) with transcription factors or products of tumor suppressor genes.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following: (a) peptide (II) comprising part of the LEF-1/TCF-4 transcription factors, or their variants and mutants; (b) peptide and related molecules (III) from the armadillo domain (arm units 3-8) of bC, and mutants of the complete bC molecule, that include at least one of the specific interaction domains for LEF-1, TCF-4, APC, conductin or E-cadherin; and (c) enzyme-linked immunosorbent assay (ELISA) for screening substance libraries for compounds that modulate interaction of bC with LEF-1/TCF, APC, conductin or E-cadherin.

ACTIVITY - Antitumor.

MECHANISM OF ACTION - bC is a key compound in the Wnt signaling pathway and is involved in development of tumors.

Generally its interaction with LEF-1 or TCF-4 is oncogenic but interaction with APC, conductin or E-cadherin is anti-oncogenic.

USE - (A) which inhibit interaction are particularly used to treat tumors, especially carcinoma of the colon and melanoma, but also, where they promote interaction, to stimulate regeneration of organs and tissues, specifically hair growth. Dwg.0/6

L8 ANSWER 13 OF 22 MEDLINE

DUPLICATE 6

ACCESSION NUMBER:

2000047719

MEDLINE

DOCUMENT NUMBER:

20047719 PubMed ID: 10580987

TITLE:

beta-catenin signaling and cancer.

AUTHOR:

Morin P J

CORPORATE SOURCE:

Laboratory of Biological Chemistry, Gerontology Research Center, National Institute on Aging, 5600

Nathan Shock Drive, Baltimore, MD 21224, USA..

MorinP@grc.nia.nih.gov

SOURCE:

BIOESSAYS, (1999 Dec) 21 (12) 1021-30. Ref: 88

Journal code: 9YY; 8510851. ISSN: 0265-9247.

PUB. COUNTRY:

ENGLAND: United Kingdom

Journal; Article; (JOURNAL ARTICLE)

General Review; (REVIEW)

(REVIEW, TUTORIAL)

LANGUAGE:

English

FILE SEGMENT:

Priority Journals

ENTRY MONTH:

200002

ENTRY DATE:

Entered STN: 20000209

Last Updated on STN: 20000209 Entered Medline: 20000203

Since its discovery as a protein associated with the cytoplasmic AB region of E-cadherin, beta-catenin has been shown to perform two apparently unrelated functions: it has a crucial role in cell-cell adhesion in addition to a signaling role as a component of the Wnt/wg pathway. Wnt/wg signaling results in beta-catenin accumulation and transcriptional activation of specific target genes during development. It is now apparent that deregulation of beta-catenin signaling is an important event in the genesis of a number of malignancies, such as colon cancer, melanoma, hepatocellular carcinoma, ovarian cancer. endometrial cancer, medulloblastoma pilomatricomas, and prostate cancer. beta-catenin mutations appear to be a crucial step in the progression of a subset of these cancers , suggesting an important role in the control of cellular proliferation or cell death. The APC/beta-catenin pathway is highly regulated and includes players such as GSK3-beta, CBP, Groucho, Axin, Conductin, and TCF. c-MYC and cyclin D1 were recently identified as a key transcriptional targets of this pathway

#### 09/587574

and additional targets are likely to emerge. Published 1999 John Wiley & Sons, Inc.

L8ANSWER 14 OF 22 MEDLINE DUPLICATE 7

ACCESSION NUMBER: 2001120045 MEDLINE

PubMed ID: 11212302 DOCUMENT NUMBER: 21079826

Signaling through beta-catenin and Lef/Tcf. TITLE:

AUTHOR: Novak A; Dedhar S

Cancer Research, S-218, Sunnybrook Health Science CORPORATE SOURCE:

Centre, Toronto, Ontario, Canada.

CELLULAR AND MOLECULAR LIFE SCIENCES, (1999 Oct 30) SOURCE:

\_56\_(5-6)\_523-37. Ref: 167\_\_\_\_\_

Journal code: CLE. ISSN: 1420-682X.

Switzerland PUB. COUNTRY:

Journal; Article; (JOURNAL ARTICLE)

General Review; (REVIEW)

(REVIEW, ACADEMIC)

English LANGUAGE:

Priority Journals FILE SEGMENT:

200102 ENTRY MONTH:

Entered STN: 20010322 ENTRY DATE:

> Last Updated on STN: 20010322 Entered PubMed: 20010209 Entered Medline: 20010215

Beta-catenin plays a structural role in cell adhesion by binding to AB cadherins at the intracellular surface of the plasma membrane and a signaling role in the cytoplasm as the penultimate downstream mediator of the wnt signaling pathway. The ultimate mediator of this pathway is a nuclear complex of beta-catenin acting as a coactivtor with lymphoid enhancer factor/T cell factor (Lef/Tcf) transcription factors to stimulate transcription of a variety of target genes. Signaling through beta-catenin is regulated by modulating its degradation and nuclear translocation. In the absence of an activating signal, phosphorylation of beta-catenin by glycogen synthase kinase 3 (GSK3) acting in conjunction with adenomatous polyposis coli and axin/conductin causes beta-catenin to interact with the beta-transducin repeat-containing protein which results in its ubiquitination and degradation. Signaling from the wnt pathway activates dishevelled which, in an as yet undefined manner, inhibits the activity of GSK3 resulting in an increase in the cytoplasmic free pool of beta-catenin, and translocation into the nucleus. The integrin-linked kinase (ILK) pathway also activates beta-catenin-Lef/Tcf signaling. ILK phosphorylates GSK3 to inhibit its activity and translocates beta-catenin into the nucleus. In addition, ILK downregulates the expression of E-cadherin and upregulates Lef-1 expression. In the final step of the beta-catenin-Lef/Tcf signaling pathway, nuclear beta-catenin binds pontin52-TATA binding protein and displaces Groucho-related gene or

> 308-4994 Shears Searcher

# 09/587574

CREB-binding protein corepressors from Lef/Tcf resulting in stimulation of transcription. During development, beta-catenin-Lef/Tcf signaling is involved in the formation of dorsal mesoderm and dorsal axis. Furthermore, defects in the beta-catenin-Lef/Tcf pathway are involved in the development of several types of cancers.

L8 ANSWER 15 OF 22 MEDLINE

DUPLICATE 8

ACCESSION NUMBER:

1999457298

MEDLINE

DOCUMENT NUMBER:

99457298 PubMed ID: 10526234

TITLE:

Identification and characterization of E-APC, a novel

Drosophila homologue of the tumour

suppressor APC.

**AUTHOR:** 

SOURCE:

Hamada F; Murata Y; Nishida A; Fujita F; Tomoyasu Y;

Nakamura M; Toyoshima K; Tabata T; Ueno N; Akiyama T

CORPORATE SOURCE:

Department of Oncogene Research, Research Institute

for Microbial Diseases, Osaka University, 3-1

Yamadaoka, Suita 565-0871, Japan. and. GENES TO CELLS, (1999 Aug) 4 (8) 465-74.

Journal code: CUF; 9607379. ISSN: 1356-9597.

PUB. COUNTRY:

ENGLAND: United Kingdom

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE:

English

FILE SEGMENT:

Priority Journals

ENTRY MONTH:

199912

ENTRY DATE:

Entered STN: 20000113

Last Updated on STN: 20000915 Entered Medline: 19991223

BACKGROUND: Mutations in the adenomatous polyposis coli (APC) AB tumour suppressor gene are implicated in the genesis of colorectal cancers. The product of the APC gene forms a complex with beta-catenin, glycogen synthase kinase 3beta (GSK-3beta) and Axin/conductin, and induces the degradation of beta-catenin. RESULTS: We have identified a novel Drosophila homologue of APC, E-APC, which is similar to but differs in several respects from D-APC. The E-APC cDNA encodes a protein of predicted 1067 amino acids, with seven armadillo repeats, two copies of the 15-amino acid repeat, five copies of the 20-amino acid repeat, and one Axin/conductin binding site. E-APC directly interacts with D-Axin and Armadillo (Arm, the Drosophila homologue of beta-catenin) in vitro, destabilizes intracellular beta-catenin, and suppresses beta-catenin/TCF-regulated transcription in APC-/- colon cancer cells. The E-APC mRNA is ubiquitously expressed throughout all developmental stages in Drosophila. CONCLUSION: Our findings suggest that E-APC may be universally involved in the regulation of the Wingless signalling pathway by down-regulating the level of Arm in Drosophila.

ANSWER 16 OF 22 MEDLINE

**DUPLICATE 9** 

ACCESSION NUMBER:

1999168905

MEDLINE

DOCUMENT NUMBER:

99168905 PubMed ID: 10049590

TITLE:

Cloning of the human homolog of conductin

(AXIN2), a gene mapping to chromosome 17q23-q24.

AUTHOR:

Mai M; Qian C; Yokomizo A; Smith D I; Liu W

CORPORATE SOURCE:

Department of Laboratory Medicine and Pathology, Mayo

Clinic/Foundation, Rochester, Minnesota 55905, USA.

CONTRACT NUMBER:

CA48031 (NCI)

SOURCE:

GENOMICS, (1999 Feb 1) 55 (3) 341-4.

Journal code: GEN; 8800135. ISSN: 0888-7543.

PUB. COUNTRY:

United States

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE:

English

FILE SEGMENT:

Priority Journals GENBANK-AF078165

OTHER SOURCE: ENTRY MONTH:

199905

ENTRY DATE:

Entered STN: 19990607

Last Updated on STN: 19990607 Entered Medline: 19990524

Conductin or Axil, an Axin homolog, plays an important AB role in the regulation of beta-catenin stability in the Wnt signaling pathway. To facilitate the molecular analysis of the human gene, we isolated the human homolog, AXIN2. The cDNA contains a 2529-bp open reading frame and encodes a putative protein of 843 amino acids. Compared with rat and mouse homologs, AXIN2 shows an overall 89% amino acid identity. Several functional domains in this protein are highly conserved including the GRS (95.9%), GSK-3beta (96.3%), Dsh (98%), and beta-catenin (89.9%) domains. Radiation hybrid mapping localized the AXIN2 gene to human chromosome 17q23-q24, a region that shows frequent loss of heterozygosity in breast cancer, neuroblastoma, and other tumors. Human AXIN2 is thus a very strong candidate involved in multiple tumor types.

ACCESSION NUMBER:

ANSWER 17 OF 22 SCISEARCH COPYRIGHT 2001 ISI (R) 2000:63768 SCISEARCH

THE GENUINE ARTICLE: 274MZ

TITLE:

Modulation of Wnt signaling by Axin and Axil

AUTHOR:

Kikuchi A (Reprint)

CORPORATE SOURCE:

HIROSHIMA UNIV, SCH MED, DEPT BIOCHEM, MINAMI KU,

1-2-3 KASUMI, HIROSHIMA 7348551, JAPAN (Reprint)

COUNTRY OF AUTHOR:

JAPAN

SOURCE:

CYTOKINE & GROWTH FACTOR REVIEWS, (SEP-DEC 1999)

Vol. 10, No. 3-4, pp. 255-265.

Publisher: ELSEVIER SCI LTD, THE BOULEVARD, LANGFORD LANE, KIDLINGTON, OXFORD OX5 1GB, OXON, ENGLAND.

ISSN: 1359-6101.

DOCUMENT TYPE:

Article; Journal

LANGUAGE:

English

REFERENCE COUNT:

97

\*ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS\* AΒ The Wnt signaling pathway is conserved in various species from worms to mammals, and, plays important roles in development, cellular proliferation, and differentiation. The molecular mechanisms by which the Wnt signal regulates cellular functions are becoming increasingly well understood. Wnt stabilizes cytoplasmic beta-catenin, which stimulates the expression of genes including c-myc, c-jun, fra-1, and cyclin D1. Axin and its homolog Axil, newly recognized as components of the Wnt signaling pathway, negatively regulate this pathway. Other components of the Wnt signaling pathway, including DvI, glycogen synthase kinase-3 beta (GSK-3). beta), beta-catenin, and adenomatous polyposis coli (APC), interact with Axin, and the phosphorylation and stability of beta-catenin are regulated in the Axin complex. Axil has similar functions to Axin. Thus, Axin and Axil act as scaffold proteins in the Wnt signaling pathway, thereby modulating the Wnt-dependent cellular functions. (C) 2000 Elsevier Science Ltd. All rights reserved.

L8 ANSWER 18 OF 22 MEDLINE

DUPLICATE 10

ACCESSION NUMBER:

1999147086 MEDLINE

DOCUMENT NUMBER:

99147086 PubMed ID: 10021369

TITLE:

Identification of APC2, a homologue of the

adenomatous polyposis coli tumour

suppressor.

**AUTHOR:** 

SOURCE:

van Es J H; Kirkpatrick C; van de Wetering M;

Molenaar M; Miles A; Kuipers J; Destree O; Peifer M;

Clevers H

CORPORATE SOURCE:

Department of Immunology, University Hospital, P.O.

Box 85500, 3508 GA, Utrecht, The Netherlands. CURRENT BIOLOGY, (1999 Jan 28) 9 (2) 105-8.

Journal code: B44; 9107782. ISSN: 0960-9822.

PUB. COUNTRY:

ENGLAND: United Kingdom

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE:

English

FILE SEGMENT:

Priority Journals

OTHER SOURCE:

GENBANK-AF091430; GENBANK-AJ012652; GENBANK-AJ130783; GENBANK-AJ130784; GENBANK-AJ130785; GENBANK-AJ130786; GENBANK-AJ130787; GENBANK-AJ130788; GENBANK-AJ130789;

GENBANK-AJ130790; GENBANK-AJ130791; GENBANK-AJ130792; GENBANK-AJ130793; GENBANK-AJ130794; GENBANK-AJ130795;

GENBANK-AJ130796; GENBANK-AJ131187

ENTRY MONTH:

199903

ENTRY DATE:

Entered STN: 19990402

Last Updated on STN: 20000303 Entered Medline: 19990323

Searcher

Shears

308-4994

The adenomatous polyposis coli (APC) tumour-suppressor protein controls the Wnt signalling pathway by forming a complex with glycogen synthase kinase 3beta (GSK-3beta), axin/ conductin and betacatenin. Complex formation induces the rapid degradation of betacatenin. In colon carcinoma cells, loss of APC leads to the accumulation of betacatenin in the nucleus, where it binds to and activates the Tcf-4 transcription factor (reviewed in [1] [2]). Here, we report the identification and genomic structure of APC homologues. Mammalian APC2, which closely resembles APC in overall domain structure, was functionally analyzed and shown to contain two SAMP domains, both of which are required for binding to conductin. Like APC, APC2 regulates the formation of active betacatenin-Tcf complexes, as demonstrated using transient transcriptional activation assays in APC -/- colon carcinoma cells. Human APC2 maps to chromosome 19p13.3. APC and APC2 may therefore have comparable functions in development and cancer.

L8 ANSWER 19 OF 22 JICST-EPlus COPYRIGHT 2001 JST

ACCESSION NUMBER:

990756513 JICST-EPlus

TITLE:

Arthroscopic treatment for dorsal wrist ganglion.

**AUTHOR:** 

NISHIKAWA SHINJI; ARAI KOICHI; TAKEUCHI KAZUNARI;

FUKUDA AKIRA; WADA KAN'ICHIRO

CORPORATE SOURCE:

Mutsu Gen. Hosp.

SOURCE:

Kansetsukyo (Arthroscopy), (1999) vol. 24, no. 1, pp.

85-90. Journal Code: L0107A (Fig. 7, Ref. 9)

ISSN: 0910-223X

PUB. COUNTRY:

Japan

DOCUMENT TYPE:

Conference; Article

LANGUAGE:

Japanese

STATUS:

New

In excising a ganglion located at the dorsum of the wrist joint, one AB may lose sight of the base of the ganglion, which may result in a recurrence of the condition; or the surgical procedure may leave a large, unsightly surgical cicatrix on the dorsum of the hand due to the size of the lesion. To eliminate these problems, we have been conductin surgery on ganglions of the dorsal wrist joint under arthroscopy. The details are reported below. A total of 16 joints(10 right and 6 left) in 16 patients(7 males and 9 females, ages ranging from 12 to 83 years, with a mean of 42 years) have undergone the arthroscopic procedure. A nodule was palpated at the center of the dorsum of the wrist in each patients and all reported pain that was associated with movement. Six had experienced repeated recurrences for six months or more; the condition had developed for the first time in eight (among whom, two had been subjected to repeated aspiration therapy); and the condition had returned in one following surgical therapy. MRI was conducted prior to surgery to confirm that there was communication between the ganglion and the

scapholunate joint(SL joint). Arthroscopy was conducted at portals I-II and a probe and a shaver were inserted through portals IV-V. The position of the base of the ganglion that was palpated at the dorsum of the scapholunate ligament(SL ligament) was confirmed under arthroscopy and excised with the shaver. No recurrence was noted and the postoperative course was satisfactory for a follow-up period that lasted from 2 to 15 months (mean, 6.4). The method introduced above applies to all ganglions that originate at the SL joint: but it is particularly suitable for large growths that are likely to leave prominent surgical scars or for radical treatment of those that return repeatedly after aspiration and cause pain associated with wrist movement. (author abst.)

L8 ANSWER 20 OF 22 BIOSIS COPYRIGHT 2001 BIOSIS

ACCESSION NUMBER:

1999:174930 BIOSIS

DOCUMENT NUMBER:

PREV199900174930

TITLE:

Cloning of the human homolog of conduction (AXIN2), a

gene mapping to chromosome 17q23-24.

AUTHOR (S):

Mai, M. (1); Qian, C.; Yokomizo, A.; Smith, D. I.;

Liu, W.

CORPORATE SOURCE:

(1) Div. Exp. Pathol., Dep. Lab. Med. Pathol.,

Rochester, MN 55905 USA

SOURCE:

Proceedings of the American Association for Cancer Research Annual Meeting, (March, 1999) Vol. 40, pp.

Meeting Info.: 90th Annual Meeting of the American

Association for Cancer Research Philadelphia, Pennsylvania, USA April 10-14, 1999 American

Association for Cancer Research

. ISSN: 0197-016X.

DOCUMENT TYPE:

Conference

LANGUAGE:

English

ANSWER 21 OF 22 BIOSIS COPYRIGHT 2001 BIOSIS 1999:165640 BIOSIS

DUPLICATE 11

ACCESSION NUMBER: DOCUMENT NUMBER:

PREV199900165640

TITLE:

APC protein: Protein interactions and cellular

functions.

AUTHOR (S):

Jais, Philippe (1); Laurent-Puig, Pierre; Olschwang,

Sylviane

CORPORATE SOURCE:

(1) Unite Marqueurs Genet. Cancers, Inst.

Gustave-Roussy, 39 rue Camille-Desmoulins, 94805

Villejuif Cedex France

SOURCE:

Gastroenterologie Clinique et Biologique, (Dec.,

1998) Vol. 22, No. 12, pp. 1071-1080.

ISSN: 0399-8320.

DOCUMENT TYPE:

General Review

LANGUAGE:

French

Searcher Shears L8 ANSWER 22 OF 22 MEDLINE DUPLICATE 12

ACCESSION NUMBER: 1998221239

MEDLINE

DOCUMENT NUMBER:

98221239 PubMed ID: 9554852

TITLE:

Functional interaction of an axin homolog, conductin, with beta-catenin, APC, and

GSK3beta.

AUTHOR:

Behrens J; Jerchow B A; Wurtele M; Grimm J; Asbrand

C; Wirtz R; Kuhl M; Wedlich D; Birchmeier W

CORPORATE SOURCE:

Max Delbruck Center for Molecular Medicine,

Robert-Rossle-Strasse 10, 13122 Berlin, Germany.

SCIENCE, (1998 Apr 24) 280 (5363) 596-9.

Journal code: UJ7; 0404511. ISSN: 0036-8075.

PUB. COUNTRY:

United States

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE:

English

FILE SEGMENT:

Priority Journals GENBANK-AF073788

OTHER SOURCE: ENTRY MONTH:

199805

ENTRY DATE:

Entered STN: 19980514

Last Updated on STN: 20000303 Entered Medline: 19980507

Control of stability of beta-catenin is central in the wnt signaling AB pathway. Here, the protein conductin was found to form a

complex with both beta-catenin and the tumor suppressor gene product adenomatous polyposis coli (APC). Conductin induced beta-catenin degradation, whereas mutants of

conductin that were deficient in complex formation

stabilized beta-catenin. Fragments of APC that contained a

conductin-binding domain also blocked beta-catenin degradation. Thus, conductin is a component of the

multiprotein complex that directs beta-catenin to degradation and is located downstream of APC. In Xenopus embryos, conductin

interfered with wnt-induced axis formation.

(FILE 'CAPLUS' ENTERED AT 11:20:11 ON 11 JUN 2001)

150 SEA FILE=CAPLUS ABB=ON PLU=ON CONDUCTING (3A) (PROTEIN L9

OR PEPTIDE)

3 SEA FILE=CAPLUS ABB=ON PLU=ON L9 AND (TUMOUR OR TUMOR L10

OR NEOPLAS? OR CANCER? OR CARCIN?)

3 S L10 NOT L6 L11

L11 ANSWER 1 OF 3 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER:

1996:427508 CAPLUS

DOCUMENT NUMBER:

125:135608

TITLE:

Co-translational effects of temperature on

Searcher

Shears

308-4994

### 09/587574

membrane insertion and orientation of

P-glycoprotein sequences

AUTHOR(S):

Zhang, Jian-Ting; Chong, Crispina H.

CORPORATE SOURCE:

Dep. Physiol. Biophys., Univ. Texas Med. Branch,

Galveston, TX, 77555-0641, USA

SOURCE:

Mol. Cell. Biochem. (1996), 159(1), 25-31

CODEN: MCBIB8; ISSN: 0300-8177

DOCUMENT TYPE:

Journal English

LANGUAGE:

P-glycoprotein (pgp) is a membrane transport protein that causes multidrug resistance (MDR) by actively extruding a wide variety of cytotoxic agents out of cells. In may also function as a peptide transporter, a vol.-regulated chloride channel, and an ATP channel. Previously, it has been shown that hamster pgp1 Pgp is expressed in more than one topol. form and that the generation of these structures is modulated by charged amino acids flanking the predicted transmembrane (TM) segments 3 and 4 and by sol. cytoplasmic factors. Different topol. structures of Pgp may be related to its different functions. This study examd. the effects of translation temp. on the membrane insertion process and the topologies of Pgp. The rabbit reticulocyte lysate expression system was used to show that translation at different temps. affects the membrane insertion and orientation of the putative TM3 and TM4 of hamster pgpl Pgp in a co-translational manner. This observation suggests that the membrane insertion process of TM3 and TM4 of Pgp mols. may involve a protein conducting channel and/or the interaction between TM3 and TM4, which act in a temp. sensitive manner. Manipulating temp. may provide a way to understand the structure-function relationship of Pgp and help overcome Pgp-related multidrug resistance of cancer cells.

L11 ANSWER 2 OF 3 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER:

1982:400304 CAPLUS

DOCUMENT NUMBER:

97:304

TITLE:

Antitumor agents. XLVIII: structure-activity relationships of quassinoids as in vitro protein

synthesis inhibitors of P-388 lymphocytic

leukemia tumor cell metabolism

AUTHOR(S):

Liou, Y. F.; Hall, I. H.; Okano, M.; Lee, K. H.;

Chaney, S. G.

CORPORATE SOURCE:

Sch. Med., Univ. North Carolina, Chapel Hill,

NC, 27514, USA

SOURCE:

J. Pharm. Sci. (1982), 71(4), 430-5

CODEN: JPMSAE; ISSN: 0022-3549

DOCUMENT TYPE:

LANGUAGE:

Journal

English

GI

I,  $R=CHMe_2$ , Z=H, n=1

II, R=Me, Z=H, n=1

III, R=Me, Z=COCH2CO, n=2

AB A series of brusatol, bisbrusatol, and bruceantin esters were examd. for their ability to inhibit protein synthesis in P-388 lymphocytic leukemia cells. Compds. which produced high antileukemic activities resulted in ID50 of 5.4-15.5 .mu.M for inhibition of whole cell protein synthesis, ID50 of 1.3-13 .mu.M for inhibition of endogenous protein synthesis in cell homogenates, and ID50 of 1.9-6 .mu.M for inhibition of polyuridine directed polyphenylalanine synthesis using runoff ribosomes and a pH 5 enzyme prepn. The polyuridine directed polyphenylalanine synthesis requires neither initiation nor termination factors, suggesting that quassinoids are exclusively elongation inhibitors. bruceantin (I) [41451-75-6], brusatol (II) [14907-98-3], and bisbrusatolyl malonate (III) [80096-78-2] allowed a runoff of the polyribosomes to 80-S free ribosomes. However, formation of the ternary complex and 80-S initiation complex were not inhibited by the quassinoids. Thus, these agents do not affect the individual steps leading to the formation of a stable 80-S initiation complex in P-388 cells. Brusatol, bruceantin, and bisbrusatolyl malonate inhibited the formation of the first peptide bond between puromycin and [3H] methionyl-transfer RNA bound to the initiation complex, indicating peptidyl transferase activity is inhibited by the quassinoids in P-388 cells. Apparently, the free 80-S ribosome is the site of binding by the quassinoid. Ribosomes actively conducting protein synthesis will continue protein synthesis and terminate before the quassinoids bind. Thus, quassinoids are elongation inhibitors of tumor cells. A strong correlation was obsd. between potent antileukemic activity and the ability to inhibit protein synthesis in P-388 lymphocytic leukemia cells.

L11 ANSWER 3 OF 3 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER:

1960:24381 CAPLUS

DOCUMENT NUMBER:

54:24381

ORIGINAL REFERENCE NO.: 54:4860c-d

TITLE:

The nature of the interaction of biologically

active agents with tissue constituents

AUTHOR (S):

Mason, R.

CORPORATE SOURCE:

Univ. Coll., London

SOURCE:

Acta Unio Intern. contra Cancrum (1959), 15,

650-1

DOCUMENT TYPE:

Journal

LANGUAGE:

Unavailable

The electronic structure of carcinogen-protein mol. complexes was examd. theoretically and the possibility of charge transfer in the complex discussed. A banded-electronic model of a protein suggests that electron transfer within such a mol. complex will take place only when the energy levels of the mols. of the complex are closely matched. Aromatic carcinogens satisfy a precise criterion for such matching of levels, and carcinogenesis is to be assocd. with the induction of conducting properties in the protein.

(FILE 'MEDLINE, BIOSIS, EMBASE, WPIDS, CONFSCI, SCISEARCH, JICST-EPLUS, JAPIO, CANCERLIT' ENTERED AT 11:22:50 ON 11 JUN 2001)

L12

18 S L10

L13

18 S L12 NOT (L2 OR L7)

L14

9 DUP REM L13 (9 DUPLICATES REMOVED)

L14 ANSWER 1 OF 9 WPIDS COPYRIGHT 2001 DERWENT INFORMATION LTD

ACCESSION NUMBER: DOC. NO. NON-CPI:

2001-266373 [27] WPIDS

DOC. NO. CPI:

N2001-190479 C2001-080736

TITLE:

Detection of proteins by using a protein

fingerprinting system which comprises linearizing the protein, labeling a first amino acid residue type and detecting first and second residue types,

useful in the diagnosis of cancer.

DERWENT CLASS:

B04 D16 S03

INVENTOR(S):

BRENT, R; BURBULIS, I E; CARLSON, R H

PATENT ASSIGNEE(S):

(MOLE-N) MOLECULAR SCI INST INC

COUNTRY COUNT:

93

PATENT INFORMATION:

PATENT NO KIND DATE

WO 2001025794 A2 20010412 (200127) \* EN

RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TZ UG ZW

> Searcher Shears

W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CR CU CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG UZ VN YU ZA ZW

### APPLICATION DETAILS:

PATENT NO KIND APPLICATION DATE

WO 2001025794 A2 WO 2000-US26958 20000929

PRIORITY APPLN. INFO: US 1999-412732 19991005

AN 2001-266373 [27] WPIDS

AB WO 200125794 A UPAB: 20010518

NOVELTY - A new method (M1) for detecting proteins having at least two different types of residues comprises giving a detectable set of distinguishing ancillary properties (a 'fingerprint') to the proteins and then detecting the fingerprint by linearizing the protein, labeling the first type of residue and detecting first and second amino acid residues.

DETAILED DESCRIPTION - A new method (M1) for detecting proteins having at least two different types of residues comprises giving a detectable set of distinguishing ancillary properties (a 'fingerprint') to the proteins and then detecting the fingerprint by linearizing the protein, labeling the first type of residue and detecting first and second amino acid residues.

In detail, M1 comprises:

- (a) linearizing the protein molecule with a denaturation means;
- (b) labeling each of the first type of amino acid residue with a tag;
- (c) detecting the fingerprint of the protein with a detection means, by detecting a first fingerprint constituent imparted by the tag and a second fingerprint constituent imparted by the second type of amino acid residue.

INDEPENDENT CLAIMS are also included for the following:

- (1) identifying a protein molecule having at least two different amino acid residue types in a sample containing several proteins, by linearizing each protein as in M1 step (a), isolating the **protein**, **conducting** steps (b) and (c) of M1, and comparing the fingerprint obtained (optionally using a computer receiving signals from the detection means) to a library of fingerprints of known protein molecules;
- (2) a library of fingerprint values of known proteins, listing the identity of the proteins and first and second (and optionally third) fingerprint constituents of each protein, being representative of the number and sequence of the first and second

(and optionally third) types of amino acid residues respectively;

- (3) characterizing protein molecules, by isolating the protein and using M1 which is modified such that first and second types of amino acid types are both labeled with different tags;
- (4) protein molecules having an identifiable fingerprint, comprising two amino acid residue types each separately tagged, or three amino acid types (optionally including tryptophan), imparting up to six fingerprint constituents by using combinations of excitation and emitted radiations; and
- (5) identifying a protein in a sample containing several proteins, following the method of (1) which is modified such that first and second residue types are both labeled with different tags.

USE - The method is useful to enable rapid identification of protein molecules, especially in biological samples e.g. plant, microorganism or animal (especially human) tissues or cells e.g. in clinical or research applications to identify aberrant or mutant forms of proteins involved in diseases such as cancers or inherited disorders such as cystic fibrosis and hemophilia. It also enables the production of a library of known proteins and their corresponding fingerprints, useful to identify unknown proteins in a sample.

Dwg.0/33

L14 ANSWER 2 OF 9 WPIDS COPYRIGHT 2001 DERWENT INFORMATION LTD

ACCESSION NUMBER:

2001-050022 [06] WPIDS

DOC. NO. NON-CPI:

N2001-038339

DOC. NO. CPI:

C2001-013790

TITLE:

Assessing translocation of proteins such as glucose transporter GLUT4, cystic fibrosis transmembrane conductance regulator by using modified protein of interest comprising the protein and detectable

tags.

DERWENT CLASS:

B04 D16 S03

INVENTOR (S):

BOGAN, J S; LODISH, H

PATENT ASSIGNEE(S):

(GEHO) GEN HOSPITAL CORP; (WHED) WHITEHEAD INST

BIOMEDICAL RES

COUNTRY COUNT:

PATENT INFORMATION:

PATENT NO KIND DATE WEEK LA

WO 2000075188 A1 20001214 (200106) \* EN 75

RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TZ UG ZW

W: AE AG AL AM AT AU AZ BA BB BG BR BY CA CH CN CR CU CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU

# ZA ZW AU 2000054775 A 20001228 (200119)

### APPLICATION DETAILS:

		KIND		PLICATION	DATE	
	2000075188			2000-US15904		
ΑU	2000054775	5 A	ΑU	2000-54775	2000060	9

### FILING DETAILS:

PATENT NO	KIND	PATENT NO
	<b></b>	
AU 20000547	775 A Based on	WO 200075188

PRIORITY APPLN. INFO: US 1999-154078 19990915; US 1999-138237 19990609

AN 2001-050022 [06] WPIDS

AB WO 200075188 A UPAB: 20010126

NOVELTY - Translocation of a protein of interest from an intracellular location to the plasma membrane in mammalian cells, when the cells are exposed to a condition or a stimulus, is assessed by using a modified protein of interest (MP) comprising the protein of interest and an epitope tag in an extracellular domain and a fluorescent tag in an intracellular domain.

DETAILED DESCRIPTION - Translocation of a protein of interest from an intracellular location to the plasma membrane in mammalian cells, when the cells are exposed to a condition or a stimulus, is assessed by using a modified protein of interest (MP) comprising the protein of interest and an epitope tag in an extracellular domain and a fluorescent tag in an intracellular domain.

The method (I) comprises:

- (a) culturing mammalian cells (test cells) expressing MP, under a condition or a stimulus to be assessed for its effects on translocation of the protein of interest;
- (b) determining a value corresponding to proportion of MP at the cell membrane to total MP in the test cells that produces a test value; and
- (c) comparing the test value with a control value, where the control value corresponds to the proportion of MP at the cell membrane to MP in control cells, where the control cells are the same cells as are cultured in (a), except that the control cells are not cultured under the condition or stimulus to be assessed, where the test value greater than the control value indicates that translocation of MP has occurred.

INDEPENDENT CLAIMS are also included for the following:

(1) determining (II) whether a protein of interest undergoes

translocation from an intracellular location to the plasma membrane in mammalian cells in the presence of a condition or stimulator, comprising:

- (a) culturing cells that express MP in the absence of the stimulator producing cultured cells;
- (b) determining the relative proportion of MP at the plasma membrane of cultured cells to total MP in the cultured cells, by producing a control value;
- (c) culturing cells that express MP under the same conditions as in (a) and in the presence of the stimulator, by producing test cells;
- (d) determining the relative proportion of MP at the plasma membrane of test cells to total MP in the test cells, by producing a test value; and
- (e) comparing the control value and the test value, where a test value that is greater than the control value indicates that protein of interest undergoes translocation following stimulation of the cells by the stimulator;
- (2) identifying (III) a drug which enhances translocation of a protein of interest from an intracellular location to the plasma membrane in mammalian cells by:
- (a) culturing cells which express RT in the presence of a candidate drug;
- (b) determining the relative proportion of MP at the plasma membrane of cultured cells to total MP in the cultured cells, producing a test value; and
- (c) comparing the test value with the control value, which is the relative proportion of the protein of interest at the plasma membrane to MP in cells cultured under same conditions in the absence of drug, where the test value greater than the control value indicates that the candidate drug enhances translocation of the protein of interest; and
- (3) eukaryotic cells (IV) expressing MP comprising a protein of interest and a detectable tag in an extracellular domain and at least 1 detectable tag in an intracellular domain, where the tags are different from each other and the protein of interest undergoes translocation in the eukaryotic cells upon contact with or exposure to a condition.
- USE The method is useful for determining translocation of a protein of interest such as aquaporin-2, cystic fibrosis transmembrane conductance regulator, gastric H+/K+ATPase, in particular GLUT4 from an intracellular location to the plasma membrane in mammalian cells in the presence of a condition or a stimulator. (III) is useful for assessing the effect of a drug on translocation of a protein such as GLUT4. Such drugs are useful in treating insulin resistance such as in adult-onset diabetes, obesity and polycystic ovary syndrome.

ADVANTAGE - Translocation of the protein of interest can be

# 09/587574

easily assessed using the tags. The tags can be detected individually, quantified and the addition of tags does not alter trafficking of the protein of interest. Dwg.0/7

L14 ANSWER 3 OF 9 WPIDS COPYRIGHT 2001 DERWENT INFORMATION LTD

1999-571821 [48] WPIDS ACCESSION NUMBER:

C1999-166854 DOC. NO. CPI:

New isolated RGS-GEF polypeptides, used to develop TITLE:

products for modulating, e.g. cell proliferation

and integrin-mediated interactions.

DERWENT CLASS: B04 D16

BOLLAG, G; HART, M J; JIANG, X; KOZASA, T; POLAKIS, INVENTOR(S):

P; ROSCOE, W; STERNWEIS, P

(ONYX-N) ONYX PHARM INC; (TEXA) UNIV TEXAS SYSTEM PATENT ASSIGNEE(S):

COUNTRY COUNT:

PATENT INFORMATION:

PATENT NO KIND DATE WEEK LΑ PG

A2 19990923 (199948)\* EN

RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL OA PT SD SE SL SZ UG ZW

W: AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI GB GE GH GM HR HU ID IL IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL

TJ TM TR TT UA UG UZ VN YU ZW

AU 9931038 A 19991011 (200008)

A2 20010103 (200102) EN EP 1064373

R: AT BE CH CY DE DK ES FI FR GB GR IE IT LI LU MC NL PT SE

# APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 9947557	A2	WO 1999-US6051	19990318
AU 9931038	A	AU 1999-31038	19990318
EP 1064373	A2	EP 1999-912727	19990318
		WO 1999-US6051	19990318

# FILING DETAILS:

PATENT NO	KIND	PATENT NO
AU 9931038	A Based on	WO 9947557
EP 1064373	A2 Based on	WO 9947557

PRIORITY APPLN. INFO: US 1998-78634 19980318

AN 1999-571821 [48] WPIDS

AB

WO 9947557 A UPAB: 19991122

NOVELTY - Isolated RGS-guanine nucleotide exchange factor (GEF) polypeptides are new.

DETAILED DESCRIPTION - A novel isolated RGS-GEF polypeptide or a biologically active fragment consists of an RGS domain of a GEF protein.

INDEPENDENT CLAIMS are also included for the following:

- (1) an isolated RGS-GEF polypeptide or a biologically active fragment comprising an RGS domain of a GEF protein, with the proviso that the polypeptide does not comprise a dbl homology (DH) domain or a pleckstrin homology (PH) domain;
- (2) an isolated RGS-GEF polypeptide, or a biologically active fragment, where the polypeptide is selected from p115 Rho-GEF, Lsc, KIAA380, and where the polypeptide is mutated in the RGS domain, and where the polypeptide has a specific binding affinity for a G protein alpha subunit (GAS), or a GTPase activating activity for a GAS;
- (3) an isolated RGS-GEF nucleic acid consisting of a nucleotide sequence (NS) encoding a polypeptide comprising an RGS domain of a GEF protein;
- (4) a nucleic acid as in (3) but, where the polypeptide does not include a DH domain or a PH domain;
  - (5) a transformed cell containing a nucleic acid as in (4);
  - (6) a vector comprising a nucleic acid as in (4), and
  - (7) identifying or assaying a molecule that:
- (a) inhibits or enhances binding of a monomeric G protein guanine nucleotide exchange factor to a GAS comprising:
- (i) incubating the GAS, or fragments with the monomeric G protein nucleotide exchange factor, or fragments, in the presence and absence of a test molecule, and
- (ii) determining whether the presence of the test molecule inhibits or enhances binding between the monomeric G-protein guanine nucleotide exchange factor and the GAS;
- (b) inhibits or enhances a stimulatory effect of a GEF on a GAS GTPase activity comprising:
  - (i) as in (ai), and
- (ii) determining whether the presence of the test molecule inhibits or enhances the stimulatory effect of the GEF protein on GAS GTPase activity;
- (c) specifically inhibits the stimulatory effect of an activated GAS on GEF mediated nucleotide exchange of a monomeric G protein, comprising conducting a first assay by:
- (i) incubating an activated GAS, or its fragments, with a GEF protein, or fragments, and a monomeric G protein, or its fragments, in the presence and absence of a test inhibitor;
- (ii) conducting a second assay by incubating a GEF protein, or fragments, and a monomeric G protein. or fragments in the presence

and absence of the test inhibitor, and

- (iii) determining whether any inhibitory effect of the test inhibitor in the first assay is greater than any inhibitory effect of the test inhibitor in the second assay;
- (d) specifically enhances the stimulatory effect of an activated GAS on GEF mediated nucleotide exchange of a monomeric G protein, comprising:
- (i) conducting a first assay by incubating an activated GAS, or fragments with a GEF protein. and fragments, and a monomeric G protein, or fragments in the presence and absence of a test enhancer;
- (ii) as in (cii), but in the presence/absence of the test enhancer, and
- (iii) determining whether any enhancing effect of the test enhancer in the first assay is greater than any enhancing effect of the test enhancer in the second assay;
- (e) mimics the stimulatory effect of an activated GAS on GEF mediated nucleotide exchange of a monomeric G protein comprising:
- (i) identifying a test compound that exhibits a binding affinity for the RGS domain of GEF proteins, or fragments, incubating a GEF protein or fragments, and monomeric G protein, or fragments in the presence or absence of the test compound, and
- (ii) determining whether the test compound exhibits a stimulatory effect on GEF mediated nucleotide exchange of a monomeric G protein, and
- (f) mimics the stimulatory effect of an RGS domain of a GEF protein on GTPase activity of a GAS comprising:
- (i) identifying a test compound that exhibits a binding affinity for a GAS, and
- (ii) incubating a GTP loaded GAS in the presence or absence of the test compound to determine whether the test compound has a stimulatory effect on GAS GTPase activity.
- USE The RGS-GEF polypeptides can be used for modulating an activity of a GAS (claimed). The products can be used for the regulation of biological pathways in which a RGS-GEF polypeptide is involved, particularly pathological conditions, e.g. cell proliferation (e.g. cancer), growth control, morphogenesis, stress fiber formation, and integrin-mediated interactions, such as embryonic development, tumor cell growth and metastasis, programmed cell death, hemostasis, leukocyte homing and activation, bone resorption, clot retraction, and the response of cells to mechanical stress. The products can also be used for detection, diagnosis and production of transgenic animals.

ADVANTAGE - None given. Dwg.0/18

L14 ANSWER 4 OF 9 MEDLINE ACCESSION NUMBER: 1999439712

MEDLINE

DUPLICATE 1

#### 09/587574

DOCUMENT NUMBER: 99439712 PubMed ID: 10508919

TITLE: A novel ADP-ribosylation like factor (ARL-6),

interacts with the protein-

conducting channel SEC61beta subunit.

AUTHOR: Ingley E; Williams J H; Walker C E; Tsai S; Colley S;

Sayer M S; Tilbrook P A; Sarna M; Beaumont J G;

Klinken S P

CORPORATE SOURCE: Laboratory for Cancer Medicine, Department of

Biochemistry, The University of Western Australia and

Royal Perth Hospital, Perth, W.A., Australia.

SOURCE: FEBS LETTERS, (1999 Oct 1) 459 (1) 69-74.

Journal code: EUH; 0155157. ISSN: 0014-5793.

PUB. COUNTRY: Netherlands

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

OTHER SOURCE: GENBANK-AF031903; GENBANK-AF133669; GENBANK-AF133670;

GENBANK-AF133910; GENBANK-AF133911; GENBANK-AF133912;

GENBANK-AF133913

ENTRY MONTH: 199911

DAME ---- 3 C

ENTRY DATE: Entered STN: 20000111

Last Updated on STN: 20000111

Entered Medline: 19991101

AB We report here the isolation of a new member of the ADP-ribosylation factor (ARF)-like family (ARL-6) present in the J2E erythroleukemic cell line, but not its myeloid variants. Consistent with this lineage-restricted expression, ARL-6 mRNA increased with

erythropoietin-induced maturation of J2E cells, and decreased with interleukin 6-induced differentiation of M1 monoblastoid cells. In tissues, ARL-6 mRNA was most abundant in brain and kidney. While ARL-6 protein was predominantly cytosolic, its membrane association increased following exposure to GTP-gammaS, like many members of the ARF/ARL family. Using the yeast two-hybrid system, six molecules which interact with ARL-6 were identified including SEC61beta, a subunit of the heterotrimeric protein conducting

channel SEC61p. Co-immunoprecipitation of ARL-6 confirmed a stable association between ARL-6 and SEC61beta in COS cells. These results demonstrate that ARL-6, a novel member of the ADP-ribosylation factor-like family, interacts with the SEC61beta subunit.

L14 ANSWER 5 OF 9 JAPIO COPYRIGHT 2001 JPO

ACCESSION NUMBER:

1997-183797

TITLE:

PHYSIOLOGICALLY ACTIVE PROTEIN RHOTEKIN

**JAPIO** 

INVENTOR:

NARUMIYA SHU

PATENT ASSIGNEE(S):

KIRIN BREWERY CO LTD, JP (CO 330755)

PATENT INFORMATION:

PATENT NO KIND DATE

ERA MAIN IPC

19970715 JP 09183797 A Heisei (6) C07K014-47

JP

APPLICATION INFORMATION

ST19N FORMAT:

JP1995-354328

19951228

ORIGINAL:

JP07354328

Heisei

SOURCE:

PATENT ABSTRACTS OF JAPAN (CD-ROM), Unexamined

Applications, Vol. 97, No. 7

1997-183797 JAPIO AN

PURPOSE: TO BE SOLVED: To obtain a new protein having activated AB

Rho-protein binding ability, inhibiting Rho-protein GTPase activity,

thus capable of inhibiting tumor development and

metastasis through neutralizing Rho-protein involving tumor

development and metastasis.

CONSTITUTION: protein is a new physiologically active protein Rhotekin (or its modified product), which has activated Rho-protein binding ability and inhibits Rho-protein GTPase activity, containing part or the whole of an amino acid sequence of the formula, or an equivalent sequence thereto. This protein is capable of neutralizing the Rho protein closely involving tumor development and metastasis, thus of inhibiting tumor development and metastasis. This new protein is obtained by conducting a library screening by yeast-two-hybrid system using mouse fetal cDNA library to isolate the gene of mouse's activated Rho- protein-binding protein followed by integrating a vector with the gene which is then manifested in host cells.

L14 ANSWER 6 OF 9 MEDLINE **DUPLICATE 2** 

ACCESSION NUMBER:

96408699 MEDLINE

DOCUMENT NUMBER:

96408699 PubMed ID: 8813706

TITLE:

Co-translational effects of temperature on membrane

insertion and orientation of P-glycoprotein

sequences.

**AUTHOR:** 

Zhang J T; Chong C H

CORPORATE SOURCE:

Department of Physiology and Biophysics, University of Texas Medical Branch, Galveston 77555-0641, USA.

CONTRACT NUMBER:

CA-64539 (NCI)

SOURCE:

MOLECULAR AND CELLULAR BIOCHEMISTRY, (1996 Jun 7) 159

(1) 25-31.

Journal code: NGU; 0364456. ISSN: 0300-8177.

PUB. COUNTRY:

Netherlands

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE:

English

FILE SEGMENT:

Priority Journals

ENTRY MONTH:

199612

ENTRY DATE:

Entered STN: 19970128

Last Updated on STN: 19970128

Searcher

Shears

308-4994

#### Entered Medline: 19961210

AB P-glycoprotein (pgp) is a membrane transport protein that causes multidrug resistance (MDR) by actively extruding a wide variety of cytotoxic agents out of cells. It may also function as a peptide transporter, a volume-regulated chloride channel, and an ATP channel. Previously, it has been shown that hamster pgp 1 Pgp is expressed in more than one topological form and that the generation of these structures is modulated by charged amino acids flanking the predicted transmembrane (TM) segments 3 and 4 and by soluble cytoplasmic factors. Different topological structures of Pgp may be related to its different functions. In this study, we examined the effects of translation temperature on the membrane insertion process and the topologies of Pgp. Using the rabbit reticulocyte lysate expression system, we showed that translation at different temperatures affects the membrane insertion and orientation of the putative TM3 and TM4 of hamster pgp 1 Pgp in a co-translational manner. This observation suggests that the membrane insertion process of TM3 and TM4 of Pgp molecules may involve a protein conducting channel and/or the interaction between TM3 and TM4, which act in a temperature sensitive manner. We speculate that manipulating temperature may provide a way to understand the structure-function relationship of Pop and help overcome Pgp-related multidrug resistance of cancer cells.

L14 ANSWER 7 OF 9 MEDLINE

DUPLICATE 3

ACCESSION NUMBER:

96381595 MEDLINE

DOCUMENT NUMBER:

96381595 PubMed ID: 8789608

TITLE:

Expression of mRNAs of multiple growth factors and

receptors by neuronal cell lines: detection with

RT-PCR

**AUTHOR:** 

Zaheer A; Zhong W; Lim R

CORPORATE SOURCE:

Department of Neurology, University of Iowa College of Medicine and Veterans Affairs Medical Center, Iowa

City 52242, USA.

SOURCE:

NEUROCHEMICAL RESEARCH, (1995 Dec) 20 (12) 1457-63.

Journal code: NX9; 7613461. ISSN: 0364-3190.

PUB. COUNTRY:

United States

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE:

English

FILE SEGMENT:

Priority Journals

ENTRY MONTH:

199610

ENTRY DATE:

Entered STN: 19961106

Last Updated on STN: 20000303 Entered Medline: 19961018

AB Neurons and glia are capable of both secreting and responding to a large variety of growth factors. However, information on multiple expression of growth factors and their receptors was usually obtained from uncorrelated observations, using cells from various

animals of origin, developmental stages, growth phases, culture ages and culture conditions. Because of its specificity and extreme sensitivity, reverse transcription-polymerase chain reaction (RT-PCR) is uniquely suitable to study a large panel of growth factors and their receptors from a limited cell sample, free of these intervening variables. In this paper we evaluate the expression of mRNA of a total of 35 growth factor-related proteins by conducting RT-PCR on three neuronal cell lines: the PC12 rat pheochromocytoma line, the MAH rat sympathoadrenal progenitor line, and the N18 mouse neuroblastoma line. Three types of results are presented. The first confirms the existing knowledge such as the presence of Trk-A (NFG receptor) in PC12. The second consists of new information that expands and extends earlier observations, such as the presence of CNTF receptor complex in PC12, which explains our previous report that CNTF enhances the biological effects of NGF on these cells. The third consists of novel information that leads the way to further experimentation by the more conventional methods. These include the strong expression of Trk-B by MAH, predicting the biological responsiveness of MAH to BDNF and NT-4, and the expression of CNTF receptor in N18. Our results also suggest that CNTF is an autocrine factor for PC12 and MAH, since both lines express the growth factor as well as the receptor. Thus, RT-PCR is a valuable tool in growth factor research that can be used in complement to, and interactively with, other approaches such as bioassay, receptor binding, and immunochemical determination. It will be particularly useful for screening a large number of growth factors in minute areas of the brain in patients suffering from neurodegenerative diseases such as Parkinson's and Alzheimer's.

L14 ANSWER 8 OF 9 BIOSIS COPYRIGHT 2001 BIOSIS

ACCESSION NUMBER: 1991:333595 BIOSIS

DOCUMENT NUMBER: BR41:30145

DOCUMENT NUMBER: BR41:30145

TITLE: REGULATION OF SQUAMOUS CELL MARKER SMALL PROLINE-RICH

PROTEIN IN CONDUCTING AIRWAY

EPITHELIUM.

AUTHOR(S): AN G; ROBINSON C B; TESFAIZZI J; CARLSON D M; WU R

CORPORATE SOURCE: CALIF. PRIMATE RES. CENT., UNIV. CALIF., DAVIS,

CALIF. 95616.

SOURCE: INTERNATIONAL CONFERENCE OF THE AMERICAN LUNG

ASSOCIATION AND THE AMERICAN THORACIC SOCIETY, ANAHEIM, CALIFORNIA, USA, MAY 12-15, 1991. AM REV

RESPIR DIS, (1991) 143 (4 PART 2), A515.

CODEN: ARDSBL. ISSN: 0003-0805.

DOCUMENT TYPE:

Conference

FILE SEGMENT:

BR; OLD

LANGUAGE:

English

# 09/587574

L14 ANSWER 9 OF 9 MEDLINE

DUPLICATE 4

ACCESSION NUMBER:

82216354 MEDLINE

DOCUMENT NUMBER:

82216354 PubMed ID: 7086652

TITLE:

Antitumor agents XLVIII: Structure-activity relationships of quassinoids as in vitro protein synthesis inhibitors of P-388 lymphocytic leukemia

tumor cell metabolism.

**AUTHOR:** 

Liou Y F; Hall I H; Okano M; Lee K H; Chaney S G

CONTRACT NUMBER:

CA 17625 (NCI) CA 22929 (NCI) CA 26466 (NCI)

SOURCE:

JOURNAL OF PHARMACEUTICAL SCIENCES, (1982 Apr) 71 (4)

430-5.

Journal code: J07; 2985195R. ISSN: 0022-3549.

PUB. COUNTRY:

United States

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE:

English

FILE SEGMENT:

Priority Journals

ENTRY MONTH:

198208

ENTRY DATE:

Entered STN: 19900317

Last Updated on STN: 19980206 Entered Medline: 19820826

AΒ A series of brusatol, bisbrusatol, and bruceantin esters were examined for their ability to inhibit protein synthesis in P-388 lymphocytic leukemia cells. Compounds which produced high T/C % values (170-272) resulted in ID50 of 5.4-15.5 microM for inhibition of whole cell protein synthesis, ID50 of 1.3-13 microM for inhibition of endogenous protein synthesis in cell homogenates, and ID50 of 1.9-6 microM for inhibition of polyuridine directed polyphenylalanine synthesis using "runoff" ribosomes and a "pH 5" enzyme preparation. The polyuridine directed polyphenylalanine synthesis requires neither initiation nor termination factors, suggesting that quassinoids are exclusively elongation inhibitors. Bruceantin, brusatol, and bisbrusatolyl malonate allowed a runoff of the polyribosomes to 80S free ribosomes. However, formation of the ternary complex and 80S initiation complex were not inhibited by the quassinoids. Thus, these agents do not affect the individual steps leading to the formation of a stable 80S initiation complex in P-388 cells. Brusatol, bruceantin, and bisbrusatolyl malonate inhibited the formation of the first peptide bond between puromycin and [3H] methionyl-transfer RNA bound to the initiation complex, indicating peptidyl transferase activity is inhibited by the quassinoids in P-388 cells. These studies also suggest that the free 80S ribosome is the site of binding by the quassinoid. Ribosomes actively conducting protein synthesis will continue protein synthesis and terminate before the quassinoids bind. This proves quassinoids are elongation inhibitors of tumor cells. A strong correlation was observed between

# 09/587574

potent antileukemic activity and the ability to inhibit protein synthesis in P-388 lymphocytic leukemia cells.

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N-PSDB; X23370.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 If it invention describes a lover human conductin, and introduced the presence or amount of conductin, at protein or nucleic acid levels, is used to diagnose tumours, while agents that (re)activate conductin are used for tumour therapy. Conductin binds to beta-catenin and induces its cytoplasmic degradation, resulting in blockade of the Wnt/Wingless signalling pathway in vertebrates. Conductin also binds to Adenomatous Polyposis Coli (APC) fragments and, in conjunction with APC, acts as a tumour suppressor.
                                                                                                                                                                                                                                                                                                                                                         Human conductin protein
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                                                                                                                                                                                                                                                                                                  suppressor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       840 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                             783..833
                                                                                                                                                                              397..465
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                                                                                                                                                                  /note=
                                                                                                                                                                                                              343..396
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                                                                                                                                                                                                                                            Location/Qualifiers 78..200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
                                                                                                                                                       "Beta-catenin
claim 14"
                                                                                                                                                                                                                      "Regulator of described in
                                                                                                                        "Dishevilled homology region as claim 15"
                                                                                                                                                                                  "GSK 3-beta binding region as described claim 13"
                                                                                                                                                      claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 639; DB 20;
Pred. No. 2.7e-66;
); Mismatches 0;
                                                                                                                                                             binding domain
                                                                                                                                                                                                                      G protein signalling domain as claim 12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                               as
                                                                                                                               described
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                840;
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RESULT
W96265
AC W9
AC W
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Matches 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Axin; cancer; breast cancer; colorectal cancer; gastrointestinal cancer; esophageal cancer; carcinoma; melanoma; diagnosis; treatment; therapy; thyroid carcinoma; tumorigenesis;
Newly isolated nucleic acid encoding "axis inhibition" (Axin) - useful for detecting, diagnosing and treating
                                                                                     N-PSDB; X09013.
                                                                                                              WPI; 1999-120510/10.
                                                                                                                                                                  Constantini F,
                                                                                                                                                                                                                                                                          10-JUL-1997;
                                                                                                                                                                                                                                                                                                                            09-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                21-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                               W09902179-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Murine axin.
                                                                                                                                                                                                                      (UYCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     beta-catenin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W96265;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W96265 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes a novel human conductin protein which has anti-tumour activity. Detecting the presence or amount of conductin, at protein or nucleic acid levels, is used to diagnose tumours, while agents that (re)activate conductin are used for tumour therapy. Conductin binds to beta-catenin and induces its cytoplasmic degradation, resulting in blockade of the Wnt/Wingless signalling pathway in vertebrates. Conductin also binds to Adenomatous Polyposis Coli (APC) fragments and, in conjunction with APC, acts as a tumour suppressor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tumor-suppressing protein conductin diagnosis of tumors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Behrens J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
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                                                                                                                                                                                                                   ) UNIV COLUMBIA NEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1999-214706/18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         840 AA;
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                                                                                                                                                                                                                                                                        97US-0890865
                                                                                                                                                                                                                                                                                                                         98WO-US14414
                                                                                                                                                               Zeng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 639; DB 20;
Pred. No. 2.7e-66;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ,
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  cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CC Nucleic acids encoding mutant and wild type Axin and CC oligonucleotides derived from them are useful for detecting mutations in the Axin gene and for determining whether a subject is likely to develop cancer (including breast, colorectal, The wild gastrointestinal, esophageal, carcinomas or melanomas). The wild cype Axin and homologues of Axin are useful for treating subjects who are likely to develop cancer (thyroid carcinomas). The nucleic acids are also useful for diagnosing cancer and for detecting mutations in cancerous cells. Wild type Axin, its antisense molecule and identified compounds form pharmaceutical compositions in the treatment of cancer. The compositions are also useful for treating cancer by inhibiting tumorigenesis (by inducing degradation of beta-catenin). The nucleic acid encoding Axin acts through negative regulation of the Wnt pathway in the Nieuwkoop Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 78; Conserv
                                                                                                                                                                                                                                                                                                   Axin; cancer; breast cancer; colorectal cancer;
gastrointestinal cancer; esophageal cancer; carcinoma; melanoma;
                                                 WPI; 1999-120510/10.
N-PSDB; X09012.
                                                                                                                                                                                                                        W09902179-A1
                                                                                                                                                                                                                                                                                     diagnosis;
                                                                                                                                                                                                                                                                                                                                         Human axin
                                                                                                                                                                                                                                                                                                                                                                   14-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                              W96264;
                                                                                                                                                                                                                                                                                                                                                                                                                      W96264 standard; Protein; 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim
          Newly isolated nucleic acid encoding "axis inhibition" protein (Axin) - useful for detecting, diagnosing and treating cancer
                                                                                       Constantini F,
                                                                                                                                                                    09-JUL-1998;
                                                                                                                                                                                              21-JAN-1999
                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                           beta-catenin.
                                                                                                                 (UYCO ) UNIV COLUMBIA NEW YORK
                                                                                                                                          10-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       334 diyley 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Figure 8;
                                                                                                                                                                                                                                                                                       treatment; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                992 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                          97US-0890865
                                                                                                                                                                    98WO-US14414.
                                                                                     Zeng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95pp; English
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61.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 407; DB
Pred. No. 5.3e
21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                        À
                                                                                                                                                                                                                                                                                       thyroid carcinoma; tumorigenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 20;
5.3e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 992;
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RESULT Y97153 ID Y99 AC Y9 AC Y9 AC Y9 AC Y9 AC XX RG KW GG 
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding mutant and wild type Axin and oligonucleotides derived from them are useful for detecting mutations in the Axin gene and for determining whether a subject is likely to develop cancer (including breast, colorectal, gastrointestinal, esophageal, carcinomas or melanomas). The wild type Axin and homologues of Axin are useful for treating subjects who are likely to develop cancer (thyroid carcinomas). The nucleic acids are also useful for diagnosing cancer and for detecting mutations in cancerous cells. Wild type Axin, its antisense molecule and identified compounds form pharmaceutical compositions in the treatment of cancer. The compositions are also useful for
                                                                                                               /note- *forms Misc-difference 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RGS; regulators of G-protein signaling; GTPase activating protein; GAP; G-alpha protein; cell adhesion; chemotaxis; vulnerary; immunosuppressor; anti-rheumatic; anti-arthritic; anti-diabetic; anti-inflamatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                treating cancer by inhibiting tumorigenesis (by inducing degradation of beta-catenin). The nucleic acid encoding Axin acts through negative regulation of the Wnt pathway in the Nieuwkoop Center.
                             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human regulator of G-protein signaling protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-DEC-2000 (first entry)
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                                                                           Misc-difference
                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytostatic; hepatotropic; anti-anaemic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Y97153 standard; Protein; 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             182
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| 242 diyley 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117 DIYLEY 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        900 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
82..201
                                                                                 109
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  "Makes direct contact with G-alpha-i"
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Novel regulator of G-protein signaling useful as diagnostic and investigative signaling disorders nucleic acids and polypeptides, tools and to treat G-protein G-protein

Claim 8; Page 102; 105pp; English.

The RGS (regulators of G-protein signaling) protein genes, clones h16395 and m1975, were identified in human and murine spleen cDNA libraries, respectively. Both proteins have unique N- and C-terminal sequences. The C-terminal location of the RGS domain is consistent with RGSs known to act as GTPase activating proteins (GAPs) for G-alpha proteins. G-alpha-i linked receptors support rapid adhesion and directed migration of leukocytes and other cell types. The novel RGS proteins may be used to modulate cell adhesion and chemotaxis, e.g. for alding wound repair. The RGS proteins, related cDNAs and anti-RGS antibodies are useful for modulation, diagnosis and treatment of immune and respiratory disorders.

Sequence 235

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Best Local Similarity 34.0
Matches 44; Conservative
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Pred. No. 5.9e-14;
5; Mismatches 43
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Matches
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Misc-difference 184
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                                                                                                waesfdkllshrdgvdaftrflktefseenlefwvacedfkkck-epqqiilkakaiyek 141
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                                                                                                                                                                  Score 177.5;
Pred. No. 6.
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Y41020
ID Y41020 standard; protein; 116 AA XX
AC Y41020;
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AC Y41020;
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Protein RGS region.
XX
RGS; guanine nucleotide exchange with the protein RGS region.
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RGS; guanine nucleotide exchange with the protein alpha subunit; cell protein morphogenesis; stress fiber form the morphogenesis; stress fiber form embryonic development; tumor cell protein and protein homology domain.
XX
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Unidentified.
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Unidentified.
XX
RO9947557-A2.
XX
VAY
RO994757-A2.
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VAY
RO9947557-A2.
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                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                   Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to isolated RGS-guanine nucleotide exchange factor (GEF) polypeptides. The novel isolated RGS-GEF polypeptide consists of an RGS domain of a GEF protein and does not comprise a dbl homology (PH) domain or a pleckstrin homology (PH) domain. The RGS-GEF polypeptides can be used for modulating an activity of a G protein alpha subunit (GAS). The products can be used for the regulation of biological pathways in which a RGS-GEF polypeptide is involved, particularly pathological conditions, e.g. cell proliferation (e.g. cancer), morphogenesis, growth conditions, e.g. cell proliferation (e.g. cancer), morphogenesis, growth as embryonic development, tumor cell growth and metastasis, programmed cell death, hemostasis, leukocyte homing and activation, bone resorption, clot retraction, and the response of cells to mechanical stress. The products can also be used for detection, diagnosis and production of several
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated RGS-GEF polypeptides, used modulating, e.g. cell proliferation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               embryonic development; tumor cell
bone resorption; clot retraction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GS; guanine nucleotide exchange factor; GEF; RGS domain; GAS; cancer; protein alpha subunit; cell proliferation; growth control; hemostasis; orphogenesis; stress fiber formation; integrin-mediated interaction; mbryonic development; tumor cell growth; cell death; leukocyte homing; one resorption; clot retraction; dbl homology domain; mechanical stress;
   60
                                                                  61 YIENNSVVSKQLKPATKTYIRDGIKKQQIGSVMFDQAQTEIQAVMEENAYQVFLTSDIY 119
fiekeapkeinidfqtktliaqni--qeatsgcfttaqkrvyslmennsyprflesefy
                                                                                                                                            wseafdellaskyglaafraflksefceeniefwlacedfkktk-spqklsskarkiytd
                                                                                                                                                                                                            WTKSLHSLLGDQDGAYLFRTFLEREKCVDTLDFWFACNGFRQMNLKDTKTLRVAKAIYKR 60
                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75pp; English
                                                                                                                                                                                                                                                                                                                       26.2%;
                                                                                                                                                                                                                                                                                         20;
                                                                                                                                                                                                                                                                                      Score 167.5; DB
Pred. No. 4e-12;
0; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polakis P, Sternweis P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to develop products for integrin-mediated interactions
                                                                                                                                                                                                                                                                                         57;
                                                                                                                                                                                                                                                                                                                                                            20;
                                                                                                                                                                                                                                                                                                                                                     Length 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kozasa
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                                                                                                                                                                                                                                                                                      Gaps
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Best Local
                                                                                                                                                                                                                                                                                                                         F15566 to F16505 encode the human prostate cancer associated proteins, called prostate cancer antigens, given in B56363 to B57302. The prostate cancer antigens can have neuroprotective, cytostatic, cardioactive, immunomodulatory, muscular, vulnerary, gastrointestinal, nephrotropic, antiinfective, gynaecological and antibacterial activities, and can be used in gene therapy. The prostate cancer antigen polynucleotides may be used for detection of prostate cancer antigen polynucleotides may be chromosome markers, and for numerous other diagnostic or research purposes. The prostate cancer antigens may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, polynonary, cardiovascular, renal, and proliferative disorders, wounds, and infectious diseases. F16506 to F16514 to B57303 represent sequences used in the exemplification of the present invention.
           B43847 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prostate cancer associated gene sequences, referred to as prostate cancer antigens, useful for treatment, prevention, and diagnosis of
                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 11; Page 1946-1947; 2338pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         disorders such as prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gastrointestinal; pulmonary:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-MAR-2000; 2000WO-US05988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200055174-A1
                                                                                             148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HUMA-) HUMAN
(ROSE/) ROSEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gastrointestinal; pulmonary;
wound; infectious disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vulnerary; gastrointestinal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B56929 standard; Protein; 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-MAR-2001
                                                                                                                         61
                                                                                                                                                         9
                                                                                                                                                                                                                                      Local Similarity
                                             ø
                                                                                                       YIENNSVVSKQLKPATKTYIRDGIKKQQIGSVMFDQAQTEIQAVMEENAYQVFLTSDIY 119 :|| : ::|| |:| || :| | 119 :|
                                                                                   fiekeapkeinidfqtktliaqni~~qeatsgcfttaqkrvyslmennsyprflesefy
                                                                                                                                                 wseafdellaskyglaafraflksefceeniefwlacedfkktk-spqklsskarkiytd 147
                                                                                                                                                                                  WTKSLHSLLGDQDGAYLFRTFLEREKCVDTLDFWFACNGFRQMNLKDTKTLRVAKAIYKR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000-587513/55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        prostate cancer antigen protein sequence
                                                                                                                                                                                                                                                                                                    220 AA;
                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0124270.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer; prostate cancer antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cytostatic;
                                                                                                                                                                                                                                    26.2%;
             217 AA
                                                                                                                                                                                                                Score 167.5; DB 21;
Pred. No. 9.1e-12;
Pred. No. 9.7e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cardiovascular; proliferative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nephrotropic; antiinfective; gynaecological;
neural; immune; reproductive; renal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cardioactive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ingen; detection; diagnosis;
immunomodulatory; muscular;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ
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59 KRYIENNSVVSKQLKPATKTYIRDGIKKQQIGSVMFDQAQTEIQAVMEENAYQVFLTSDI 118

1 WTKSLHSLLGDQDGAYLFRTFLEREKCVDTLDFWFACNGFR--QMNLKDTKTLRVAKAIY 58 wsqslekllanqtgqnvfgsflksefseeniefwlacedykktesdllpck----aeeiy 145

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CC B4338 to B4239. The proteins can have activities based on the tissues CC and cells the genes are expressed in Example of activities include: CC cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; CC antiasthmatic; antiahematic; antiabeterial; antiviral; dermatological; CC antityroid; antiahlergic; antibacterial; antiviral; dermatological; CC neuroprotective; cardiant; thrombolytic; coagulant; nootropic; artipsoriatic and antianglogenic. The polynucleotides and CC vasotropic; antipsoriatic and antianglogenic. The polynucleotides and CC polypeptides can be used for preventing, treating or ameliorating medical CC conditions and diagnosing pathological conditions. Polynucleotides, CC polypeptides, antibodies, agonists and antagonists from the present CC invention may be used to treat immune disorders by activating or inhibiting the proliferation, differentiation or mobilisation of immune CC cells, to treat disorders of haematopoietic cells, autoimmune disorders, callergic reactions, syraft versus host disease and organ rejection, CC concers, cardiovascular disorders, neurological disease and bacterial or ciral infections. The peptides, nucleotides, antibodies, agonists and CC antagonists may be also be used in drug screens. C78449 to C78457 and CC invention.
    Matches
                                         Query Match
                                                                                                  Sequence
                                                                                                                                          invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated nucleic acids comprising sequences encoding peptides useful for treating or diagnosing {\it e.g.} cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral; antiinflammatory; antiithyroid; antiallergic; antibacterial; cardiant; dermatological; neuroprotective; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-MAR-2000; 2000WO-US05882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200055350-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neurological disease; drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammati
immune disorder; haematopoietic cell disorder; autoimmune disorder;
allergic reaction; graft versus host disease; organ rejection;
haemostatic; thrombolytic; cardiovascular disorder; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; cancer associated gene; cancer antigen; detection; diagnosis; cytostatic; proliferative; vulnerary; immunomou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B43847;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC
                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000-587533/55
    40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to C78448 encode the human cancer associated proteins given in
                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C78056
                                                                                                  217
    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  associated protein sequence SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0124270
                    25.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2352pp; English.
    28;
                Score 165; DB 21;
Pred. No. 1.8e-11;
    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vulnerary; immunomodulator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NO:1292
                                     Length 217;
    Indels
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Gaps
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RESULT 10

Y41021

XX Y41021

XX Y41021

XX O6-DEC

XX RGS;

KW GFG;

KW GF
                            S
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                                                                                         Matches
                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                   (GEF) polypeptides. The novel isolated RGS-GEF polypeptide consists of an RGS domain of a GEF protein and does not comprise a dbl homology (DH) domain or a pleckstrin homology (PH) domain. The RGS-GEF polypeptides can be used for modulating an activity of a G protein alpha subunit (GAS). The products can be used for the regulation of biological pathways in which a RGS-GEF polypeptide is involved, particularly pathological conditions, e.g. cell proliferation (e.g. cancer), morphogenesis, growth control, stress fiber formation, and integrin-mediated interactions, such as embryonic development, tumor cell growth and metastasis, programmed cell death, hemostasis, leukocyte homing and activation, bone resorption, clot retraction, and the response of cells to mechanical stress. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated RGS-GEF polypeptides, used modulating, e.g. cell proliferation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bollag G,
Jiang X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       morphogenesis; stress fiber formation; integrin-mediated interaction; embryonic development; tumor cell growth; cell death; leukocyte homing; bone resorption; clot retraction; dbl homology domain; mechanical stress;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Y41021;
                                                                                                                                                                                                                                                                                                          products can also be used for transgenic animals. Sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to isolated RGS-guanine nucleotide exchange factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 18; 75pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W09947557-A2
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                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ONYX-) ONYX PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pleckstrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RGS3 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                204 yl 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SS; guanine nucleotide exchange factor; GEF;
protein alpha subunit; cell proliferation; g
1 WTKSLHSLLGDQDGAYLFRTFLEREKCVDTLDFWFACNGFRQMNLKDTKTLRVAKAIYKR 60 | | :|| || :| :| || || :: :| :| || || ::
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                                                                                      39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hart MJ,
                                                                                                                                                                                                                                  116
                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RGS region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   domain
                                                                                                                 25.7%;
32.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Roscoe
                                                                                    22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ξ
                                                                                 Score 164.5; DB Pred. No. 9e-12; Mismatches
                                                                                                                                                                                                                                                                                                                detection, Y41014-028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polakis P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to develop products for
integrin-mediated interactions
                                                                                                                                                                                                                                                                                                             diagnosis and production of represent RGS regions of several
                                                                                                                                           DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sternweis P,
                                                                                    55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RGS domain; GAS;
                                                                                      Indels
                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 control;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kozasa
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Query Match Best Local (

Similarity

25.2%; Score 161; DB 20; 32.2%; Pred. No. 2.3e-11;

Conservative

28;

Mismatches

46;

8;

Gaps

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                                          RGS domain of a GEF protein and does not comprise a dbl homology (DH) domain or a pleckstrin homology (PH) domain. The RGS-GEF polypeptides can be used for modulating an activity of a G protein alpha subunit (GAS). The products can be used for the regulation of biological pathways in which a RGS-GEF polypeptide is involved, particularly pathological conditions, e.g. cell proliferation (e.g. cancer), morphogenesis, growth control, stress fiber formation, and integrin-mediated interactions, such as embryonic development, tumor cell growth and metastasis, programmed cell death, hemostasis, leukocyte homing and activation, bone resorption, clot retraction, and the response of cells to mechanical stress. The products can also be used for detection, diagnosis and production of several transgenic animals. Sequences Y41014-028 represent RGS regions of several
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bollag G,
Jiang X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RGS; guanine nucleotide exchange factor; GEF; RGS domain; GAS; cancer; G protein alpha subunit; cell proliferation; growth control; hemostasis; morphogenesis; stress fiber formation; integrin-mediated interaction; embryonic development; tumor cell growth; cell death; leukocyte homing; bone resorption; clot retraction; dbl homology domain; mechanical stress;
Sequence
                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 18; 75pp; English
                                                                                                                                                                                                                                                                                                                                                                                   New isolated RGS-GEF polypeptides, used to develop products for modulating, e.g. cell proliferation and integrin-mediated interactions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Y41019 standard; protein; 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ONYX-) ONYX PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Н
                                                                                                                                                                                                                                                      invention relates to isolated RGS-guanine nucleotide exchange factor F) polypeptides. The novel isolated RGS-GEF polypeptide consists of a domain of a GEF protein and does not comprise a dbl homology (DH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                yiaiqackevnldsytrehtkdnl--qsvtrgcfdlaqkrifglmekdsyprflrsdly 116
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115 AA;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Fig 2; 40pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalian p26 proteins and their related DNA - useful for screening for de-phosphorylase inhibitory compounds
                                                                                                    154 kh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            useful as a reagent for screening for compounds having dephosphorylase inhibitory activity. It is also useful as a treating and preventive agent for diseases related to the haematogenic system.
                                                                                                                                               121 EY 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W44834 standard; peptide; 181 AA
                                                                                                                                                                                                        97
                                                                                                                                                                                                                             61 YIENNSYVSKOLKPATKTYIRDGIKKQQIGSVMFDQAQTEIQAVMEENAYQVFLTSDIYL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human p26 protein
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                                                                                                                                                                                                                                                                                                                                 WTKSLHSLLGDQDGAYLFRTFLEREKCVDTLDFWFACNGFRQMNLKDTKTLRVAKAIYKR 60
                                                                                                    155
                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 AA;
                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                               30;
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 160; DB 19;
Pred. No. 5.4e-11;
                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                             49;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 181;
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64 waaslenlledpegvkrfreflkkefseenvlfwlacedfkkmgdk-tqmgekakelymt 122

1 WTKSLHSLLGDQDGAYLFRTFLEREKCVDTLDFWFACNGFRQMNLKDTKTLRVAKAIYKR 60

Query Match Best Local S Matches 39

Similarity

25.0%;

Score 160; DB 21; Pred. No. 6.4e-11; Mismatches

Length 207; Indels

4.

Conservative

30;

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C called pancreatic cancer antigens, given in B54008 to B54465. The human communomodulatory, relaxant, contraceptive, gynaecological, cardiant and cantinflammatory activities, and can be used in gene therapy. The complication of a medical condition or in assays for diagnosing a compartment to the proteins and the activity of the proteins can be used to gene therapy. The compartment to the proteins and the activity of the proteins can be compared to detect, treat compartments to the proteins and the activity of the proteins can be compared to the proteins and the activity of the proteins can be used to detect, treat compared to the antigens can be used to design nucleit cancer antigens can be used to design polynucleotides can be screened for. The pancreatic cancer antigen polynucleotides can be screened for. The pancreatic cancer composes that can be used to design nucleic acid hybridisation dentification and/or typing and a variety of forensic and diagnostic compared to the proteins can be used to generate antibodies which are used to purify, detect and target the polypeptides, including both in vivo cand in vitro diagnostic and therapeutic methods. The proteins can be used to treat or prevent neural, immune system, muscular, reproductive, considered to considered to consider the proteins can be considered to considered to consider the proteins can be considered to considered to considered to consider the proteins can be considered to considered t
  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C98773 to C99231 encode the human pancreatic cancer associated proteins called pancreatic cancer antiques, given in B44008 to B54466 The human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid that is a pancreatic cancer antigen for preventing, treating, or ameliorating a medical condition, particular pancreatic cancer, or for use in assays for diagnosing a pathological condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME
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linkage analysis; tissue identification; tissue typing; forensic;
neural; immune system; muscular; reproductive; gastrointestinal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              detection; diagnosis; identification; cytostatic; neuroprotective;
nootropic; immunomodulatory; relaxant; contraceptive; gynaecological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; pancreas; pancreatic cancer; pancreatic cancer antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human pancreatic cancer antigen protein sequence SEQ ID NO:812
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Page 1267-1268; 1379pp; English.
207 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0124270
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                New regulators of G-protein signalling - useful for, e.g. diagnosis, prevention and treatment of cancer and inflammation
                                                                                WPI; 1998-557112/47.
N-PSDB; V45442.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Regulator of G-protein signalling 2; RGPS-2; human; G protein coupled receptor; signal transduction; in cell proliferation; cancer; diagnosis; therapy.
                                                                                                                                                      Goli SK,
                                                                                                                                                                                                (INCY-) INCYTE PHARM INC
                                                                                                                                                                                                                                                                                           31-MAR-1998;
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                                                                                                                                                   Hillman JL
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                                                                                                                                                                                                                                                                                                                                                                                                                                "potential protein kinase C phosphorylation
site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RGS; guanine nucleotide exchange factor; GBF; RGS domain; GAS; cancer; G protein alpha subunit; cell proliferation; growth control; hemostasis; morphogenesis; stress fiber formation; integrin-mediated interaction; embryonic development; tumor cell growth; cell death; leukocyte homing; bone resorption; clot retraction; dbl homology domain; mechanical stress;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 19; Page 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Y41001;
WPI; 1999-571821/48
                                                       Jiang X;
                                                                                        Bollag G,
                                                                                                                                                                                                                                                                               18-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                 23-SEP-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Y41001 standard; protein; 118 AA
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                                                                                                                                                      (ONYX-) ONYX PHARM INC.
                                                                                                                                                                                                                    18-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 WTKSLHSLLGDQDGAYLFRTFLEREKCVDTLDFWFACNGFRQMNLKDTKTLRVAKAIYKR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                        Hart MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                  99WO-US06051.
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                                                                                           Roscoe
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The invention relates to isolated RGS-guanine nucleotide exchange factor CC (GEF) polypeptides. The novel isolated RGS-GEF polypeptide consists of an CC RGS domain of a GEF protein and does not comprise a dbl homology (PH) CC domain or a pleckstrin homology (PH) domain. The RGS-GEF polypeptides can be used for modulating an activity of a G protein alpha subunit (GAS). CC which a RGS-GEF polypeptide is involved, particularly pathological cc conditions, e.g. cell proliferation (e.g. cancer), morphogenesis, growth CC control, stress fiber formation, and integrin-mediated interactions, such CC as embryonic development, tumor cell growth and metastasis, programmed CC clot retraction, and the response of cells to mechanical stress. The CC products can also be used for detection, diagnosis and production of CC transgenic animals. Sequences Y41000-008 represent conserved domain
                                                                                                                                                                                                                                             Query Match 24.5
Best Local Similarity 31.1
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated RGS-GEF polypeptides, used to develop products for modulating, e.g. cell proliferation and integrin-mediated interactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Fig 1; 75pp; English.
1 WTKSLHSLLGDQDGAYLFRTFLEREKCVDTLDFWFACNGFRQMNLKDTKTLRVAKAIYKR 60
                                                                                                                                                                                                                                                                                                                                                                                               118 AA;
                                                                                                                                                                                                                                                                        24.5%; Score 156.5; DB 20; Length 118; 31.1%; Pred. No. 8e-11;
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Search completed: June 7, 2001, 02:01:15
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
  Score
                                                                                                                                                                                                                                                                                                                                                                                                                                               158
158
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3: /cgn2_6/ptodata/2,
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5: /cgn2_6/ptodata/2,
6: /cgn2_6/ptodata/2,
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Match
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US-08-8460-505-32
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US-08-829-110-6
US-08-829-110-6
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US-08-94-004-2
US-08-94-004-2
US-08-461-379A-2
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US-08-463-074B-2
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Query Match
Best Local Similarity
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45	44	43	42	41	40	39	38	37	36	35 5	34	မ	32	31	30	29	28
6 <b>4</b>	64	64	101	101	113	113	113	114	114	114	116	116	124.5	124.5	124.5	133	133
10.0	10.0	10.0	15.8	15.8	17.7	17.7	17.7	17.8	17.8	17.8	18.2	18.2	19.5	19.5	19.5	20.8	20.8
764	764	764	420	420	119	119	119	123	123	123	118	118	555	555	555	123	123
U	ω	Н	σ	N	σı	w	N	G	ω	N	G	N	Ç	ω	N	ر.	N
PCT-US95-16930-4	US-09-177-431-4	US-08-375-300-4	PCT-US96-08295-40	US-08-588-258B-40	PCT-US96-08295-30	US-08-460-505-30	US-08-588-258B-30	PCT-US96-08295-1	US-08-460-505-1	US-08-588-258B-1	PCT-US96-08295-38	US-08-588-258B-38	PCT-US96-08295-24	US-08-460-505-24	US-08-588-258B-24	PCT-US96-08295-39	US-08-588-258B-39
Sequence 4, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 40, Appl	Sequence 40, Appl	Sequence 30, Appl	Sequence 30, Appl	Sequence 30, Appl	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 38, Appl	Sequence 38, Appl	Sequence 24, Appl	Sequence 24, Appl	Sequence 24, Appl	Sequence 39, Appl	Sequence 39, Appl

ALIGNMENTS

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US-08-748-483-4
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; Patent No. 5955314
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                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: US
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/748,41
FILING DATE: Herewith
                                                                                                                                                                                                    FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: PF-0:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-845-4166
TELEPAX: 415-845-4166
                                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: A NOVEL REGULATOR OF CELL SIGNALLING
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                      IMMEDIAȚE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                             LENGTH:
            CLONE:
                                                                     TYPE: amino acid
STRANDEDNESS: sin
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Palo Alto
STATE: CA
                  LIBRARY: GenB
CLONE: 292037
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STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                               211 amino acids
                                                                                         single
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26.2%;

Score 167.5; DB 2 Pred. No. 2.3e-13;

2

Length 211;

Matches

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US-08-460-505-31
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US-08-588-258B-31
                  Sequence 31, Application US/08460505
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 32.8:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/588,2
FILING DATE: January 12, 1996
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GENERAL INFORMATION:
APPLICANT: H. Robert Horvitz et al.
APPLICANT: TOVENTION: REGULATORS OF G-PROTEIN SIGNALLING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
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LENGTH: 119 amino acids
                                                                                                                                                        116 YL 117
                                                                                                                                                                                                      119 YL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 39,109
REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Bieker-Brady, Kristina
REGISTRATION NUMBER: 39,109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                         59 KRYIENNSVYSKQLKPATKTYIRDGIKKQQIGSVMFDQAQTEIQAVMEENAYQVFLTSDI 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDITION OF THE STREET: 1. STREET: 1. STREET: 1. AND THE STREET S
                                                                                                                                                                                                                                              58 KAFVHSDA--AKQINIDFRTRESTAKKIKAPTPTCFDEAQKVIYTLMEKDSYPRFLKSDI 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DATE: January 12, 1996
CLASSIFICATION: 435
TORNEY/AGENT TWO-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 617-428-7045
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: US
ZIP: 02110
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                                                                                                                                                                                                                                                                                                                                                 WSQSLEKLLANQTGQNVFGSFLKSEFSEENIEFWLACEDYKKTESDLLPCK----AEEIY 57
                                                                                                                                                                                                                                                                                                                                                                                                  WTKSLHSLLGDQDGAYLFRTFLEREKCVDTLDFWFACNGFR--QMNLKDTKTLRVAKAIY 58
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PCT-US96-08295-31
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                                                                                                                                                                                                                                 Sequence 31, Application PC/TUS9608295
GENERAL INFORMATION:
APPLICANT: Massachusetts Institute of Technology
TITLE OF INVENTION: REGULATORS OF G-PROTEIN SIGNALLING
NUMBER OF SEQUENCES: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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  COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Bieker-Brady, Kristina REGISTRATION NUMBER: 39,109 REFERENCE/DOCKET NUMBER: 019: TELECOMMUNICATION INFORMATION: TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
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ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          116 YL 117
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                                                                                                           STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 01.
                                                                                                                                                      ADDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58 KAFVHSDA--AKQINIDERTRESTAKKIKAPTPTCFDEAQKVIYTLMEKDSYPRELKSDI 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59 KRYIENNSVVSKQLKPATKTYIRDGIKKQQIGSVMFDQAQTEIQAVMEENAYQVFLTSDI 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 02-JUN-1995
FILING DATE: 02-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 WTKSLHSLLGDQDGAYLFRTFLEREKCVDTLDFWFACNGFR--QMNLKDTKTLRVAKAIY 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE:
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                                                                                                                                      Boston
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USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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Floppy disk
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32.8%;
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Pred. No. 2.2e-13;
8; Mismatches 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Version #1.30
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application US/08829110 Patent No. 5882890
                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Hillman, Jenni
APPLICANT: Goli, Surya K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATA:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/588,258
APPLICATION NUMBER: 12-JAN-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Bicker-Brady, Kristina
REGISTRATION NUMBER: 39,109
REFERENCE/DOCKET NUMBER: 01997/216001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                  SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: NOVEL REGULATORS OF G-PROTEIN TITLE OF INVENTION: SIGNALING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119 YL 120
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                                                                                                                                                                                                     STREET: 3174 POI
CITY: Palo Alto
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TYPE: amino acid
STRANDEDNESS: not relevi
APPLICATION NUMBER: FILING DATE: Filed
                                                                                                                                                     COUNTRY: U
ZIP: 94304
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                                                                             OPERATING SYSTEM:
                                                                                         COMPUTER: IBM Compatible
                                                                                                                                                                                            STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59 KRYIENNSVVSKQLKPATKTYIRDGIKKQQIGSVMFDQAQTEIQAVMEENAYQVFLTSDI 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/
FILING DATE: 31-MAY-1996
                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 WTKSLHSLLGDQDGAYLFRTFLEREKCVDTLDFWFACNGFR--QMNLKDTKTLRVAKAIY 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELEPHONE: 61//542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KAFVHSDA--AKQINIDFRTRESTAKKIKAPTPTCFDEAQKVIYTLMEKDSYPRFLKSDI 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WSQSLEKLLANQTGQNVFGSFLKSEFSEENIEFWLACEDYKKTESDLLPCK----AEEIY 57
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                                                                                                                                                                                                                             E: Incyte Pharmaceuticals, Inc 
3174 Porter Drive
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                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                         Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
 Filed Herewith
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25.8%; Score 165; DB 5; Length 119 32.8%; Pred. No. 2.2e-13;
                     US/08/829,110
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Best Local Similarity
Matches 40; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/08748483 Patent No. 5955314
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                    OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                     CLASSIFICATION: 530 PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatii
                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: INCYTE PE
                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: À NOVEL REGULATOR OF CELL SIGNALLING NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hillman, Jenni
APPLICANT: Goli, Surya K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         183 YL 184
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LIBRARY: Gen-
ONE: 299705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            125 KAFVHSDA--AKQINIDERTRESTAKKIKAPTPTCFDEAQKVIYTLMEKDSYPRFLKSDI 182
                                                                                                                                                        APPLICATION NUMBER: US FILING DATE: Herewith CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: 8
                                                                                                                                                                                                                                                                                                                                             CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 KRYIENNSVVSKQLKPATKTYIRDGIKKQQIGSVMFDQAQTEIQAVMEENAYQVFLTSDI 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69 WSQSLEKLLANQTGQNVFGSFLKSEFSEENIEFWLACEDYKKTESDLLPCK----AEEIY 124
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                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                           ZIP: 94304
                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                               STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 WTKSLHSLLGDQDGAYLFRTFLEREKCVDTLDFWFACNGFR--QMNLKDTKTLRVAKAIY 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                           3174 Porter Drive
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                                                                                                                                                                                                                                                      IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hillman, Jennifer L.
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                                       PF-0157 US
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Pred. No. 4.3e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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US-08-829-110-3
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                          INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 243 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 40; Conserv
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Sequence 3, April
5882890
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                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
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LENGTH: 196 amino acids
                                                                                                                                           TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                          CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
MMEDIATE SOURCE
                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: GO11, SUTYA K.

TITLE OF INVENTION: NOVEL REGULATORS OF G-PROTEIN
TITLE OF INVENTION: SIGNALING
NUMBER OF SEQUENCES: 6
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LIBRARY: GenBa
CLONE: 728966
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                                                                                                                             TELEPHONE:
                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/8
FILING DATE: Filed Herewith
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                                                                                                                               415-855-0555
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                                                                                                                                                           PF-0259 US
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61 YIENNSVYSKQLKPATKTYIRDGIKKQQIGSVMFDQAQTEIQAVMEENAYQVFLTSDIY 119

1 WTKSLHSLLGDQDGAYLFRTFLEREKCVDTLDFWFACNGFRQMNLKDTKTLRVAKAIYKR 60

Indels

2; Gaps

2 WSEAFDELLASKYGLAAFRAFLKSEFCEENIEFWLACEDFKKTK-SPQKLSSKARKIYTD 60

Matches

Local Similarity 31.9 nes 38; Conservative

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US-08-588-258B-32
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                       Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 32, Application US/08588258B Patent No. 5929207
                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Bicker-Brady, Kristina
REGISTRATION NUMBER: 39,109
REFERENCE/DOCKET NUMBER: 01997
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
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Best Local Similarity 32.0
Matches 39; Conservative
                                                                                             TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: Windows 95 SOFTWARE: Fastseq Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALL.
STREET: 1.
CITY: Boston
"TATE: MA
"TSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                         TELEFAX:
                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: Januar CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100 WAASLENLLEDPEGVKRFREFLKKEFSEENVLFWLACEDFKKMODK-TOMOEKAKEIYMT 158
                                                                                                                                                                        LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 YIENNSVVSKQLKPATKTYIRDGIKKQQIGSVMFDQAQTEIQAVMEENAYQVFLTSDIYL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION:
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                                                                                                                                                      amino acid
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                                                                                                                                                                    121 amino acids
                                                                                                                                                                                                                                          617-428-7045
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176 Federal Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              H. Robert Horvitz et al.
VENTION: REGULATORS OF G-PROTEIN SIGNALLING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            THYMNOT 02
                                                                                                                                                                                                                                                                                                                                                                           January 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Floppy disk
                                                                                                                                    not relevant
24.7%; Score 158; DB 2; J
31.9%; Pred. No. 1.7e-12;
7ative 20; Mismatches 59;
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Best Local Similarity
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                                                                                                                                                                                                                ·-US96-08295-32
                                                                                                                                                             equence 32, Application PC/TUS9608295
GENERAL INFORMATION:
APPLICANT: Massachusetts Institute
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INFORMATION FOR SEQ ID NO:
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                                                                                                                      APPLICANT: Massachusetts Institute of Technology TITLE OF INVENTION: REGULATORS OF G-PROTEIN SIGNALLING NUMBER OF SEQUENCES: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Bleker-Brady, Kristina REGISTRATION NUMBER: 39,109 REFERENCE/DOCKET NUMBER: 01997/214001 TELECOMMUNICATION INFORMATION: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS: ADDRESSEE: F1sh & Richardson P.C.
                                                                                                     CORRESPONDENCE ADDRESS:
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                                                  CITY:
                                                                  STREET:
                                                                                                                                                                                                                                                                                          61 FIEKEAPKEINIDFQTKTLIA-AQNIQEATSGCFTTAQKRVYSLMENNSYPRFLESEFY 118
                                                                                                                                                                                                                                                                                                                             61 YIENNSVVSKQLKPATKTYIRDGIKKQQIGSVMFDQAQTEIQAVMEENAYQVFLTSDIY 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 121 amino acids
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STATE: MA
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STREET: 27
             COUNTRY:
                                                                                   ADDRESSEE:
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MA
USA
                                              Boston
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                                                                  E: Fish & Richardson P.C
225 Franklin Street
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RESULT
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Best Local Similarity
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SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
                                                                                                                 ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                            APPLICANT: GOL1, SURYA K.
TITLE OF INVENTION: NOVEL
TITLE OF INVENTION: SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 617/542-5070
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                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: (CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: 1
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                    APPLICATION NUMBER: FILING DATE: Filed
                                                                                                                                                                                                        STREET: 3174 PO: CITY: Palo Alto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
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CLASSIFICATION:
                                                                     SOFTWARE:
                                                                                COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 YIENNSVVSKQLKPATKTYIRDGIKKQQIGSVMFDQAQTEIQAVMEENAYQVFLTSDIY 119
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REGISTRATION NUMBER: 39,109
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3174 Porter Drive
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                                                                     FastSEQ for Windows Version 2.0
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                                                                                                                        Diskette
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12-JAN-96
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                Filed Herewith
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                                  US/08/829,110
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US-08-748-483-5
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                          FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
NEGISTRATION NUMBER: 36,749
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INFORMATION FOR SEQ ID NO: 6:
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                            CLASSIFICATION: 530
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                           OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
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                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Hillman, Jennifer L. APPLICANT: Goli, Surya K.
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LIBRARY: GenBank
CLONE: 1216373
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LENGTH: 205 amino acid:
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                                                                                                                                                               APPLICATION NUMBER: US
FILING DATE: Herewith
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CITY: Palo Alto
STATE: CA
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TOPOLOGY: lir
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REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
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                                                                                                                                                                                                                                                                                                                                                                                                                             A NOVEL REGULATOR OF CELL SIGNALLING
                                                                                                                                                                               US/08/748,483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26; Mismatches
                               PF-0157 US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 155.5; DB 2
Pred. No. 7.2e-12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               205;
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US-08-748-483-1
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; CLONE: 1216373
US-08-748-483-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/08748483 Patent No. 5955314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 30.8
40; Conservative
                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/I
FILING DATE: Herewith
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                       NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 317.
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION: NAME: Billings, Lucy J.
                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Goli, Surya K.
TITLE OF INVENTION: A NOV
NUMBER OF SEQUENCES: 5
MMEDIATE SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             169 LKSRFYLDLV 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          114 LTSDIYLEYV 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116 ----NEFISVQ----ATKEVNLDSCTREETSRNMLEPTITCFDEAQKKIFNLMEKDSYRRF 168
               TOPOLOGY:
                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM CO.
OPERATING SYSTEM:
                                                                                                                  TELEX
                                                                                                                                TELEFAX: 415-845-4166
                                                                                                                                                                                                                                               FILING DATE:
                                                                LENGTH:
                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: INCLIDENCE OF STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 YIENNSVYSKQLKPATKTYIRDGIKKQQIGSVM-----FDQAQTEIQAVMEENAYQVF 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59 WAESLENLISHECGLAAFKAFLKSEYSEENIDFWISCEEYKKIK-SPSKLSPKAKKIY-- 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 WTKSLHSLLGDQDGAYLFRTFLEREKCVDTLDFWFACNGFRQMNLKDTKTLRVAKAIYKR 60
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                                                amino acid
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                                                          181 amino acids
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               linear
                                                                                                                                                                                                                                                                                                                                                                                           IBM Compatible
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RESULT 14
US-08-726-228-2
; Sequence 2, Application
; Patent No. 5846780
; PATENT INFORMATION:
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US-08-748-483-1
                                                                                                                             Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: LBUTA A. COTUZZI
REGISTRATION UNUBER: 30,742
REFERENCE/DOCKET NUMBER: 7853
TELECOMMUNICATION INFORMATION:
TELECHIONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,228
FILING DATE: 04-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS LENGTH: 201 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Levinson, Douglas A. APPLICANT: Gimeno, Carlos J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 EYV 123
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nes 36; Conserv
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ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: New York
STATE: New Yor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 YIENNSVVSKQLKPATKTYIRDGIKKQQIGSVMFDQAQTEIQAVMEENAYQVFLTSDIYL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 WRDSLDKLLQNNYGLASFKSFLKSEFSEENLEFWIACEDYKKIK-SPAKMAEKAKQIYEE 119
61 YIENNSV----VSKQLKPATKTYIRDGIKKQQIGSVMFDQAQTEIQAVMEENAYQVFLTS 116
                                                                                                                                                                                                                                        TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                      TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
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                                    WRESFOLLLNSKNGVAAFHAFLKTEFSEEALEFWLACEEFKKIR-SATKLASRAHHIFDE 119
                                                                     WTKSLHSLLGDQDGAYLFRTFLEREKCVDTLDFWFACNGFRQMNLKDTKTLRVAKAIYKR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New York
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                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pennie & Edmonds LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RATH GENES AND POLYPEPTIDES AND METHODS
FOR THE TREATMENT AND DIAGNOSIS OF IMMUNE DISORDERS
                                                                                                                             22.0%; Score 140.5; DB 2; 29.3%; Pred. No. 5.3e-10;
                                                                                                          23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25;
                                                                                                                                                                                                                                                                                                                                                                                                            7853-063
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Pred. No. 8.1e-12;
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                                                                                                              Mismatches
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                                                                                                            Indels 11;
                                                                                                                                               Length 201;
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                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Levinson, Douglas A.

APPLICANT: Gimeno, Carlos J.

TITLE OF INVENTION: RATH GENES AND POLYPEPTIDES AND METHODS

TITLE OF INVENTION: FOR THE TREATMENT AND DIAGNOSIS OF IMMUNE DISORDERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Laura A. COTUZZI
REGISTRATION NUMBER: 30,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           174 PAY 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 YIRSEAPKEVNIDHETRELIKTNL-----QAATTSCFDVAQGKTRTLMEKDSYPRELKS 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117 DIY 119
174 PAY 176
                                117 DIY 119
                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/0 FILING DATE: 06-JUN-1997 CLASSIFICATION: 435
                                                                                              61 YIENNSY----VSKQLKPATKTYIRDGIKKQQIGSVMFDQAQTEIQAVMEENAYQVFLTS 116
                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX:
                                                                                                                                  61 WRESFDLLLNSKNGVAAFHAFLKTEFSEEALEFWLACEEFKKIR-SATKLASRAHHIFDE 119
                                                                                                                                                                1 WTKSLHSLIGDQDGAYLFRTFLEREKCVDTLDFWFACNGFRQMNLKDTKTLRVAKAIYKR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                              212) 790-9090
(212) 896-8864/9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                            linear
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                                                                                                                                                                                                                        22.0%;
29.3%;
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                                                                                                                                                                                                                        Score 140.5; DB 3
Pred. No. 5.3e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7853-074
                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                          DB 3;
                                                                                                                                                                                                                                        Length 201;
                                                                                                                                                                                                        Indels
                                                                                                                                                                                                        11;
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Search completed: June 7, 2001, 02:02:09 Job time: 5402 sec

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd

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Result
No.
                                                                                                                                                                                                                                                                                                                                                           Database
                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB
Maximum DB
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                         407
172.5
167.5
160
158.5
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143.5.5
143.5.5
133
133
133
134.5
121.5
121.5
121.5
111.5
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1112.5
107.6
97.5
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JC5502
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11.0	11.0	11.0	11.0	11.0	11.0	11.0	11.0	11.1	11.2	11.2	11.2	11.3	11.3	11.4	11.4
190	1607	949	798	785	421	413	268	157	1305	1131	190	431	382	1291	1276
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translation elonga	hypothetical prote	isoleucyl-tRNA syn	hypothetical prote	cullin 3 homolog -	cullin-3 - fission	MG349 homolog G12_	cymJ protein - Kle	MHC class I protei	DNA-directed RNA p	major DNA binding	probable translati	hypothetical prote	myosin-like protei	probable tail-host	probable tail-host

### ALIGNMENTS

Axin homolog Axil - rat

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N;Alternate names: Axil
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jul-2000
C;Accession: T08423
R;Yanamoto, H.; Kishida, S.; Uochi, T.; Ikeda, S.; Koyama, S.; Asashima, M.; Kikuchi, R;Yanamoto, H.; Kishida, S.; Uochi, T.; Ikeda, S.; Koyama, S.; Asashima, M.; Kikuchi, Mol. Cell. Biol. 18, 2867-2875, 1998
A;Title: Axil, a member of the Axin family, interacts with both glycogen synthase kin A;Reference number: Z16414; MUID:98226558
A;Title: Axil, a member of the Axin family, interacts with both glycogen synthase kin A;Reference number: Z16414; MUID:98226558
A;Cccssion: T08423
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Ccoss: preliminary; translated from GB/EMBL/DDBJ
A;Cross: references: EMBL;AF017757; NID:g3080758; PIDN:AAC40089.1; PID:g3080759
A;Note: interacts with GSK-3beta and beta-catenin
C;Keywords: phosphoprotein; signal transduction
                                                                    negative regualtor axin [imported] - rat
N;Alternate names: rAxin
C;Species: Rattus norvegicus (Norway rat)
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jul-2000
C;Accession: T08422
R;Ikeda, S.; Yamamoto, H.; Murai, H.; Kishida, S.; Kikuchi, A.
EMBO J. 17, 1371-1384, 1998
A;Title: Axin, a negative regulator of the Wnt signaling pathway, forms a cc
A;Reference number: Z16413; MUID:98151361
A;Accession: T08422
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T08422
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A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: mRNAA;Residues: 1-832 <IKE>
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Local Similarity 100.0%;
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Pred. No. 7.6e-53;
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G-0/G-1 switch regulatory protein 8 - human N;Alternate names: helix-loop-helix phosphoprotein; C;Species: Homo sapiens (man) C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #C;Accession: I53020; I65984 R;Siderovski, D.P.; Heximer, S.P.; Forsdyke, D.R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:U27655; NID:g1216368; PID:g1216369 R;Druey, K.M.; Blumer, K.J.; Kang, V.H.; Kehrl, J.H. Nature 379, 742-746, 1996 A;Title: Inhibition of G-protein-mediated MAP kinase activa: A;Reference number: A58012; MUID:96178495 A;Accession: S68436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-519 < DRU>
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C;Species: Homo sapiens (man)
C;Date: 04-Dec-1997 #sequence_revision 12-
C;Accession: S78089; S68436
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; S68436
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Pred. No. 8.2e-09;
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Pred. No. 7.8e-31;
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                               #text_change 29-Sep-1999
                                                             regulator of G-protein signaling
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hypothetical protein F56B6.2 - C; Species: Caenorhabditis elega

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A;Accession: S71812
A;Status: preliminary; nucleic acid sequence not shown;
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A; Residues: 1-173 <HUN>
C; Superfamily: B-cell activation
                                                                                                                                                                                                                                                                                                                        A; Title: RGS10 is a selective activator of Galpha(i) GTPase activity A; Reference number: S71812; MUID:96371048
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                                                                                                                                                                                                                                                                                                                                                                                                           C; Accession: S718
                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Homo sapiens (man)
C;Date: 14-Apr-1998 #sequence_revision 24-Apr-1998 #text_change 17-Mar-1999
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A:Introns: 37/2; 71/2; 92/1; 147/3
C:Superfamily: B-cell activation protein BL34
C:Keywords: phosphoprotein
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A;Cross-references: GDB:355647; OMIM:600861
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A;Accession: I65984
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A; Reference number:
A; Accession: I53020
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A;Title: A human gene encoding a putative basic helix-loop-helix phosphoprotein whose A;Reference number: I53020; MUID:94235158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: GB:L13463;
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A; Residues: 1-211 < RES>
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                                          WAASLENLLEDPEGVKRFREFLKKEFSEENVLFWLACEDFKKMQDK-TQMQEKAKEIYMT
YIENNSVVSKQLKPATKTYIRDGIKKQQIGSVMFDQAQTEIQAVMEENAYQVFLTSDIYL 120
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                                                                                                                        39; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        translated from GB/EMBL/DDBJ
                                                                                                                                             25.0%;
32.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26.2%;
32.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NID:g292054; PIDN:AAC37587.1;
                                                                                                                          30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20;
                                                                                                                                                                                                                           protein BL34
                                                                                                                                           Score 160; DB 2; Pred. No. 3.7e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 167.5; DB Pred. No. 9e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                          Mismatches
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C.Species: Homo Sapiens (man)
C.Species: Homo Sapiens (man)
C.Species: Homo Sapiens
C.Species: Homo Sa
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A;Experimental source: strain Bristol N2
C;Genetics:
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                                                                                                                                                                                                                                                                             A;Gene: GDB:RGS1; IER1; 1R20; IR20; BL34
A;Cross-references: GDB:439178; OMIM:600323
A;Map position: 1q31-1q31
C;Superfamily: B-cell activation protein BL34
C;Keywords: B-cell; phosphoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-180,'D',182-196 <HON>
A;Cross-references: GB:S59049; NID:g299704; PIDN:AAB26289.1; PID:g299705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: Isolation and characterization of a novel B cell activation A;Reference number: I56165; MUID:93232596 A;Accession: I56165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:X73427; NID:g313214; PIDN:CAA51826.1; R;Hong, J.X.; Wilson, G.L.; Fox, C.H.; Kehrl, J.H. J. Immunol. 150, 3895-3904, 1993
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A; Introns: 39/3; 235/2; 259/2; 322/3; 360/2; 405/1; 461/3; 503/2
A; Note: F5686.2
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A; Residues: 1-533 <STE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: 220957
A; Accession: T31002
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A;Description: The sequence of C. elegans cosmid F5686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Accession: T31002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-196 < NEW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N; Alternate names: B-cell activation protein 1r20; regulator of G-protein signaling 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary; translated from GB/EMBL/DDB.
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                                                                                                         Query Match
Best Local S
Matches 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 24.8
Best Local Similarity 30.7
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cell activation protein BL34 - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 29-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               115 TSDIYLE 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 451 SEFVAEHSPKEVNLDSDTRAATKAAVEAGCKPD----TFALAQSRVEQLMSKDSYRRFL 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59
WTKSLHSLLGDQDGAYLFRTFLEREKCVDTLDFWFACNGFR--QMNLKDTKTLRVAKAIY 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HILLIANKEGCALERGELKKEESDENMDEWLECEEFKKM--KDGKKSTTQKAIEIY 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WTKSLHSLLGDQDGAYLFRTFLEREKCVDTLDFWFACNGFRQMNLKDTKTLRVAKA--IY 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RDRLFLD 512
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                                                                                                                                          Similarity
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                                                                                                      24.7%; Score 158; DE 32.0%; Pred. No. 6.66 32.0%; Mismatches
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                                                                                                         3; DB 2; 1
. 6.6e-08;
cches 47;
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                                                                                                                                                                           Length 196
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                                                                                                             80
                                                                                                      Gaps
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Db
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RESULT 9
JC7228
G-protein signaling regulator 5 homolog - clawed frog
G-protein signaling regulator 5 homolog - clawed frog
G:Species: Xenopus sp. (clawed frog)
C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 21-Jul-2000
C:Accession: JC7228; PC7066
R:Saitch, O.; Odagiri, M.; Masuho, I.; Nomoto, S.; Kinoshita, N.
Biochem. Biophys. Res. Commun. 270, 34-39, 2000
Piochem. Biophys. Res. Commun. 270, 34-39, 2000
Note: Molecular cloning and characterization of Xenopus RGS5.
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Colecule 
                                                                                                                                                                                                 A;Title: Molécular cloning
A;Reference number: JC7228
A;Accession: JC7228
A;Molecule type: mRNA
A;Residues: 1-181 <SAI>
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578221

G-protein signaling regulator RGP4 - human

G-protein signaling regulator RGS4

N;Alternate names: G-protein signaling regulator RGS4

C;Species: Homo sapiens (man)

C;Date: 29-Jan-1998 #sequence_revision 13-Feb-1998 #t
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A;Title: Inhibition of G-protein-mediated A;Reference number: A58012; MUID:96178495
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A; Residues: 1-205 <DRU>
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A; Molecule type: protein A; Residues: 88-168 <SA2>
                                                                                                A;Cross-references: DDBJ:AB038436
A;Accession: PC7066
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R;Druey, K.M.; Blumer, K.J.; Kang, V.H.; Kehrl, J.H.
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 YL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----NEFISVQ---ATKEVNLDSCTREETSRNMLEPTITCFDEAQKKIFNLMEKDSYRRF 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YIENNSYVSKOLKPATKTYIRDGIKKQQIGSVM-----FDQAQTEIQAVMEENAYQVF 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MAP kinase activation
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source: embryo

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C;Comment: This protein has function as a genesis and cell differentiation. C;Superfamily: B-cell activation protein C;Keywords: differentiation; embryo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-284 <FAV>
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A; Introns: 43/1; 198/2
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R:Snow, B.E.; Antonio, L.; Suggs, S.; Gutstein, H.B.; Siderovski, D.P. Biochem. Biophys. Res. Commun. 233, 770-777, 1997
A:Title: Molecular cloning and expression analysis of rat Rgs12 and Rg A:Reference number: JC5502; MUID:97312490
A;Accession: JC5503
A;Molecule type: mRNA
                                                                                            G-protein signaling regulator 14 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 05-Nov-1999
C:Accession: JC5503
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| WRDSLEKLLENSYGLSVFQSFLKSEFSEENIEFWMACEDYKKAKSPSKMTTK-AKKIYEE 119
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Pred. No. 1.4
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Pred. No.
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A;Residues: 1-544 <SNO>
A;Residues: 1-544 <SNO>
A;Cross-references: GB:U92279; NID:92088555; PIDN:AAC53175.1; PID:92088556
C;Comment: This protein functions as GTPase activating protein.
F;64-113/Domain: GH1 #status predicted <GH1>
F;117-152/Domain: GH2 #status predicted <GH2>
F;117-152/Domain: GH3 #status predicted <GH3>
F;514-534/Region: conserved #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R; Kershaw, J.
submitted to the EMBL Data Library,
A; Reference number: Z19427
A; Accession: T21468
A; Accession: T21468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein F28C1.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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A; Residues: 1-558 <WIL>
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A; Introns: 7/2; 76/1; 129/1; 176/2; 313/2; 364/2;
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A;Experimental source: clone F28C1
RESULT 13
T21034
T21034
Appothetical protein F16H9.la - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #tes
C;Accession: T21034; T21270
R;Gardner, A.
submitted to the EMBL Data Library, July 1995
A;Reference number: 219363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: CESP: F28C1.2
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Matches 34
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29.6%;
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Pred. No. 9.4e-05;
23; Mismatches 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 124.5; DB 2;
Pred. No. 0.00032;
Pred. No. 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        June
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                             15-Oct-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     409/2; 515/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSPDB:GN00023; CESP:F28C1.2
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A;Map position: X
A;Introns: 16/2; 31/2; 52/1; 91/3
C;Superfamily: B-cell activation protein BL34
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submitted to the EMBL Data Library, November 1995
A;Reference number: 219398
A;Accession: T21270
                                                                                                                                                                                       A;Map position: X
A;Introns: 28/2; 43/2; 64/1; 103/3
C;Superfamily: B-cell activation protein BL34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jul-2000
C;Accession: T21035; T21272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Accession: T21034
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-169 <WIL>
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                                                                                                                                                                                                                                                                                                 A; Experimental source: clone C; Genetics:
                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-181 <WIZ>
A;Cross-references: EMBL:Z67882; PIDN:CAB54230.1; GSPDB:GN00028; CESP:F16H9.1b
                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: A; Accession: T21272
                                                                                                                                                                                                                                                                                                                                                                                                                                                              submitted to the EMBL Data Library, November 1995
A; Reference number: Z19398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:Z50005; PIDN:CAB54219.1; GSPDB:GN00028; CESP:F16H9.1b
A;Experimental source: clone F16H9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: Z19363
A; Accession: T21035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data Library, July 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein F16H9.1b - Caenorhabditis elegans
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A;Residues: 1-169 <WI2>
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                                                                                                              Query Match
Best Local :
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                                                                                      Match 19.0%; Score 121.5; DB (Local Similarity 27.5%; Pred. No. 0.00018) Nes 33; Conservative 25; Mismatches 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 WTKSLHSLLGDQDGAYLFRTFLEREKCVDTLDFWFACNGF-RQMNLKDTKTLRVAKAIYK 59
                                                                                                                                                                                                                                                                           CESP: F16H9.1b
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                                      WTKSLHSLLGDQDGAYLFRTFLEREKCVDTLDFWFACNGF-RQMNLKDTKTLRVAKAIYK 59
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27.5%;
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                                                                                                                                  DB 2;
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WSQSFENLMKHRAGQKYFAEFLKGEYSDENILFWQACEELKREKNAE--KIEEKARIIYE 109

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C;Accession: JC5502
C;Accession: JC5502
R;Snow, B.E.; Antonio, L.; Suggs, S.; Gutstein, H.B.; Siderovski, R;Snow, B.E.; Antonio, L.; Suggs, S.; Gutstein, H.B.; Siderovski, R;Snow, Biophys. Res. Commun. 233; 770-777, 1997
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JC5502
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A; Residues: 1-1387 <SNO>
A; Cross-references: GB:U92280; NID:g2088557; PIDN:AAC53176.1; PID:g2088558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochem. Biophys. Res. Commun. 233; 770-777, 1997
A;Title: Molecular cloning and expression analysis of rat Rgs12 and Rgs14.
A;Reference number: JC5502; MUID:97312490
A;Accession: JC5502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G-protein signaling regulator 12 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 05-Nov-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Comment: This protein funcitons as GTPase activating F;18-80/Domain: rhophilin-like #status predicted <RHO>
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                        712 WAVSFERLLQDPVGVRYFSDFLRKEFSEENILFWQACECFSHVPAHDKKELSYRAREIFS 771
                                                                                                                              826 QLYQECV 832
                                                                                                                                                                                 117 DIYLEYV 123
                                                                                                                                                                                                                                    772 KFL----CSKATTPVNIDSQAQLADDILNAPHPD-MFKEQQLQIFNLMKFDSYTRFLKS
                                                                                                                                                                                                                                                                                     60 RYIENNSVVSKQLKPA---TKTYIRDGIKKQQIGSVMFDQAQTEIQAVMEENAYQVFLTS 116
                                                                                                                                                                                                                                                                                                                                                                                           1 WTKSLHSLLGDQDGAYLFRTFLEREKCVDTLDFWFACNGFRQMNLKDTKTLRV-AKAIYK 59
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                        June
                        7,
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                        2001, 02:03:20
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Title:
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                                                                                              US-09-587-574-2
639
1 WTKSLHSLLGDQDGAYLFRT.....VMEENAYQVFLTSDIYLEYV 123
93435 seqs, 34255486 residues
                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                             GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

93435

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

33 33 33	22 22 23 24 25 26	20 20 20	Result
139.5 136.5 136.5 133	149.55	639 639 620 560 420,5 407 407 407 401 1172.5 1167.5 1167.5 1168.5 1158.5 1158.5 1159.5	Score
00111		100.0 100.0 87.6 65.8 65.7 63.7 63.7 63.7 63.7 63.7 63.7 63.7 63	Query Match I
217 159 202 284	180 205 199 181 181 201	833 8440 8812 8812 8812 8812 8812 8812 8812 881	Length
			DB
GAIP_HUMAN RGSD_HUMAN RGSG_HUMAN YTN3_CAEEL RGSE_RAT	RGSB_RAT RGS4_MOUSE RGSG_RAT RGSG_RAT RGS5_MOUSE RGS5_MOUSE RGS5_MOUSE GAIP RAT	AXN2_RAT AXN2_HOMAN AXN2_HOMAN AXN2_BRARE AXN1_ERAFE AXN1_ERAFE AXN1_RAT AXN1_HOUSE AXN1_HOMAN RGS2_HOMAN RGS4_HOMAN RGS4_RAT RGS4_RAT RGS4_RAT	ID
homo sa homo sa homo sa caenorl	rattu mus m bos t rattu mus m rattu rattu	240 rattus no 2566 mus muscu 251 homo sapi 095 brachydan 094 brachydan 094 brachydan 097 rattus no 625 mus muscu 400 gallus sapi 1796 homo sapi 1797 prattus no 1797 rattus no 1799 rattus no	Description

130 20.3 547 1 KGSE_MOUSE 124.5 19.5 555 1 EGIO_CABELI 121.5 19.0 169 1 YUE1_CABELI 118 18.5 467 1 RGSB_HUMAN 118 18.5 675 1 RGS9_RAT 118 18.5 677 1 RGS9_RAT 117 18.3 484 1 RGS9_BOVIN 116.5 18.2 374 1 RGS9_HUMAN 115 18.0 1387 1 RGSC_RAT 115 18.0 1447 1 RGSC_RAT	19.0 169 1 19.0 169 1 18.5 675 1 18.5 677 1 18.5 677 1 18.3 484 1 18.3 374 1 18.0 1387 1 16.8 254 1	45	44	43	42	41	40	39	38	37	36	3 5	34
5547 169 1 467 1 675 1 677 1 484 1 374 1 1374 1 254 1	557 1 EG10_CAREL P49809 169 1 YUE1_CAREL P49809 169 1 YUE1_CAREL P49808 467 1 RGSB_HUMAN O94810 675 1 RGSS_RAT O46869 677 1 RGSS_RAT O46869 484 1 RGSS_BOVIN P79348 674 1 RGSS_HOVIN P79348 1674 1 RGSS_HOVIN O75916 1785 1 RGSS_HOWAN O75916 1785 1 RGSS_HOWAN O75916 1785 1 RGSS_HOWAN O97914 1785 1 R	107.5	115	115	115	116.5	117	118	118	118	121.5	124.5	130
	1 KGSE_MOUSE P4949819 1 EG10_CAREEL P49809 1 YUE1_CAREEL P49808 1 KGSB_HUMAN O94810 1 RGSB_HOWAN O94810 1 RGSB_RAT P49805 1 RGSB_BOVIN P39488 1 RGSB_BOVIN P39488 1 RGSB_HUMAN O75916 1 RGSC_RAT O75916 1 RGSC_RAT O74924 1 RGSC_HUMAN O08774 1 RGSC_HUMAN O0874 1 RGSC_HUMAN P3495	16.8	18.0	18.0	18.0	18.2	18.3	18.5	18.5	18.5	19.0	19.5	20.3
I KGSE_MOUSE I EGG10_CARELI I YUE1_CAEEL I YUE1_CAEEL I RGSB_HUMAN I RGS9_RAT I RGS9_BOVIN I RGS9_BOVIN I RGS9_HUMAN I RGSC_HUMAN I RGSC_HUMAN I YKO7_CAEEL	P9/49809 P49809 P49808 O94810 O54828 P49805 O46469 P793489 P79316 O08774 O14924 P34995	254	1447	1387	674	374	484	677	675	467	169	555	547
EGIO_CAEEL YUE1_CAEEL	P494899 P49809 P49808 O94810 O54828 P49805 O46469 P79348 P79348 O75916 O08774 O14924 P34995	щ	<u>,                                    </u>	$\vdash$	<u>, , , , , , , , , , , , , , , , , , , </u>	_	-	1	L	$\vdash$	٢	Н	۰
		YKO7_CAEEL	RGSC_HUMAN	RGSC_RAT	RGS9_HUMAN	RGSX_BOVIN	RGS9_BOVIN	RGS9_RAT	RGS9_MOUSE	RGSB_HUMAN	YUE1_CAEEL	EG10_CAEEL	KGSE_MOUSE

# ALIGNMENTS

FT COR	8888888888	24888888888888	R R R R R R R R R R R R R R R R R R R	RESULT AXN2_R ID AC O DT O DT O DT O DE A DE A
AP017757; AAC40089.1; P49799; lAGR. P49799; lAGR. P7000342; P7001158; P700615; RGS; 1. PF00778; DIX; 1. PF00778; DIX; 1. PF00778; DIX; 1. Opmental protein; Phosphorylation. N 81 200 RGS. N 327 413 GSK-3B BINDING SITE (BY SIMILARITY N)	ARITY: CONTAINS 1 RGS DOMAIN.  ARITY: CONTAINS 1 DIX DOMAIN.  S-PROT entry is copyright. It is produced through a c the Swiss Institute of Bioinformatics and the EMBL bean Bioinformatics Institute. There are no restrict non-profit institutions as long as its content is and this statement is not removed. Usage by and fo requires a license agreement (See http://www.isb-sib.n email to license@isb-sib.ch).	MAI. Cell. Biol. 18:2867-2875(1998).  MAI. CELL. BIOL. 18:2867-2875(1998).  -!- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES BETA-CATENIN. PROBABLY FACTILITATE THE PHOSPHORYLATION OF BETA-CATENIN AND APC BY GSK-3B (BY SIMILARITY).  -!- SUBURIT: INTERACTS WITH GLYCOGEN SYNTHASE KINASE-3 BETA (GSK-3B) AND BETA-CATENIN THE INTERACTION BETWEEN AXIN AND BETA-CATENIN OCCURS VIA THE ARMADILLO REPEATS CONTAINED IN BETA-CATENIN.  -!- SUBCELLULAR LOCATION: CYTOPLASMIC.  -!- SUBCELLULAR LOCATION: CYTOPLASMIC.  -!- TISSUE SPECIFICITY: EXPRESSED IN LUNG AND THYMUS.  -!- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY PP2A.	ta; Metaia; Metaia; Euthera; Euthera; ErROM N Brain; =98226555 H., Kiu A.; a member shrungs	1 XN2_RAT STA 70240; 1-OCT-2000 (Rel. 1-OCT-2000 (Rel. 1-OCT-2000 (Rel. 1-OCT-2000 (Rel. XIN 2 (AXIS INHIB AXIL).

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RESULT 2
AXNO_MANOSE
ID AXNOZE
ID 01-OCT
01-OCT
DT 01-OCT
DT 01-OCT
DE AXIN2
OC EUARIY
OC IT CATENIA
RI SCIENC
RP SEQUEN
RA Jenkin
RT CATENIA
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OB8566; Q9QXJ6;
01-OCT-2000 (Rel. 4
01-OCT-2000 (Rel. 4
01-OCT-2000 (Rel. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Behrens J., Jerchow B.-A., Wuertele M., Grimm J., Wirtz R., Kuehl M., Wedlich D., Birchmeier W.; "Functional interaction of an axin homolog, conducatenin, APC, and GSK3beta."; Science 280:596-599(1998).
                                                 This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
       entities
                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN
BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zhang T., Fagotto F., Hsu W., Zeng L., Gilbert D., Cope. Jenkins N.A., Marburton D., Costantini F.; Properties of mouse Axin2 and human AXIN2: chromosomal expression pattern, interaction with Axin and effects of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AXIN 2 (AXIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-98221239; PubMed-9554852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                               CATENIN AND APC BY GSK-3B (BY SIMILARITY).

-I- SUBUNIT: INTERACTS WITH GLYCOGEN SYNTHASE AND AND BETA-CATENIN. THE INTERACTION BETWEEN AXIN AND BET OCCURS VIA THE ARMADILLO REPEATS CONTAINED IN BETA-CAT TERNARY COMPLEX (BY SIMILARITY).

-I- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).

-I- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORY PP2A (BY SIMILARITY).

-I- SIMILARITY: CONTAINS 1 RGS DOMAIN.
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    pean Bioinformatics Institute. The non-profit institutions as long a and this statement is not removed. requires a license agreement (See )
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(Rel. 40, Last annotation update)
INHIBITION PROTEIN 2) (CONDUCTIN)
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Pred. No. 8.1e-53
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                             Usage
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AXIN AND BETA-CATENIN
) IN BETA-CATENIN.
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Q9Y271; Q9UH84;
01-OCT-2000 (Rel. 40, Created)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
AXIN 2 (AXIS INHIBITION PROTEIN 2) (CONDUCTIN)
                                                                                                                                                     Mai M., Qian C., Yokomizo A., "Cloning of the human homolog chromosome 17q23-q24."; Genomics 55:341-344(1999).
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                  expression pattern, interaction with Axin
                                    SEQUENCE FROM N.A.
TISSUE-Brain, and Lymphoblast;
Zhang T., Fagotto F., Hsu W., Zeng L., Gilbert D., Copeland N.G.,
Jenkins N.A., Warburton D., Costantini F.;
"Properties of mouse Axin2 and human AXIN2: chromosomal location,
                                                                                                                                                                                                                                                                                                                                  Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                          AXIN2
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                                                                                                                                                                                                                                    MEDLINE=99168905;
                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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BETA-CATENIN BINDING SITE (BY
SIMILARITY).
POLY-HIS.
DIX.
R -> K (IN REF. 2).
H -> Y (IN REF. 2).
S -> P (IN REF. 2).
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G -> A (IN REF. 2).
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Pred. No. 8.2
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                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata;
Catarrhini; Hominidae
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5 -> P (IN REF. 2).
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5 -> S (IN REF. 2).
6 -> A (IN REF. 2).
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No. 8.2e-53;
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                        and
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RESULT 4
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ID AXN2_B
AC P57095
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Best Local
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                     AXN2_BRARE
P57095;
01-OCT-2000
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Developmental protein; Phosphorylation.
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InterPro; IPR001158; -.
Pfam; PF00615; RGS; 1.
Pfam; PF00778; DIX; 1.
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EMBL; AF205888; AAF22799.1;
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SUBUNIT: INTERACTS WITH GLYCOGEN SYNTHASE KINASE-3 BETA (GSK-3B)
AND BETA-CATENIN. THE INTERACTION BETWEEN AXIN AND BETA-CATENIN
OCCURS VIA THE ARMADILLO REPEATS CONTAINED IN BETA-CATENIN.
TERNARY COMPLEX (BY SIMILARITY).
SUBCELLULAR LOCATION: CYTOPLASMIC.
TISSUE SPECIFICITY: EXPRESSED IN BRAIN AND LYMPHOBLAST.
PYM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: CONTAINS 1 RGS DOMAIN. SIMILARITY: CONTAINS 1 DIX DOMAIN.
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761
37
(Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation updats
s INHIBITION PROTEIN 2).
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MISSING
P -> S (
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BETA-CATENIN BINDING SITE (BY
SIMILARITY).
POLY-HIS.
DIX.
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Pred. No. 2.1e-51;
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Q -> R (IN REF. 2).
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H (IN REF. 2).
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  RESULT 5
AXN1_BRARE
ID AXN1_B
AC P57094
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Query Match
Best Local Similarity
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Rasborinae; Danio.
AXN1_BRARE STANDARD; PRT; 8
p57094;
01-OCT-2000 (Rel. 40, Created)
01-OCT-2000 (Rel. 40, Last sequence up
01-OCT-2000 (Rel. 40, Last annotation
AXIN 1 (AXIS INHIBITION PROTEIN 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Pfam; PF00778; DIX; 1.
PROSITE; PS50132; RGS;
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HSSP; P49799; 1AGR.
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InterPro; IPR001158; -.
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BETA-CATENIN BIN
SIMILARITY).
POLY-SER.
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Pred. No. 2.2e-45;
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BINDING SITE (BY
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01-0CT-2000 (Rel. 40, I
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AXIN OR AXN.
                                                                                               XENLA
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Cooperative roles of Bozozok/Dharma and Nodal-related proteins in the formation of the dorsal organizer in zebrafish.";

Mech. Dev. 91:293-303(200).

-I- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-CATENIN AND APC BY GSK-3B (BY SIMILARITY).

-I- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).

-I- PIM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi
Cypriniformes; Cyprinidae; Rasborinae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AB032262; HSSP; P49799; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shimizu
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50132; RGS; Developmental protein;
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SIMILARITY: CONTAINS 1 RGS DOMAIN.
SIMILARITY: CONTAINS 1 DIX DOMAIN.
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                                                                                                                                                                             IYLEY 122
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Hirano T.
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Phosphorylation.
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GSK-3B BINDING :
BETA-CATENIN BII
SIMILARITY).
DIX.
                                                                                                                                                                                                                                                                                                               Score 420.5; DB Pred. No. 3.2e-320; Mismatches 2
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BINDING SITE (BY
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A Hedgepeth C.M., Deardorff M.A., Klein P.S.;

A Hedgepeth C.M., Deardorff M.A., Klein P.S.;

Yenopus axin interacts with glycogen synthase kinase-3 beta and remain and the anterior midbrain.";

T expressed in the anterior midbrain.";

Mech. Dev. 80:147-151(1999).

C -!- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULA C. -!- FUNCTION. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA CATENIN AND APC BY GSK-3B (BY SIMILARITY).

C -!- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).

C -!- FUNCTION: CYTOPLASMI
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Best Local
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TANI_RAT STANDARD 070239; 01-0CT-2000 (Rel. 40, C 01-0CT-2000 (Rel. 40, L 01-0CT-2000 (Rel. 40, L AXIN 1 PROTEIN (AXIS IN
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SEQUENCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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pfam; pF00778; DIX; 1.
pROSITE; pS50132; RGS; 1.
Developmental protein; Phosphorylation.
Developmental protein; Phosphorylation.
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DOMAIN 88 2
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HSSP; P49799; 1AGR
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SIMILARITY: CONTAINS 1 RGS DOMAIN.
SIMILARITY: CONTAINS 1 DIX DOMAIN.
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INHIBITION PROTEIN 1) (R
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Pred. No. 3.6e-32;
5; Mismatches 20;
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BETA-CATENIN BINDING SITE (BY
SIMILARITY).
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RA Ikeda S., Kishida S., Yamamoto H., Murai H., Koyama S., Kikuchi A.;
RT "AXIn, a negative regulator of the Wnt signaling pathway, forms a
rt complex with GSK-3beta and beta-catenin and promotes GSK-3beta-
rt dependent.phosphorylation of beta-catenin.";
RL EMBO J. 17:1371-1384(1998).

C. I- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
RETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
C. CATENIN AND APC BY GSK-3B (BY SIMILARITY).
C. CATENIN AND APC BY GSK-3B AND BETA-CATENIN. THE INTERACTION
RETWEEN AXIN AND BETA-CATENIN OCCURS VIA THE ARMADILLO REPEATS
C. CONTAINED IN BETA-CATENIN. TERNARY COMPLEX. ALSO BINDS TO
PLAKOGLOBIN (GAMMA-CATENIN). APC, DUL AND PP2A (BY SIMILARITY).
C. TISSUE SPECIFICITY: HIGHLY EXPRESSED IN TESTIS, THYMUS AND LUNG
FOLLOWED BY CEREBRUM, CEREBELLUM, HEART, KIDNEY, SKELETAL MUSCLE,
SPLEEN AND LIVER.
C. PART DE STATE OF THE STATE OF THE SPLEEN AND LUNG
SPLEEN AND LIVER.
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Best Local Similarity
Matches 78; Conserv
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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SIMILARITY: CONTAINS 1 RGS DOMAIN.
SIMILARITY: CONTAINS 1 DIX DOMAIN.
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                                                                       DIYLEY 276
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Pred. No. 6.4e-31;
1; Mismatches 23
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GSK-3B BINDING SITE.
BETA-CATENIN BINDING
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214 WAESLHSLLDDQDGISLFRTFLKQEGCADLLDFWFACSGFRKLEPCDSNEEKRLKLARAI 58 YKRYI-ENNSVYSKQLKPATKTYIRDGIKKQQIGSVMFDQAQTEIQAVMEENAYQVFLTS 116

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01-OCT-2000 (Rel. 40, Created)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
AXIN 1 (AXIS INHIBITION PROTEIN 1) (FUSED PROTEIN) (FRAGMENT)
AXIN 1 (AXIS INHIBITION PROTEIN 1) (FUSED PROTEIN)
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SEQUENCE
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DOMAIN
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Pfam; PF00778; DIX; 1.
PROSITE; PS50132; RGS; 1.
PROSITE; protein; Phosphorylation; Alternative splicing.
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InterPro; IPR000342; -.
InterPro; IPR001158; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zeng L., Fagotto F., Zhang T., Hsu W., Vasicek T.J., Perry W.L. III,
Lee J.J., Tilghman S.M., Gumbiner B.M., Costantini F.;
"The mouse Fused locus encodes Axin, an inhibitor of the Wnt signaling
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- FUNCTION: INHIBITOR OF THE WIT SIGNALING PATHWAY. DOWN REGULATES BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090
                                                                                                                                                                                                                                                                                                                                       Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                      DOMAIN
1 WTKSLHSLLGDQDGAYLFRTFLEREKCVDTLDFWFACNGFRQMNLKDT---KTLRVAKAI 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BETWEEN AXIN AND BETA-CATENIN OCCURS VIA THE ARMADILLO REPEATS CONTAINED IN BETA-CATENIN. TERNARY COMPLEX. ALSO BINDS TO PLAKOGLOBIN (GAMMA-CATENIN), APC, DVL AND PP2A (BY SIMILARITY). SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY). ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE PRODUCED BY ALTERNATIVE SPLICING. PRODUCED BY ALTERNATIVE SPLICING. TISSUE SPECIFICITY: EXPRESSED IN EMBRYONIC STEM CELLS. DEVELOPMENTAL STAGE: WIDELY EXPRESSED AT E10.5 TO E16.5 DAY. PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: CONTAINS 1 RGS DOMAIN. SIMILARITY: CONTAINS 1 DIX DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATENIN AND APC BY GSK-3B (BY SIMILARITY).
SUBUNIT: INTERACTS WITH GSK-3B AND BETA-CATENIN. THE INTERACTION
                                                                                                                                                                                                                                                                                                                                       PF00615; RGS; 1.
                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the Swiss Institute of Bioinformatics and the EMBL outstation
                                                   Conservative
                                                                                                                                   3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                           AAC53285.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=9230313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ISOFORMS 1 AND
                                                                                                                                   895
109917
                                                                                                                                                                                                     18
340
561
630
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Rodentia;
                                                                 63.7%;
                                                   21;
                                                                                                                                   ¥.
                                                   Score 407; DB 1; 1
Pred. No. 7.2e-31;
1; Mismatches 23;
                                                                                                                                                                                 GSK-3B BINDING SITE (BY SIMILARITY).
BETA-CATENIN BINDING SITE (BY
SIMILARITY).
                                                                                                                                   MISSING (IN ISOFORM 2).
N; 70EEB53D387BD26F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                992
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                                                                                                    Query Match
Best Local S
Matches 77
                                                                                                                                                                                                                                    DOMAIN
SEQUENCE
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01-OCT-2000 (Rel. 40, Last sequence up
01-OCT-2000 (Rel. 40, Last annotation
AXIN (AXIS INHIBITION PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00615; RGS; 1.
Pfam; PF00778; DIX; 1.
PROSITE; PS50132; RGS; 1.
Developmental protein; Phosphorylation.
Developmental Protein; RGS.
DOMAIN 88 211 RGS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zeng L., Fagotto F., Zhang T., Hsu W., Vasicek T.J., Perry W.L. III, Lee J.J., Tilghman S.M., Gumbiner B.M., Costantini F.; "The mouse Fused locus encodes Axin, an inhibitor of the Wnt signaling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Embryo;
MEDLINE-97373830; PubMed-9230313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Archosauria; Aves; Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AXIN OR AXN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     042400;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P49799;
                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000342; -. InterPro; IPR001158; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             334 DIYLEY 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117
  85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PP2A (BY SIMILARITY).
SIMILARITY: CONTAINS 1 RGS DOMAIN.
SIMILARITY: CONTAINS 1 DIX DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGUL BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BET CATENIN APC BY GSK-3B (BY SIMILARITY).

SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).

DEVELOPMENTAL STAGE: EXPRESSED AT STAGE 12 TO 15.

PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DIYLEY 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  way that regulates embryonic axis formation."; 90:181-192(1997).
  WAESLHSLIDDQDGINLFRTFLKQEDCADLLDFWFACSGFRKLEPCVSNEEKRLKLAKAI 144
                             WTKSLHSLLGDQDGAYLFRTFLEREKCVDTLDFWFACNGFRQNN---LKDTKTLRVAKAI 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AF009012;
                                                                                                    , Similarity 61.77; Conservative
                                                                                                                                                                                                                                    759
841 i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LAGR
                                                                                                                                                                                                                                      AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAC60245.1;
                                                                                                                                                                                                                                         841
94931
                                                                                                                                                                                                                                                                                                                     433
508
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                                                                                                                               63.5%;
                                                                                                                                                                                                                                         ₩.;
                                                                                                         22;
                                                                                                    Score 406; DB Pred. No. 7.5e 22; Mismatches
                                                                                                                                                                                                                                                               DIX
                                                                                                                                                                                                                                                                                       GSK-3B BINDING SITE (BETA-CATENIN BINDING SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                      400D0C90E72506FE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              841 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       update)
                                                                                                                                  DB 1;
.5e-31;
                                                                                                                                                        Length 841;
                                                                                                                                                                                                                                                                                                                                                (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                     SITE
                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                     (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGULATES
                                                                                                         4;
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RESULT 10
AXN1_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2000 (Rel. 40, Created)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
AXIN 1 (AXIS INHIBITION PROTEIN 1) (HAXIN) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AXN1_HUMAN
015169;
                                                                    NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zeng L., Fagotto F., Zhang T., Hsu W., Vasicek T.J.,
Lee J.J., Tilghman S.M., Gumbiner B.M., Costantini F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97373830;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AXIN1 OR AXIN
  SEQUENCE
               DOMAIN
                                          DOMAIN
                                                                                                                                      InterPro; IPR000342; -
InterPro; IPR001158; -
Pfam; PF00615; RGS; 1.
                                                                                                                                                                                 MIM; 603816;
                                                                                                                                                                                            HSSP;
                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          145 YKKYILDNNGIVSRQIKPATKSFIKDCVMKLQIDPDMFDQAQTEIQCMIEDNTYPLFLKS
                                                        DOMAIN
                                                                                                Developmental protein;
                                                                                                             PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         205 DIYLEY 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58
                                                                                                                                                                                                                                                                                                                                                                                                                            BETA CATENIN. PROBABLY FACILIATION.

BETA CATENIN AND APC BY GSK-3B.

GATENIN AND APC BY GSK-3B.

SUBUNIT: INTERACTS WITH GLYCOGEN SYNTHASE KINASE-3 BETA (GSK-3B)

SUBUNIT: INTERACTS WITH GLYCOGEN BETWEEN AXIN AND BETA-CATENIN.

AND BETA-CATENIN. THE INTERACTION BETWEEN AXIN AND BETA-CATENIN.

OCCURS VIA THE ARMADILLO REPEATS CONTAINED IN BETA-CATENIN.

OCCURS VIA THE ARMADILLO REPEATS CONTAINED IN GAMMA-CATENIN),
                                                                                                                                                                                                                                                                                                                                           SIMILARITY: CONTAINS 1 RGS DOMAIN. SIMILARITY: CONTAINS 1 DIX DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: CYTOPLASMIC. TISSUE SPECIFICITY: UBIQUITOUSLY E PTM: PROBABLY PHOSPHORYLATED BY GS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DIYLEY 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YKRYI-ENNSVVSKQLKPATKTYIRDGIKKQQIGSVMFDQAQTEIQAVMEENAYQVFLTS
                                                                                                                         PF00778; DIX; 1.
                                                                                                                                                                                            AF009674; AAC51624.1; P49799; 1AGR.
                                                                                                             PS50132; RGS;
    900
                 818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Human).
AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=9230313;
    900
99803
                                                                                              Phosphorylation.
     W.
  RGS.
GSK-3B BINDING SITE (BY SIMILARITY).
BETA-CATENIN BINDING SITE (BY
SIMILARITY).
DIX.
EE5F990B11FC7B3B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                       GSK-3B
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                                                                                                                                                                                                                                                                                                                                                                                                     EXPRESSED
                                                                                                                                                                                                                                                                                                                                                                                       AND
                                                                                                                                                                                                                                                                                                                                                                                         DEPHOSPHORYLATED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 III,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           116
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Query Match Best Local

Similarity

62.8%; 62.7%;

Score Pred.

401; No.

L; DB 1; . 2.4e-30;

Length 900;

5 5 5 5

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Query Match
Best Local :
                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                 MIM; ""
InterPro; IPROUUS;",
InterPro; IPROUUS;",
Pfam; PF00615; RGS; 1.
PRINTS; PR01301; RGSPROTEIN.
PPOSITE; PS50132; RGS; 1.
PPOSITE; PS50132; RGS; 1.
RG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     _HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
RECULATOR OF G-PROTEIN SIGNALING 3 (RGS3) (RGP3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collabora between the Swiss Institute of Bioinformatics and the EMBL outstatisthe European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=96178495; PubMed=8602223;
Druey K.M., Blumer K.J., Kang V.H.,
"Inhibition of G-protein-mediated Mammmalian gene family.";
Nature 379:742-746(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                               Signal transduction in DOMAIN 394 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U27655; AAC50394.1; -. HSSP; P49799; 1AGR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RGS3_HUMAN P49796;
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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       EΥV
                                                                                                                                             YKRYI-ENNSYVSKQLKPATKTYIRDGIKKQQIGSVMFDQAQTEIQAVMEENAYQVFLTS
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                                                   YIAIQACKEVNLDSYTREHTKDNL--QSVTRGCFDLAQKRIFGLMEKDSYPRFLRSDLYL
                                                                                                 YIENNSVVSKQLKPATKTYIRDGIKKQQIGSVMFDQAQTEIQAVMEENAYQVFLTSDIYL 120
                                                                                                                                                                                                                                                 60;
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                                                                                                                                                                                                                                                                        Score 172.5;
Pred. No. 4.
                                                                                                                                                                                                                                                                                                                                                                       F1CFE3F27D4673A0 CRC64;
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AP kinase activation
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                                                                                               RESULT 12
RRGS2_HRGS2_HRGS2_HRGS2_HRGS2_HRGS2_HRGS2_HRGS2_OC 01-FEB
DT SEQUEN
RR SEQUEN
RR SEQUEN
RR SEQUEN
RR SEQUEN
RR MEDILIN
RA WU H.-
RA WU H.-
RA WU H.-
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TH 1431."
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Query.Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RGS2 OK GOOD,
HOMO Sapiens (Human),
Eukaryota; Metazoa; Chordata;
Eukaryota; Metazoa; Primates;
                                                                                                                                                                                                                                                                           EMBL; AL035407; CAB62512.1; -. HSSP; P49799; 1AGR. MIM; 600861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene, '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-CCT-2000 (Rel. 40, Last annotation update)
REGULATOR OF G-PROTEIN SIGNALING 2 (RGS2) (G0/G1 SWITCH REGULATORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wu H.-K., Heng H.H., Shi X.-M., Forsdyke D.R., Tsui L.-C., Mak T.W. Minden M.D., Siderovski D.P.; minden M.D., Siderovski D.P.; "Differential expression of a basic helix-loop-helix phosphoprotein gene, GOS8, in acute leukemia and localization to human chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "A human gene encoding a putative basic helix-loop-helix phosphoprottein whose mRNA increases rapidly in cyclohexin blood mononuclear cells.";
DNA Cell Biol. 13:125-147(1994).
                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                              EMBL; L13391; AAA20680.1; -. EMBL; L13463; AAC37587.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHARACTERIZATION.
MEDLINE-95371353; Pubmed-7643615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RGS2 OR GOS8.
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                                                                                                                             Signal transduction B3
                                                                                                                                                                       PRINTS; PR01301; RGSPROTEIN. PROSITE; PS50132; RGS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             508
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: CONTAINS 1 RGS DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTM: COULD BE PHOSPHORYLATED. MIGHT BE FUNCTIONALLY REGULATED BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEIN KINASE(S)
                                                                                                                                                                                                                                                                      600861;
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                                                                                                                                                                                                                       Pro; IPR000342; -. PF00615; RGS; 1.
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211 AA;
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                                                                                                                             199
                                                                                                                                             inhibitor; Cell cycle;
                                                                                                 24382 MW;
. 2 8
8 8
                                                                       RGS:
; EFFE4AE47EF9AD8F CRC64;
Pred. No. 4.8e-09;
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                         DB 1;
                                                                                                                                                     Phosphorylation.
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RESULT 14
RGSA_HUMAN
ID RGSA_H
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use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by an
entities requires a license agreement (See http://www.isb-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Characterization of a novel mammalian RGS protein that binds to Galpha proteins and inhibits pheromone signaling in yeast.";
J. Biol. Chem. 272:8679-8685(1997)
-1- FUNCTION: INHIBITS SIGNAL TRANSDUCTION BY INCREASING THE GTPASE ACTIVITY OF G PROTEIN ALPHA SUBUNITS THERBBY DRIVING THEM INTO THEIR INACTIVE GDP-BOUND FORM. MAY PLAY A ROLE IN LEUKEMOGENESIS.
-1- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.
-1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
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     RGSA_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000342; - Pfam; PF00615; RGS; 1.
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                                                                                                                               FIEKEAPKEINIDFQTKSLIAQNI--QEATSGCFTTAQKRYYSLMENNSYPRFLESEFY 195
                                                                                                                                                                            YIENNSVVSKQLKPATKTYIRDGIKKQQIGSVMFDQAQTEIQAVMEENAYQVFLTSDIY 119
                                                                                                                                                                                                                                                                            WTKSLHSLLGDQDGAYLFRTFLEREKCVDTLDFWFACNGFRQMNLKDTKTLRVAKAIYKR 60
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                                                                                                                                                                                                                                    WAEAFDELLASKYGLAAFRAFLKSEFCEENIEFWLACEDFKKTK-SPQKLSSKARKIYTD 138
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(Rel. 35, Last sequence update)
(Rel. 40, Last annotation update)
F G-PROTEIN SIGNALING 2 (RGS2).
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     STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  inhibitor; Cell cycle
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20; Mismatches
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; 61FAA2DC9B0C4DF9 CRC64;
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Best Local
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15-DEC-1998;
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                                                          Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                          Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Trac
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Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGULATOR OF
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Pfam; PF00615; RGS; 1
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(Rel. 37, Last sequence update)
(Rel. 40, Last annotation updat)
F G-PROTEIN SIGNALING 10 (RGS10)
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19608 MW;
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                                                                                                                                                                                 Last sequence update)
Last annotation updat
PROTEIN) (DAXIN) (D-A
                                                                                                                                                                                                                                                                      Created)
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; EF36915F1AA23F3B CRC64;
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                                                                                                               Tracheata; Hexapoda; Insecta;
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10 (RGS10).
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RA Merkulov G., Milshina N.V., McDerry C., McIeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., McDarry C.W., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzary D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Syirskas R., Tector C., Turner R., Etrong R., Sun E.,
RA Syirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
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RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Besson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Barokstein P., Brottler P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Gebat S., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gelbat W.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hastin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshhna N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshhna N.V., Mobarry C., Morris J., Moshrefi A.,
                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-99387984; PubMed-10457025; Willert K., Logan C.Y., Arora A., Fish M., Nusse R.; Willert K., Logan C.Y., Arora A., Fish M., Nusse R.; "A Drosophila Axin homolog, Daxin, inhibits wnt signaling."; A Drosophila Axin homolog, Daxin, inhibits wnt signaling."; Development 126:4165-4173(1999).

1- FUNCTION: INHIBITOR OF THE WG SIGNALING PATHWAY. DOWN REGULATES BETA-CATENIN (ARMADILLO-ARM). PROBABLY FACILITATE THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ruel L., Anthopoulos N., Goncalves J., Manoukian A.S., Woodgett J.R.; "A Drosophila homolog of the axin gene is involved in the transduction of the wingless signal regulating the stability of the armadillo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hamada F., Tomoyasu Y., Takatsu Y., Nakamura M., Nagai S.-I.,
Suzuki A., Fujita F., Shibuya H., Toyoshima K., Ueno N., Akiyama T
"Negative regulation of Wingless signaling by D-axin, a Drosophila
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Science 283:1739-1742(1999).
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                                                                                               SUBUNIT: INTERACTS WITH ZW3 AND ARM. THE INTERACTION BETWEEN AXN AND ARM OCCURS VIA THE ARMADILLO REPEATS CONTAINED IN ARM. SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).

DEVELOPMENTAL STAGE: UBIQUITOUSLY EXPRESSED THROUGHOUT THE
DEVELOPMENT.
SIMILARITY: CONTAINS 1 RGS DOMAIN.
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MEDLINE=98226558; PubMed=9566905;
Yamamoto H., Kishida S., Uochi T., Ikeda S.,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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SEQUENCE 838 AA; 92947 MW; 45B825C13BA07F37 CRC64;
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PFAM; PF00615; RGS; 1.
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Mol. Cell. Biol. 18:2867-2875(1998).
EMBL; AF017757; AAC40089.1; -.
HSSP; P49799; IAGR.
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61 YIENNSYVSKQLKPATKTYIRDGIKKQQIGSYMFDQAQTEIQAVMEENAYQVFLTSDIYL 120
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Science 2
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"Functional interaction of an axin homolog,
catenin, APC, and GSK3beta.";
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                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                              01-MAY-2000
                                                                                                                AXIN2
   Zhang T.,
                   SEQUENCE FROM N.A
                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                         198
                                                                                                                                                                                                                                                                                                                     121
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                                                                                                                                                                                                                                                                                         EYV 200
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PDD003639; -; 1.
PDD003639; -; 1.
PD003639; -; 1.
PD003639; -; 1.
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    Fagotto F.,
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ilarity 100.0%;
Conservative
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Rodentia;
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Last annotation updat
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Pred. No. 7.8e-53;
; Mismatches 0;
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                                                                  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
      Zeng
      ۲.,
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         D.,
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         Copeland N.
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Best Local S
Matches 118
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Best Local (
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9UH84;
01-MAY-2000
01-MAY-2000
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (NOV-1999) to the EMBL; AF205889; AAF22800.1; HSSP; P49799; IAGR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expression pattern, interaction with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PFAM; PF00615; RGS; 1.
PFAM; PF00778; DIX; 1.
PRINTS; PR01301; RGSPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jenkins N.A., Warburton D., Costantin "Properties of mouse Axin2 and human
                                                                                                                                                                                                                                                                                        Zhang T., Fagotto F., Hsu W., Zeng L., Gilbert D., Copeland N.G., Jenkins N.A., Warburton D., Costantini F.; "Properties of mouse Axin2 and human AXIN2: chromosomal location, expression pattern, interaction with Axin and effects on embryoni axis formation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INTERPRO; IPR000342; -.
                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9UH84
                                                                                                                                                                         PFAM; PF00615; RGS; 1.
PFAM; PF00778; DIX; 1.
PRINTS; PR01301; RGSPRC
                                                                                                                                                                                                                                               Submitted (NOV-1999) to the EMBL/GenBank/DDBJ EMBL; AF205888; AAF22799.1; -. HSSP; P49799; LAGR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AXIN2
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                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                 rissue=brain, Lymphoblast;
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                      INTERPRO; IPR001158;
                                                                                                                                                                                                                                  INTERPRO; IPRO00342; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YIENNSVYSKOLKPATKTYIRDGIKKQQIGSVMFDQAQTEIQAVMEENAYQVFLTSDIYL 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WTKSLHSLLGDQDGAYLFRTFLEKEKCVDTLDFWFACNGFRQMNLKDTKTLRVAKAIYKR 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WTKSLHSLLGDQDGAYLFRTFLEREKCVDTLDFWFACNGFRQMNLKDTKTLRVAKAIYKR 60
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                           WTKSLHSLLGDQDGAYLFRTELEREKCVDTLDFWFACNGFROMNLKDTKTLRVAKAIYKR 60
YIENNSYVSKQLKPATKTYIRDGIKKQQIGSVMFDQAQTEIQAVMEENAYQVFLTSDIYL 120
                                                                                      al Similarity
118; Conserv
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                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              (Human).
~+azoa; Chordata;
                                                                                                                                                                 AA;
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A; 92896 MW;
                                                                                                                                                               RGSPROTEIN.
A; 86857 MW;
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                                                                                                                                                                                                                                                                                                                                 ., Zeng L., Gilbert D., Copeland N.G., Costantini F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
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                                                                                         Score 624; DB 4;
Pred. No. 1.9e-51;
4; Mismatches 1
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                                                                                                                                                                  3A4943ABF430BBD3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            777
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.5e-52;
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                                                                                                                                                                    CRC64;
                                                                                                                      Length 777;
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                                                                                              Indels
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INTERPRO; IPRO01158; -.
PFAM; PF00615; RG; 1.
PFAM; PF00778; DIX; 1.
SEQUENCE 843 AA; 9355
                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9YGY0
Q9YGY0;
01-MAY-1999
01-MAY-1999
01-CCT-2000
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Q9Y2T1;
01-NOV-1999
SEQUENCE FROM N.A.

MEDLINE-99173782; PubMed-10072781;

Hedgepeth C.M., Deardorff M.A., Klein
"Xenopus axin interacts with glycogen
expressed in the anterior midbrain.";

Mech. Dev. 80:147-151(1999).
                                                                                                                                                                                                                                                                       Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea.
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-99168905; PubMed-10049590; Mai M., Qian C., Yokomizo A., Smit Colning of the human homolog of chromosome 17q23-q24.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genomics 55:341-344(1999).
EMBL; AF078165; AAD20976.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EYV 199
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9 (TrEMBLrel. 10,
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93557 MW;
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95.98;
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Pred. No. 2.1e-51
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                                                                                                            P.S.;
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Matches 78
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PFAM; PF00778; DIX; 1.
PRODOM; PD00158; -; 1.
PRODOM; PD003539; -; 1.
SEQUENCE 842 AA; 94459 M
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INTERPRO; IPR001158; -.
PFAM; PF00615; RGS; 1.
PFAM; PF00778; DIX; 1.
PRODOM; PD001580; -; 1.
PRODOM; PD003639; -; 1.
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MEDILINE-98151361; PubMed-9482734;
Ikeda S., Yamamoto H., Murai H., Kishida S., Kikuchi A.;

"Axin, a negative regulator of the Wnt signaling pathway,
complex with GSK-3beta and beta-catenin and promotes GSK-
dependent phosphorylation of beta-catenin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBO J. 17:1371-1384(1998).
EMBL; AF017756; AAC40066.1;
HSSP; P49799; LAGR.
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nes 78; Conservative
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| :||||| ||| :||||||::| | | |||||||::| |:| |::||||
85 WAESLHSLLDDQDGIHLFRTFLQQENCADLLDFWFACSGFRKLEPNDSKVEKRLKLAKAI 144
                                                                                                                                                                      WTKSLHSLLGDQDGAYLFRTFLEREKCVDTLDFWFACNGFRQMNLKDT----KTLRVAKAI 57
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                                                DIYLEY
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                                                                                              YKRYI-ENNSVVSKQLKPATKTYIRDGIKKQQIGSVMFDQAQTEIQAVMEENAYQVFLTS
                                                                                                                                               WAESLHSLLDDQDGISLFRTFLKQEGCADLLDFWFACSGFRKLEPCDSNEEKRLKLARAI 149
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77; Conser
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Last sequence update)
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Pred. No. 5.9e-32;
                                                                                                                                                                                                                                                                       Score 407; DB 1
Pred. No. 1e-30;
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Best Local Similarity
[1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-97373830; PubMed-9230313;
Zeng L., Fagotto F., Zhang T., Hsu W., Vasicek T.J., Perry W.L.,
III Lee J.J., Tilghman S.M., Gumbiner B.M., Costantini F.;
"The mouse Fused locus encodes Axin, an inhibitor of the Wnt sig
                                                                                                                                                                                                                                                                                                                                                          01-JAN-1998
01-JAN-1998
01-OCT-2000
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                                                                                                                                                                                                                                        Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zeng L.,
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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MEDLINE=97373830; PubMed=9230313;
Zeng L., Fagotto F., Zhang T., Hs
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HSSP; P49799; IAGR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DIYLEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L., Fagotto F., Zhang T., Hsu W., Vasicek T.J., Perz
Lee J.J., Tilghman S.M., Gumbiner B.M., Costantini F
mouse Fused locus encodes Axin, an inhibitor of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DIYLEY
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                                                                                                                                                                                                                                                                                                                                                          (TremBLrel. 05, Created)
(TremBLrel. 05, Last seq
(TremBLrel. 15, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               regulates embryonic axis formation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAC53285.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63.7%;
61.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 407; DB 11;
Pred. No. 1.2e-30;
1; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           841
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; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Perry W.L.,
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                                                     Wnt signaling
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Best Local
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Best Local
                                                                                                                                                                           Matches
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HSSP; P49799; lAGR.
INTERPRO; IPR000342; -.
INTERPRO; IPR001158; -.
PFAM; PF00615; RGS; 1.
PFAM; PF00778; DIX; 1.
PRODOM; PD001580; -; 1.
PRODOM; PD003589; -; 1.
PRODOM; PD003589; -; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   015169;
015169;
01-JAN-1998
01-JAN-1998
01-OCT-2000
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pathway that regulates embryonic axis Cell 90:181-192(1997). EMBL, AF009674; AAC51624.1; ... HSSP; P49799; lAGR.
                                                                                                                                                                                                                                                                                                                         PFAM; PF00615; RGS; 1.
PFAM; PF00778; DIX; 1.
PRINTS; PR01301; RGSPROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=97373830; Pul
Zeng L., Fagotto F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pathway that regulates embryonic axis Cell 90:181-192(1997)
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                                                                                   WTKSLHSLLGDQDGAYLFRTFLEREKCVDTLDFWFACNGFRQMNLKDT---KTLRVAKAI
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YRKYILDNNGIVSRQTKPATKSFIKGCIMKQLIDPAMFDQAQTEIQATMEENTYPSFLKS
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                                                                                                                                                                             79;
                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                     900
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8 (TrEMBLrel. 05,
0 (TrEMBLrel. 15,
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                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                     AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=9230313;
F., Zhang T., Hsu W., Vasicek T.J., Perry W.L.,
ghman S.M., Cumbiner B.M., Costantini F.;
locus encodes Axin, an inhibitor of the Wnt sig
                                                                                                                                                                                                                                                                                     99803 MW;
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                                                                                                                                                                                               62.8%;
62.7%;
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Last annotation update)
                                                                                                                                                                         Score 401; DB 4;
Pred. No. 4.2e-30;
17; Mismatches 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 406; DB 13;
Pred. No. 1.3e-30;
Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                     EE5F990B11FC7B3B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B.M., Costantini r.
an inhibitor of the
                                                                                                                                                                                                                    Length 900
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117 DIYLEY |||||| | 242 DIYLEY

247 122

Best Local Similarity

34.6%;

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RESULT
ID POPTP2
AC Q9
AC Q9
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D
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Q9NS28
ID 09NS28
AC Q9NS28
DT 01-OCT
DT 01-OCT
DT 01-OCT
DE REGULA
OS HOMO S
OC Eukary
OC Mammal
OX NCBI_T
RN [1]
RP SEQUEN
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RT "A nov
RL Submit
DR EMBL;
SQ SEQUEN
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Query Match
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Best Local
                                                                      SEQUENCE FROM N.A.

Zhang W., Wan T., Yuan Z., He L., Cao X.;

"A novel regulator of G-protein signaling.";

submitted (JUL-1998) to the EMBL/GenBank/DDBJ

EMBL; AF076642; AAF80227.1;

SEQUENCE 235 AA; 27582 MW; 973ABDE8EC7DE3D
                                                                                                                                                                                                                                                                                                                                                                       Q9NS28 PRELIMINARY; PRT; 235 AA.
Q9NS28;
Q1-OCT-2000 (TIEMBLrel. 15, Created)
Q1-OCT-2000 (TIEMBLrel. 15, Last sequence update)
Q1-OCT-2000 (TIEMBLrel. 15, Last annotation update)
REGULATOR OF G-PROTEIN SIGNALING 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-OVARY;
Itoh K., Antipova A., Ratcliffe M., Sokol S.;
"Dishevelled transduces a signal by displacing GSK3 from axin-GSK3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9PTP2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WTKSLHSLLGDQDGAYLFRTFLEREKCYDTLDFWFACNGFRQMNLKDTKTLRVAKAIYKR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WGRSLNLLLDDQDGATLFRMYLEGEGLGDLLTFWFACNGFRAMDPLEPKTSKTAKAIYRW 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EY 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79196 MW; C3D0AF0D9540F162 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52.6%;
  29
  . 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 336; DB 1
Pred. No. 5e-24;
Score 186.5;
                                                                               973ABDE8EC7DE3D5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ₹
₽B
                                                                                                                                                                                                                                                                                                                                                                                                        update)
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4.
                                                                                                                                  databases
                                                                               CRC64;
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; Pipidae;
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RESULT Q9JL22
ID Q9,
AC Q9,
DT 011
DT 011
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DT 011
DT REBURGE REB
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Q91L23
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DT 011
DT
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Best Local Similarity
Matches 39; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                             O9JL22 PRELIMINARY; PRT; 297 AA.

O9JL22:
O1-OCT-2000 (TrEMBLrel. 15, Created)
O1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
O1-OCT-2000 (TrEMBLrel. 15, Last annotation update)
REGULATOR OF G-PROTEIN SIGNALING 3 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9JL23
Q9JL23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Reif K., Cyster J.G.;

**RGS molecule expression in murine B lymphocytes and regulate chemotaxis to lymphoid chemokines.";

J. Immunol. 164:4720-4729(2000).

EMBL; AF215669; AAF34626.1;

EMBL; AF215669; AAF34626.1;

EMBC; AF215669; AAF34626.1;

**EMBC; AF315669; AAF34626.1;

**EMBC; AF31569; AAF34626.1;

**EMBC; AAF34626.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
REGULATOR OF G-PROTEIN SIGNALING 3S.
SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-EMBRYO;
MEDLINE-20243574; PubMed=10779778;
                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vert
Mammalia; Eutheria; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUE=KIDNEY;
MEDLINE=20243574; PubMed=10779778;
                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YIENNSVYSKQLKPATKTYIRDGIKKQQIGSVMFDQAQTEIQAVMEENAYQVFLTSDIYL 120
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31.7%;
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25; Mismatches 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 167.5; DB 1
Pred. No. 1.3e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BE66E0C1FE07952F CRC64;
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                                                                                                                                                                                                                                                                                                                                        Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                              Muridae;
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"RGS molecule expression in murine B lymphocytes and ability to down-
"regulate chemotaxis to lymphoid chemokines.";
J. Immunol. 164:4720-4729(2000).
EMBL; AF215670; AAF34627.1; -.
EMBL; AF215670; AAF34627.1; -.
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QSJHXO;

QSJHX
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STRAIN-SPRAGUE DAWLEY; TISSUE-THORACIC AORTA SMOOTH MUSCLE;
STRAIN-SPRAGUE DAWLEY; TISSUE-THORACIC AORTA SMOOTH MUSCLE;
STRAIN-SPRAGUE DAWLEY; TISSUE-THORACIC AORTA SMOOTH MUSCLE.";
"RGS2 regulates angiotensin II signaling in vascular smooth muscle.";
"RGS2 regulates angiotensin II signaling in vascular smooth muscle.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AF279918; AAF85981.1; -.

EMBL; AF279918; AAF85981.1; -.

SEQUENCE 211 AA; 24323 MW; 84B5525CB41EA964 CRC64;
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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1: /SIDS2/qcadats
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Gapop 10.0 , Gapext 0.5
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272
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/SIDS2/gcgdata/geneseq/geneseqp/AA198B.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqp/aa1981.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result No.		Query Match	Query Match Length DB ID	DB 20	ID W93570	Description Human, cond
21	272 272	100.0	840 840	20	W93570 W93569	Human conductin pr
w	142.5	52.4	992	20	W96265	Murine
4	141.5	52.0	900	20	W96264	Human axin.
u	65	23.9	462	16	R78230	Candid
σı	65	23.9	463	15	R48084	C. ant
7	61.5	22.6	995	20	Y04658	L.lactis HsdR subu
80	58	21.3	1816	21	Y95440	Caenor
9	57	21.0	115	21	в27999	Human
10	57	21.0	260	21	G56044	Arabid
11	57	21.0	260	21	G61383	Arabidopsis thalia

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B00066 Y81502 R39358	R39819 W92950 W55104	R88616 W15473 Y06427 W01535	Y86289 B53070 B11540	105393 B28212 B12426 V54496	W05394 Y31719 Y23627	W88235 Y06292 W68093	W98441 W10422 B42487	R91310 W78102 B40894	G56043 G61382 G56042 G51381
KIA Str rZP	2mp WO9 Str	TNF-R Human Mouse Cellu	Human Human SEN v	Human Novel Human	Mouse Human A hum	Human Human Human	H. py Penic Human	Funga Chime Human	Ara Ara Ara
. [0 175	$\alpha \sim 1$	TNF-R p55IC-bindin Human P100 protein Mouse circadian re Cellular homoloque	n secreted p n anglogenes virus protei	en Tie ligand Nen Tie ligand N	sH3P13 prot fibrinogen an growth fa	prothrone neuron	lori GHPO 5 illium chry ORFX ORF22	~ 5 - 1	psis thali psis thali psis thali psis thali

### ALIGNMENTS

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Tumor-suppressing protein conductin diagnosis of tumors
                                                                                                                                                                                  Conductin; tumour; diagnosis; treatment; beta-catenin; anti-tumour; therapy; cytoplasmic degradation; blockade; Wnt signalling pathway; Adenomatous Polyposis Coli; APC; tumour suppressor.
                                                                                                                                                                                                                                 Human conductin protein.
                                                                                                                                                                                                                                                                       W93570;
                                                                                                                                                                                                                                                                                        W93570 standard; Protein; 840
                                                                                                                                                                                                                                                     17-JUN-1999
                            WPI; 1999-214706/18.
N-PSDB; X23370.
                                                      Behrens J, Birchmeier
                                                                       (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX
                                                                                          02-SEP-1997;
                                                                                                             01-SEP-1998;
                                                                                                                               11-MAR-1999.
                                                                                                                                                W09911780-A2.
                                                                                                                                                                   Homo sapiens.
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Matches 54
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                                                   Tumor-suppressing protein conductin
                              diagnosis of tumors
                                                                                                                          WPI; 1999-214706/18
                                                                                                                                                                                                                                                                                                                            01-SEP-1998;
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                                                                                                      N-PSDB; X23369.
                                                                                                                                                                                                                                                                              02-SEP-1997;
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                                                                                                                                                                                                                           (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Regulator
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "GSK 3-beta binding region as claim 13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Dishevilled homology region claim 15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Beta-catenin binding domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                claim 14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 described
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 272; DB 20;
Pred. No. 4.9e-25;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of
in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G protein signalling domain claim 12"
                                                     used for treatment and
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RESULT
W96265
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Best Local
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                      Nucleic acids encoding mutant and wild type Axin and oligonucleotides derived from them are useful for detecting mutations in the Axin gene and for determining whether a subject is likely to develop cancer (including breast, colorectal, gastrointestinal, esophageal, carcinomas or melanomas). The wild type Axin and homologues of Axin are useful for treating subjects who are likely to develop cancer (thyroid carcinomas). The nucleic acids are also useful for diagnosing cancer and for detecting mutations in cancerous cells. Wild type Axin, its antisense molecule and identified compounds form pharmaceutical compositions in the treatment of cancer. The compositions are also useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            anti-tumour activity. Detecting the presence or amount of conductin, at protein or nucleic acid levels, is used to diagnose tumours, while agents that (re)activate conductin are used for tumour therapy. Conductin binds to beta-catenin and induces its cytoplasmic degradation, resulting in blockade of the Wnt/Wingless signalling pathway in vertebrates. Conductin also binds to Adenomatous Polyposis Coli (APC) fragments and, in conjunction with APC, acts as a tumour suppressor.
                                                                                                                                                                                                        Claim 8;
                                                                                                                                                                                                                                               Newly isolated nucleic acid encoding "axis inhibition"
                                                                                                                                                                                                                                                                                            WPI; 1999-120510/10.
                                                                                                                                                                                                                                                                                                                         Constantini F,
                                                                                                                                                                                                                                                                                                                                                                                   10-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                              09-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               beta-catenin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Axin; cancer; breast cancer; colorectal cancer;
gastrointestinal cancer; esophageal cancer; carcinoma; melanoma;
diagnosis; treatment; therapy; thyroid carcinoma; tumorigenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Murine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W96265 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes a novel human conductin protein which has
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 11; Fig 1; 22pp;
            treating cancer by inhibiting
                                                                                                                                                                                                                                   (Axin)
                                                                                                                                                                                                                                                                              N-PSDB;
                                                                                                                                                                                                                                                                                                                                                      (UYCO ) UNIV COLUMBIA NEW YORK
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                                                                                                                                                                                                                                   useful
                                                                                                                                                                                                      Figure 8; 95pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     840 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                              98WO-US14414
                                                                                                                                                                                                                                                                                                                         Zeng
                                                                                                                                                                                                                                  for detecting, diagnosing and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
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                                                                                                                                                                                                      English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 272; DB 20;
Pred. No. 4.9e-25;
Mismatches 0;
tumorigenesis acid encoding
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 (by inducing degr
Axin acts through
                                                                                                                                                                                                                                     treating
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                                                                                                                                                                                                                                   protein
                                                                                                                                              a subject is
               degradation
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Query Match
Best Local Similarity
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Matches
                                                                                                                                                  likely to develop cancer (including breast, colorectal, gastrointestinal, esophageal, carcinomas or melanomas). The wild type Axin and homologues of Axin are useful for treating subjects who are likely to develop cancer (thyroid carcinomas). The nucleic acids are also useful for diagnosing cancer and for detecting mutations in cancerous cells. Wild type Axin, its antisense molecule and identified compounds form pharmaceutical compositions in the treatment of cancer. The compositions are also useful for treating cancer by inhibiting tumorigenesis (by inducing degradation of beta-catenin). The nucleic acid encoding Axin acts through negative regulation of the Wnt pathway in the Nieuwkoop Center.
                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding mutant and wild type Axin and oligonucleotides derived from them are useful for detecting mutations in the Axin gene and for determining whether a subject is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Axin; cancer; breast cancer; colorectal cancer;
gastrointestinal cancer; esophageal cancer; carcinoma; melanoma;
diagnosis; treatment; therapy; thyroid carcinoma; tumorigenesis;
                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Figure 11; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Newly isolated nucleic acid encoding "axis inhibition" protein (Axin) - useful for detecting, diagnosing and treating cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-120510/10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          beta-catenin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-JUN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           negative regulation of the Wnt pathway in the Nieuwkoop Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYCO ) UNIV COLUMBIA NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-JUL-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
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30; Conserv
30;
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                                                                                                              900 AA;
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Conservative
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                     52.0%;
56.6%;
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Pred. No. 3.9e-09;
8; Mismatches 14
9
                        Score 141.5; DB 20; Pred. No. 4.7e-09;
Mismatches
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14;
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Indels
                                        Length 900;
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Gaps
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RESULT
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                                 E. colony transformants contg. Candida antarctica lipase A, chromosomal DNA of the C. antarctica strain LF058 (DSM 3855) were prepd. The colonies are screened with the 32P-phosphorylated oligo degenerate probe NOR 440, based on the N-terminal sequence determined from mature C. antarctica lipase. Plasmids were prepd. If from positive colonies and analysed by southern hybridisation. The probe for the southern is either the NOR 440 probe or a 32P-labelled probe NOR438. NOR 438 is an oligo corresp. to AA sequence of the lipase in which, at 13 posns., a base has been chosen on the basis of codons used in yeasts and filamentous fungi. (Guess positions are indicated in 094949 FT). Only one plasmid, pMT1076, contains a band which hybridises both to NOR 440 pmT1076 is restriction mapped and sequenced (see 094950). The last two AAs of the propeptide (see R78230) are a typical cleavage site for endoproteolytic processing by enzymes of the S. Cerenitains with the propeptide (see R78230) are a typical cleavage site for endoproteolytic processing by enzymes of the S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Candida antarctica DSM 3855
                                                                                                                                                                                                                                                                                                                   Aspergillus japonicus-type cells expressing heterologous protein fungal enzyme, provide high yields without significant prodn. of
                                                                                                                                                                                                                                                                                                                                                                                                       Berka RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lipase
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Sequence
                                                                                                                                                                                                                                                                            Example; Page 36-37; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                 (NOVO ) NOVO NORDISK BIOTECH INC
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DB; Q94950.
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462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'label= mature lipase
                                                                                                                                                                                                                                                                                                                                                                                                       Takagi S,
                                                                                                                                                                                                                                                                                                                                                                                                         Yoder
                                                                                                                                                                                                                                                                                                                       protease
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Ouery Match 23.9%; Best Local Similarity 48.3%; Matches 14; Conservative

Score 65; DB 16; Pred. No. 4.8; 5; Mismatches 8

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Length 462; Indels

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents the C. antartica lipase A protein. This lipase has high thermostability and is active at acid pH. A varies of the mature lipase A in which hel39 has been replaced by a Trp residue has increased specific activity compared to the parent lipase. The lipase or varient may be used in ester hydrolysis, ester synthesis or interesterification. They can also be used for avoiding pitch trouble in the process for the production of mechanical pulp or a paper-making process using mechanical pulp. They can also be used in detergents or as a digestive enzyme, eg. it the treatment of cystic fibrosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lipase A; thermostability; specific activity; mechanical ester hydrolysis; ester synthesis; interesterification; a pitch; paper-making; detergent; digestive enzyme; cystic
                                      Y04658;
                                                                                          Y04658 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 15; Page 39-40; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               compared
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New lipase variants, partic. from Candida antartica - have amino acid substitutions to increase specific activity against substrates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Borch K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-JUL-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JUL-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9401541-A.
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                                                                                                                                                                                                                         336 asytvsvpkfprfiwhaipdeivpyqpaa 364
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                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                           1 ANGQVSLPHFPR--THRLPKEMTPVEPAA 27
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                                                                                                                                                                                                                                                                                                                               l Similarity 48.3
14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                463 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93WO-DK00225
                                                                                          Protein;
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                                                                                                                                                                                                                                                                                                                                                        23.9%;
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1.9;
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cystic fibrosis.
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Best Local
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                                                                                                                         calcium release activated channel; therapy; diagnosis; lymphocyte proliferative disorder.
 30-DEC-1998;
29-JAN-1999;
                                                                                                     Caenorhabditis elegans.
                                                                                                                                                  SOC/CRAC; calcium channel; store operated channel;
                                                                                                                                                                        Caenorhabditis elegans polypeptide at the c05c12.3 locus.
                                                                                                                                                                                               10-OCT-2000
                                                                                                                                                                                                                                             Y95440 standard; Protein; 1816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 3; Page 18-22; 65pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chopin MC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-MAR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   L.lactis HsdR subunit #1.
                                 20-DEC-1999;
                                                        13-JUL-2000
                                                                               WO200040614-A2
                                                                                                                                                                                                                      Y95440;
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteriophage resistance mechanism subunit polypeptides - of lactic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (INRG ) INRA INST NAT RECH AGRONOMIQUE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lactococcus lactis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lactic acid bacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                  resistance mechanism
                                                                                                                                                                                                                                                                                                     732 pqshqipk-ltpavqelkafagedfsqiprgekdlkqfvrlgletqnqiqqlvq 784
                                                                                                                                                                                                                                                                                                                  11 PRTHRLPKEMTPV--EPAAFAAELISRLEK------LKLELESRHSLEERLQ
                                                                                                                                                                                                                                                                                                                                                           Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1999-183265/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bacteria, especially Lactococcus lactis
                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                           995 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clier F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HsdS; restriction/modification; bacteriophage; resistance;
                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                              (first entry)
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98US-0114220
99US-0120018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97FR-0010885
                                 99WO-US29996
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                                                                                                                                                                                                                                                                                                                                                            22.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                  in a lactic acid bacterium
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                                                                                                                                                                                                                                                                                                                                                   17;
                                                                                                                                                                                                                                                                                                                                                Score 61.5; D
Pred. No. 31;
17; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                         Length 995;
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99US-0140415

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RESULT
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Best Local (
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                                                                                                                                                                                                                                                                                                   Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antidicer; vulnerary; antionvulsant; antibacterial; antifungal; antiparastic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is that of a Caenorhabditis elegans polypeptide at the c05c12.3 locus. The polypeptide was identified in a database search for putative calcium channel proteins. The C05c12.3 protein was noteable cause its central pore region had some similarity to, but was clearly distinct from, members of the Trp family of calcium chennels. The polypeptide was used in BLAST screening to isolate 2 other C. elegans homologues (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New SOC/CRAC calcium channel polynucleotides and polypeptides used to diagnose and treat proliferative disorders associated with the channel and to screen for novel modulators of the channel -
Isolated nucleic acid molecule encoding a human secreted protein
                             WPI; 2000-638174/61.
                                                                                                                                                                                                                                                         Homo saplens.
                                                                                                                                                                                                                                                                                                                                                                               Human secreted protein BLAST search protein SEQ ID NO: 153
                                                                                                                                                                                                                                                                                                                                                                                                           02-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B27999 standard; Protein; 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Y95441-42) and mouse melastatin-1 (see Y95438). These were used to screen EST databases for lymphocyte homologues. Human clones (see A4992-24) encoding members (see Y95435-37) of a new family SOC (store operated channel) or CRAC (calcium release activated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-465957/40
                                                                                        (HUMA-) HUMAN GENOME SCI INC
                                                                                                                      12-MAR-1999;
23-NOV-1999;
                                                                                                                                                                09-MAR-2000;
                                                                                                                                                                                                21-SEP-2000
                                                                                                                                                                                                                            WO200055171-A1
                                                                                                                                                                                                                                                                                       neurological disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 VSLPHFPRTHRL-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page 72-76; 108pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    calcium channel polypeptides were identified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1816 AA;
                                                           Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                2000WO-US06043
                                                                                                                      99US-0124146.
99US-0167061.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21.3%;
                                                                                                                                                                                                                                                                                       infection; human; secreted protein.
                                                           Komatsoulis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----PKEMTPVEPA--AFAAELISRLEK 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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Pred. No.
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pred. No. 1.70
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                                                        16-APR-1999;
19-APR-1999;
21-APR-1999;
                                                                                                                   29-MAR-1999;
01-APR-1999;
06-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ameliorating or treating medical conditions, e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer, and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G56044 standard; Protein; 260 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                peptide fragment homologous to the protein encoded by the gene given in the descriptor line. The sequence is a search result from a BLASTX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 427-428; 438pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     used in preventing, treating or ameliorating a medical condition
                                                                                                     08-APR-1999
                                                                                                                                                                            09-MAR-1999
23-MAR-1999
                                                                                                                                                                                                        25-FEB-1999;
05-MAR-1999;
                                                                                                                                                                                                                                                                                   06-SEP-2000
                                                                                                                                                                                                                                                                                                                EP1033405-A2
                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                        Protein identification; signal transduction pathway; metabolic
                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana protein fragment SEQ ID NO: 71971.
                            23-APR-1999
23-APR-1999
                                                                                                                                                                                                                                                     25-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  homology search. The genes and proteins are useful for preventing,
                                                                                                                                                                25-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                          termination
                                                                                                                                                                                                                                                                                                                                                                                      hybridisation assay; genetic mapping; gene expression control;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :| | | :::|: | :::||::| :|| | 82 yfeslhtllmdisplfretfgsklisklselkke
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 HFPRTHRLPKEMTPVEPAAFAAELISRLEKLKLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention relates to the isolation of genes C59049-C59098 encoding human secreted proteins B27907-B27956. This sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bacterial, fungal and parasitic infections.
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                                                                                                                                                                                                                                                                                                                                                                          sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                     2000EP-0301439
            99US-0128714.
99US-0129845.
99US-0130077.
99US-0130449.
99US-0130891.
99US-0131449.
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99US-0125788.
99US-0126264.
99US-0126785.
99US-0127462.
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99US-0123180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42
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promoter;
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PR 29 - MGC-1999 99US-015566.
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PR 20 - MGC-1999 99US-01566.
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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2: /ggn2_6/ptodata/2,

3: /cgn2_6/ptodata/2,

4: /ggn2_6/ptodata/2,

5: /cgn2_6/ptodata/2,

5: /cgn2_6/ptodata/2,
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Maximum Match 100%
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   185757 seqs, 19210857 residues
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/cgn2_6/ptodata/2/18a/FCTUS_COMB.pep:*
/cgn2_6/ptodata/2/18a/PCTUS_COMB.pep:*
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     BB
US-08-458-023B-2
US-09-111-556A-2
US-08-317-401E-2
US-08-317-401E-4
US-08-315-310A-7
US-08-936-135-2
US-08-936-135-2
US-08-98-885-291-52
US-08-98-934-494-2
US-08-9143-084-2
US-08-99-103B-12
US-08-699-103B-12
US-08-699-103B-12
US-08-699-103B-12
US-08-699-103B-12
US-08-764-100-7
US-08-764-711-4
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ANGQVSLPHFPRTHRLPKEMTPVEPAA  :   :       ;   :   :   ASYTVSVPKFPRFIWHAIPDEIVPYQPAA	nilarity Conserv	GENERAL INFORMATION: APPLICANT: Yoder, Wendy APPLICANT: Yoder, Wendy APPLICANT: Takagi, Shinobu APPLICANT: Takagi, Shinobu APPLICANT: Takagi, Shinobu APPLICANT: Boominathan, Karup TITLE OF INVENTION: ASPERGILL NUMBER OF SEQUENCES: 16 CORRESSONDENCE ADDRESS: ADDRESSEE: NO. 56679900 NO. STREET: 405 Lexington Avenu CITY: New York COUNTRY: USA ZIP: 10174-6201 COMPUTER READABLE FORM: MEDIUM TYPE: FLOPPY disk COUNTRY: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS SOFTWARE: Patentin Release CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/4 FILING DATE: 01-JUN-1995 CLASSIFICATION NUMBER: 31,274 REFERENCE/DOCKET NUMBER: 31,274 REFERENCE/DOCKET NUMBER: 40 TELECOMMUTCATION INFORMATION: TELEPHONE: 212-867-0123 TELEPHONE: 212-867-0123 TELEPHONE: 212-867-0123 TELEPAX: 212-87-0123 TELEP	p1	11111111111111111111111111111111111111
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THRLPKEMTPVEPAA         :     WHAIPDEIVPYQPAA	%; Scor %; Pred 5; M	N: V4	A 8458023	1 US-0 1 US-0 2 US-0 3 US-0 3 US-0 3 US-0 3 US-0 1 US-0 1 US-0 1 US-0 1 US-0 1 US-0 2 US-0 3 US-0 2 US-0 3 US-0 3 US-0 3 US-0 5 US-0 7 US-0 8 US-0 8 US-0 8 US-0 9 US-0 9 US-0 9 US-0 9 US-0 9 US-0 1
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	2)			Sequence Sequence
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                                                                                                                                 Patent No. 6074863
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                                                                                                                                                                      08-360-758-2
                                                                                                                    GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 463 amino acid
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APPLICATION NUMBER:
FILING DATE: 03-JUN-
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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ADDRESSEE: No. 60201800 No. 6020180disk of No. 6020180th America, Inc.
                                                                                    APPLICANT:
                                                                                                    APPLICANT:
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TELECOMMUNICATION INFORMATION: 212-867-0123
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                                                                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/0 FILING DATE: 22-DEC-1994
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                                                                                                                                                                                                                                                                         1 ANGQVSLPHFPR--THRLPKEMTPVEPAA 27
OF INVENTION: C. ANTARCTICA LIPASE AND LIPASE VARIANTS
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                                                               Pathar, Shamkant A Egel-Mitani, Michi
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Egel-Mitani, Michi
                                 Clausen,
                                                   Borch, Kim
                                                                                                  Svendsen, Allan
                                                                                                                                                                                                                                                                                                              Conservative
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Best Local :
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                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA:
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              APPLICATION NUMBER: US/08/31:
FILING DATE: 03-October-1994
ATTORNEY/AGENT INFORMATION:
NAME: Harrington, James J.
                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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PRIOR APPLICATION DATA:
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CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6401
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REGISTRATION NUMBER:
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VENTION: GENES ENCODING SIGNAL RECOGNITION PARTICLE
VENTION: ASPERGILLUS NIGER
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SYSTEM: PC-DOS/MS-DOS
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Pred. No. 1
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Query Match
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Best Local Similarity
                                                                                                                                                                                         TELEPHONE: 212 867 0123
TELEFAX: 212 867 0298
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LEGITH: 552 amino acids
TYPE: amino acids
STRANDEDNESS: single
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Patent No. 592256
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                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION LONGER: U$/08/317,401E
FILING DATE: 03-October-1994
ATTORNEY/AGENT INFORMATION:
NAME: Harrington, James J.
REGISTRATION NUMBER: 38,711
REFERENCE/DOCKET NUMBER: 3448.000-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein ORIGINAL SOURCE: ORGANISM: Aspergillus
                                                                                                                                         MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 59225610 No. 5922561disk of No. 5922561th America,
STREET: 405 Lexington Avenue, Suite 6400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 534 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: GENES ENCODING SIGNAL RECOGNITION PARTICLE TITLE OF INVENTION: ASPERGILLUS NIGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 212 867 0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Thompson, Sheryl APPLICANT: Yaver, Debbie Sue
                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
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164 LTQTDPAIVAAEGVAKFKKERPEIIIVDTSGRHKQEEEL 202
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CITY: New York
STATE: New Yor)
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ZIP: 10174-6401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 534 amino acids
TYPE: amino acid
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                                                                                                                                                                               TOPOLOGY:
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                Conservative
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                                                                                                                        Aspergillus niger
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                                                                                                                                                        protein
                                20.8%; Score 56.5; 33.3%; Pred. No. 2
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Pred. No. 21
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                Mismatches
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                                                 DB 2;
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                13;
                                               Length 552;
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TELEFAX: (650
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                 APPLICANT: Tessier-La
APPLICANT: He, Zhigan
APPLICANT: Chen, Hang
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NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
                                                                                                                                                                                                                         TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin palane
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STATE: C
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                                                                            ADDRESSEE: SCIENCE DRIVE CTREET: 75 DENISE DRIVE
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STRANDEDNESS: sir
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                                                                    CITY: HILLSBOROUGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
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                                    CALIFORNIA
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75 DENISE DRIVE
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He, Zhigang
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPETIBLE
COPERATING SYSTEM: PC-DOS/MS-DOS

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                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/785,310A
FILING DATE: 21-JAN-1997
CLASSIFICATION: 536
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                                                               TELEFAX: (415) 343-4342 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (650) 343-434 (NFORMATION FOR SEQ ID NO:
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                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
                          SEQUENCE CHARACTERISTICS:
LENGTH: 824 amino acids
                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UTS
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LENGTH: 2588 amino acids
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NAME: OSMAN, RICHARD A
RECISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Neuronal PAS Domain Protein NUMBER OF SEQUENCES: 8
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STRANDEDNESS: sir
TOPOLOGY: linear
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STRANDEDNESS:
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T: 268 BUSH STREET, SUITE 3200
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Similarity 47.8%;
11; Conservative
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Pred. No. 1.5e+02;
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                                                                                                              Matches
                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No. 5874241
GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                            Best Local
                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                  TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: No.: 5874241thrup, Thomas E
REGISTRATION NUMBER: 33,268
                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
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CORRESPONDENCE ADDRESS:
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                                                       436 EASTPALPRSATLPQELPVPGLSQAATMPAPLPSPLSCDLTQQLLPQTVLQSTPAPMAQF 495
496 SAQ-FSMFQTIKDQLEQRTRILQANIRWQQEELHKIQEQL 534
                          29 AAELISRLEKLKLELESR---
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                                                                                                                                                                                                                                                        LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
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                                                                                  4 QVSLPHFPRTHRLPKEM----
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Two Prudential Plaza, Suite 4700
                                                                                                                                                                                                                                                         824 amino acids
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Pinto, Lawrence H
                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                   312-616-5460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Takahashi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             IBM PC compatible SYSTEM: PC-DOS/MS-DOS
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Pred. No. 84;
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                                                                                                                                           Length 824;
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 52
LENGTH: 824
TYPE: PRT
ORGANISM: Mus musculus
US-08-885-291-52
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US-08-934-494-2
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Best Local Similarity
Matches 20; Conserv
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Patent No. 60571
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EARLIER FILING DATE: 1997-03-13
NUMBER OF SEQ ID NOS: 55
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                                                                                                                                               FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Turek, Fred W. APPLICANT: Pinto, Lawrence H.
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                                            TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 406 amino acids
                                                                                                                                          TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                SOFTWARE: WinPatin (GECURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 mb floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    496 SAQ-FSMFQTIKDQLEQRTRILQANIRWQQEELHKIQEQL 534
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                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: South San
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                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/934,494
                                                                                                                     TELEPHONE:
              ropology:
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                               Amino Acid
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1 DNA Way
outh San Francisco
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650/952-9881
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15
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                                                                                          US-08-699-103B-10
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Best Local Similarity 34.1
Conservative
                                                           Sequence 10, Application US/08699103B Patent No. 6107462
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Patent No.
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Best Local Similarity
                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/143
FILING DATE: 28-Aug-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 406 amino acids
              APPLICANT:
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APPLICANT: Rine, Jasper D.
APPLICANT: Hampton, Randolph
TITLE OF INVENTION: GENES AND PROTEINS CONTROLLING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                         161 RRKRLPEMAQPVDP----AHNVSRLHRLPRDCQELFQVGER 197
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STATE: California
                                                                                                                                                                                     12 RTHRLPKEMTPVEPAAFAAELISRLEKLKLELESRHSLEER 52
                                                                                                                                                                                                                                                                                                                                TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
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NVENTION: Tie Ligand Homologues
STOTIFNCES: 17
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650/952-9881
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Hillan, Kenneth
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Goddard, Audrey
Godowski, Paul J.
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Pred. No.
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Pred. No.
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US-08-699-103B-12
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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NEORMATION FOR SEQ ID NO:
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NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/699,103B
FILING DATE: 16-AUG-1996
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 09
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/322-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/002,581
FILING DATE: 17-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Green, Grant D.
REGISTRATION NUMBER: 31,259
REGISTRATION NUMBER: 31,259
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LENGTH: 853 amino acid
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                                                                                                                                                 ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
SOFTWARE: FastSEQ for Windows Version CORRENT APPLICATION DATA:
CAPPLICATION NUMBER: US/08/699,103B FILLING DATA: 16-AUG-1996
PAPICATION NUMBER: 60/002,581
PAPLICATION NUMBER: 60/002,581
FILLING DATE: 17-AUG-1995
                                                                                                                                                                                                                                                                                                                       APPLICANT: Hampton, Randolph
TITLE OF INVENTION: CHOLESTEROL SYNTHESIS
                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
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STATE: CA
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STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
                                                                                                                COMPUTER: IBM CONTROL OPERATING SYSTEM:
                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                       STATE: CA
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2200 Sand Hill Road, Suite 100
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-699-103B-12
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Search completed: June Job time: 5403 sec
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Best Local Similarity 37:9
Matches 11; Conservative
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Best Local Similarity
Matches 11; Conserv
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APPLICANT: Sun, Zhong Sheng
APPLICANT: Albrecht, Urs
APPLICANT: Elchele, Gregor
TITLE OF INVENTION: Mammalian Circadian Regulator M-RIGUIZ (M-PERZ)
FILE REFERENCE: D6067
                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/220,641
CURRENT FILING DATE: 1998-12-24
EARLIER APPLICATION NUMBER: US 60/068,886
EARLIER FILING DATE: 1997-12-26
NUMBER OF SEQ ID NOS: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. 6210923
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INFORMATION FOR SEQ ID NO: 12:
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Copyright (c) 1993 - 2000 Compugen Ltd
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## ALIGNMENTS

Axin

homolog Axil -

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negative regualtor axin [imported] - rat
N;Alternate names: rAxin
C:Species: Rattus norvegicus (Norway rat)
C:Species: Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jul-2000
C;Accession: T08422
R;Ikeda, S:; Yamamoto, H:; Murai, H:; Kishida, .S.; Kikuchi, A.
EMBO J: 17, 1371-1384, 1998
A;fitle: Axin, a negative regulator of the Wnt signaling pathway, forms a co
A;Reference number: Z16413; MUID:98151361
A;Accession: T08422
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mkNA
A;Residues: 1-832 < TKE>
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C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Species: Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jul-2000
C;Accession: T08423
R;Yamamoto, H.; Kishida, S.; Uochi, T.; Ikeda, S.; Koyama, S.; Asashima, M.; Kikuchi, Roll. Cell. Biol. 18, 2867-2875, 1998
A;Title: Axil, a member of the Axin family, interacts with both glycogen synthase kin A;Reference number: Z16414; MUID:98226558
A;Accession: T08423
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A;Molecule type: mRNA
A;Residues: 1-838 <YAM>
A;Cross-references: EMBL:AF017757; NID:g3080758; PIDN:AAC40089.1; PID:g3080759
A;Note: interacts with GSK-3beta and beta-catenin
C;Keywords: phosphoprotein; signal transduction
                                                                                                         A;Cross-references: EMBL:AF017756; NID:g2982197; PIDN:AAC40066.1; PID:g2982198 A;Note: GSK-3beta interacting protein C;Keywords: phosphoprotein; signal transduction
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Query Match
Best Local Similarity
Matches 30; Conserv
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Best Local
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  Conservative
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                       56.68;
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  8; Mismatches
                     Score 142.5;
Pred. No. 9.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 272; DB 2; Pred. No. 7.1e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                       .2e-09
                                              DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 838;
                                          Length
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  Indels
                                              832;
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  Gaps
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A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serorakeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Togononi, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, R.; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A; Reference number: A69580; MUID:98044033
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C; Genetics:
A; Gene: PA1624
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R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
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C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000
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A; Residues: 1-141 <KUN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            conserved hypothetical protein yklA - Bacillus subtilis
C; Species: Bacillus subtilis
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A; Residues: 1-268 <STO>
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                                                Query Match
Best Local
                                                                                                                                                                                                                    Superfamily: hypothetical protein ykla
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    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Status: preliminary; nucleic acid sequence not shown; translation not shown
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    l Similarity
16; Conserv
23.2%;
ilarity 33.3%;
Conservative 1
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; Score 63; DB; Pred. No. 2.4; 11; Mismatches
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Pred. No. 3
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                                                                                    DB 2;
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                                                                               Length 141;
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K.; Lim,
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A;Cross-references: EMBL:AF020713; NID:g3025478; PID:g3025578; PIDN:AAC13073.1
A;Cross-references: EMBL:AF020713; NID:g3025478; PIDN:AAC13073.1
C; Bron, S; Broulllet, S; Bruschi, C.V.; Caldwell, B; Capuano, V.; Carter, N.M.;
A; Ehrlich, S.D.; Emmerson, P.T.; Entlan, K.D.; Errington, J; Fabret, C; Ferrari,
Nature 390, 249-256, 1997
A; Authors: Foulger, D; Fritz, C; Fujita, M; Fujita, Y; Fuma, S; Galizzi, A; Gal
A; Authors: Foulger, D; Fritz, C; Fujita, M; Fujita, Y; Fuma, S; Hosono, S; Hullo, M
iech, J.; Harwood, C.R.; Henaut, A; Hilbert, H; Holsappel, S; Hosono, S; Hullo, M
Koetter, P; Koningstein, G; Krogh, S; Kumano, M; Kurita, K; Lapidus, A; Lardino
A; Authors: Lauber, J; Lazarevic, V; Lee, S,M.; Levine, A; Liu, H; Masuda, S; Mau
Y, M; Ogawa, K; Ogiwara, A; Oudega, B; Park, S.H.; Parro, V.; Pohl, T.M.; Portete
Rieger, M; Rivolta, C; Rocha, E; Roche, B; Rose, M; Sadaie, Y; Sato, T; Scanl
A; Authors: Schleich, S; Schroeter, R; Scoffone, F; Sekiguchi, J; Sekowska, A; Se
akeuchi, M; Tamakoshi, A; Tamanoto, H; Yamane, K; Yasumoto, K; Yata, K; Yoshida
A; Authors: Yoshikawa, H, F; Zumstein, E; Yoshikawa, H; Danchin, A.
A; Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili
A; Molecule type: DNA
A; Residues: 1-333 <LOG>
C; Superfamily: unassigned homeobox proteins;
C; Keywords: DNA binding; homeobox; nucleus; 1
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A;Description: The complete nucleotide sequence of the Bacillus subtilis SPbeta
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C;Species: Bacillus subtilis phage SPBC2
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 20-Jun-2000
                                                                                                                                                                                                        R;Logan, C.; Hanks, M.C.; Noble-Topham, S.; Nallainathan, Dev. Genet. 13, 345-358, 1992
A;Title: Cloning and sequence comparison of the mouse, hum A;Reference number: A48423; MUID:93185339
                                                                                                                                                                                                                                                                                                                                                                                                     homeotic protein engrailed 1 - chicken
C;Species: Gallus gallus (chicken)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Oct-1997
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A; Accession: T12864
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                                                                                                                                         A; Status: preliminary; not compared with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:Z99114;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ANGQVSLPHFPRTHR-----LPKEMTPVEPAAFAAELISRLEKLKLELESRHSL 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1-251 <KUN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GB:Z99115; GB:AL009126; NID:g2634478; PIDN:CAB13985.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 62.5; DB 2; Pred. No. 5.3;
                                                                                                                                                    conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 251;
                                                                                                                                                                                                                                                                                                                                   D.; Provart, N.J.; Joyner,
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homeobox homology

regulation

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A;Map position: 3
A;Introns: 66/2; 111/3; 177/1; 217/3; 269/3
A;Note: T3A5.100
C;Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote
                                                                                                                                                                                                                                                                                                   C;Accession: T46149
R;Bloecker, H.; Mewes, H.W.; Mayer, submitted to the Protein Sequence D
                                                                                                                                                                                                                                                                                                                                                     protein kinase ATN1-like protein - Arabidopsis thaliana
N;Alternate names: protein T3A5.100
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 17-Mar-2000
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C;Superfamily: Saccharomyces cerevisiae hypothetical protein YJR003c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:x87611; NID:g854567; PIDN:CAA60924.1; R;de Haan, M.; Grivell, L.A.; Smits, P.H.M. submitted to the Protein Sequence Database, September 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein YJR003c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein J1415; hypothetical protein YJR83.3(
C;Species: Saccharomyces cerevisiae
C;Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 04-Mar-2000
C;Accession: S55190; S57018
R;de Haan, M.; Smits, P.H.M.; Grivell, L.A.
submitted to the EMBL Data Library, May 1995
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A;Experimental source: cultivar Columbia;
                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-377 <BLO>
                                                                                                                                                                                                                                                                    A; Reference number: 223024
A; Accession: T46149
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A; Residues: 1-539 <ZAG>
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A; Accession: S57018
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A; Residues: 1-539 <DEH>
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A:Accession: S55190
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Best Local S
Matches 15
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Best Local Similarity
Matches 12; Conserv
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 th 22.1%; Similarity 30.6%; P. 15; Conservative 11;
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38.8%;
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 Score 60; DB
Pred. No. 16;
11; Mismatches
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Pred. No. 16;
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Pred. No. 8.2;
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December
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r 1999
                                  Length 377;
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c;Species: Homo
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R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Hc Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complet A;Reference number: A70500; MUID:98295987
A;Accession: E70826
                                                                                                                                                                                                                                                                        C;Genetics:
A;Gene: mmp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable membrane protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:X79993; NID:g871983; PIDN:CAA56314.1; PID:g871984 C;Superfamily: kinase-related transforming protein; protein kinase homolog C;Keywords: ATP: phosphotransferase; protein kinase F;33-322/Domain: protein kinase homology <KIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mitogen-activated protein kinase N; Alternate names: MAP1 kinase
                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:AL021943; GB:AL123456; NID:g3261530; A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-964 <COL>
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A; Residues: 1-369 <HUT>
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Plant Mol. Biol. 27, 1043-1052, 1995
A;Title: Glbberellin-regulated expression
A;Reference number: S56638; MUID:95284341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Avena sativa (oat)
C;Date: 27-Oct_1995 #sequence_revision 03-Nov-1995 #text_change 18-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary; nucleic acid sequence
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11
                                                                                          7 LPHFPRTHRLPKEMTPVEPAAFAAELISRLEKLKLELESRHSLEERLQ 54
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                                                                LPLMQRLDTLMPQLTAMMP----EMIQTMKSMKAQMLSMHSTQEGLQ 663
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19; Conserv
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; Pred. No. 53;
10; Mismatches
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; Pred. No. 18;
7; Mismatches
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human (fragment) sapiens (man)

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C;Accession: A82561
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: A82561
A;Status: preliminary
A;Cross-references: GB:AE004050; GB:AE003849; NID:g9107594; PIDN:AAF85213.1; A;Experimental source: strain 9a5c R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein XF2414 [imported] - Xylella fastidiosa (strain 9a5c) C;Species: Xylella fastidiosa C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-20 C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #sequence
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A;Title: Coordinate embryonic expression of three zebraf A;Reference number: S30437; MUID:93201987
A;Accession: S30438
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C;Date: 13-Jan-1995 #sequence_revision 13
C;Accession: S30438
                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-601 <SIM>
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C;Superfamily: unassigned homeobox proteins; homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
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A; Residues: 1-231 <EKK>
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A; Residues: 1-7962 < RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 PRTHRLPKEMTPVEP-----AAFAAELISRLEKLKLELE-SRHSLEERLQ 54
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les 19; Conserv
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    Alvarenga, R.;
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A;Cross-references: EMBL:D14693; NID:g287572; C;Superfamily: unassigned homeobox proteins;
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A;Authors: Ferreira, V.C.A.; Eraga, J.S.; Franca, S.C.; Franco, M.C.; Fr J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins A;Authors: Martins, E.M.F.; Matsukuma, A.V.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C., F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, R.G.; Santelli, R.V.; Sawa A;Authors: da Silva, R.G.; Valada, H.; Vallada, H.; Valnada, H.; Valnada, H.; Valnada, H.; Valnada, H.; Valnada, M.A.; Verjovski-Almeida, S.; Vettore, A.L. A;Reference number; A59328
                                                                                                                                                                                                                                            homeotic protein En-1b - African clawed frog (fragment)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein C47D12.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
A; Molecule type: mRNA
A; Residues: 1-171 <WAT>
                                                                               A; Reference number: A; Accession: S35638
                                                                                                         A;Title: Nucleotide sequence of Xenopus homeobox gene, En-1.
A;Reference number: S35638; MUID:93281404
                                                                                                                                                            R;Watanabe, M.; Hayashida, T.; Nishimoto, T.; Kobayashi, H.
Nucleic Acids Res. 21, 2513, 1993
                                                                                                                                                                                                                  C; Accession:
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A; Introns: 40/3; 150/3; 476/3; 577/2;
C; Superfamily: threonine--tRNA ligase
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                                                        A;Status: preliminary
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A;Experimental source: clone C47D12
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A; Accession: T19994
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A; Residues: 1-725 <WIL>
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                              35 HFVNGHKMSKAPTDMAPWPAFIEERIKLWDKLKAEYDAEIAAKE 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 HFPRTHRLPKEMTPVEP-AAFAAELISRLEKLKLELESRHSLEE
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6699 phaseolus v	P25	AVU	FRI_PHAVU	-	254	19.3	52.5	44
	P14	CHAM	HMEN_SCHAM	<u>_</u>	93	19.3	52.5	43
054943 mus musculu	054	OUSE	PER2_MOUSE	_	1257	19.5	53	42
Q13200 homo sapien	Q13	JMAN	PSD2_HUMAN	ب	908	19.5	53	41
	P21	DUSE	CD72_MOUSE	ш	354	19.5	53	40
	Q62	OUSE	SH33_MOUSE	ᆫ	347	19.5	53	39
Q10552 mycobacteri	210	CTU	Y893_MYCTU	_	325	19.5	53	38
	299	JMAN	NPA2_HUMAN	ᆫ	824	19.7	53.5	37
Q9v407 drosophila	Q9ν	OME	AXN_DROME	ب	745	19.7	53.5	36
Q14314 homo sapien	Q14	JMAN	FGL2_HUMAN	ᆫ	439	19.7	53.5	35
P57722 mus musculu	P57	OUSE	PCB3_MOUSE	Н	339	19.7	53.5	34

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phorylation. RGS GSK-3B BIN	This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no we modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to licenseeisb-sib.ch).	OCCURS VIA THE ARMADILLA REPEATS CONTAINED IN BE TERNARY COMPLEX. TERNARY COMPLEX. SUBCELLULAR LOCATION: CYTOPLASMIC. TISSUE SPECIFICITY: EXPRESSED IN LUNG AND THYMUS PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHO PP2A. SIMILARITY: CONTAINS 1 RGS DOMAIN. SIMILARITY: CONTAINS 1 DIX DOMAIN.	Xenopus embryos.";  Mol. Cell. Biol. 18:2867-2875(1998).  Hol. Cell. Biol. 18:2867-2875(1998).  FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWNED BETA-CATEMIN. PROBABLY FACILITATE THE PHOSPHORYLATION CATEMIN AND APC BY GSK-3B (BY SIMILARITY).  FOR SUBUNIT: INTERACTS WITH GLYCOGEN SYNTHASE KINASE-3 BE AND BETA-CATEMIN. THE INTERACTION BETWEEN AXIN AND BE AND BETA-CATEMIN. THE INTERACTION BETWEEN AXIN AND BETA-CATEMIN.	.A.  B; PubMed-9566905;  shida S., Uochi T., Ikeda S., Koyama S.,  of the Axin family, interacts with both  3beta and beta-catenin and inhibits axin	ted) sequence update) annotation update oTEIN 2) (CONDUCTI ta; Craniata; Vert ta; Sciurognathi;	PRT;
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"Properties of mouse Axin2 and human AXIN2: chromosomal location, expression pattern, interaction with Axin and effects on embryoni axis formation.";
Gibert D., Copeland N.G., Copeland N.G., Senter D., Copeland N.G., Copeland N
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-!- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-CATENIN AND APC BY GSK-3B (BY SIMILARITY).
-!- SUBUNIT: INTERACTS WITH GLYCOGEN SYNTHASE KINASE-3 BETA (GSK-3B) AND BETA-CATENIN. THE INTERACTION BETWEEN AXIN AND BETA-CATENIN. OCCURS VIA THE ARMADILLO REPEATS CONTAINED IN BETA-CATENIN.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    088566; Q9QXJ6;
01-OCT-2000 (Re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 280:596-599(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (AXIL).
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                                                                                                                                                                                                                                                                                                                  s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - Buropean Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: CONTAINS 1 RGS DOMAIN. SIMILARITY: CONTAINS 1 DIX DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TERNARY COMPLEX (BY SIMILARITY).
SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY)
PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PP2A (BY SIMILARITY).
                                                                                                            , AF205889; AF
MGI:1270862;
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                                                                                   P49799;
                                                                                                                                                                                                                   an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         h 100.0%;
Similarity 100.0%;
54; Conservative (
                                                           IPR000342;
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AAF22800.1;
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POLY-HIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.
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Pred. No. 1.7e-24
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Best Local
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AXN2_HUMAN

Q9Y2T1; Q9UH84;

Q1-OCT-2000 (Rel
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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mai M., Qian C., Yokomizo A., "Cloning of the human homolog chromosome 17q23-q24.";
                                                                                                                                                                                                                                                                                                                                  axis formation."; Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                             Zhang T., Fagotto F., Hsu W., Zeng L., Gilbert D., Copeland N.G., Jenkins N.A., Warburton D., Costantini F.; "Properties of mouse Axin2 and human AXIN2: chromosomal location,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                           expression pattern, interaction with Axin and
                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Brain, and Lymphoblast;
Zhang T., Fagotto F., Hsu W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genomics 55:341-344(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=99168905; PubMed=10049590;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AXIN 2 (AXIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2000 (Rel. 40, Created)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR01301; RGSPROTEIN. PROSITE; PS50132; RGS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
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SIMILARITY: CONTAINS
SIMILARITY: CONTAINS
                                                                                                           OCCURS VIA THE ARMADILLO REPEATS CONTAINED TERNARY COMPLEX (BY SIMILARITY).
SUBCELLULAR LOCATION: CYTOPLASMIC.
TISSUE SPECIFICITY: EXPRESSED IN BRAIN AND PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND
                                                                                                                                                                                                                    FUNCTION: INHIBÍTOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-CATENIN AND APC BY GSK-3B (BY SIMILARITY).

SUBUNIT: INTERACTS WITH GLYCOGEN SYNTHASE KINASE-3 BETA (GSK-3B) AND BETA-CATENIN. THE INTERACTION BETWEEN AXIN AND BETA-CATENIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 100.54; Conservative
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758
101
474
484
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840
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                                           1 RGS
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R -> K (IN REF. 2)
H -> Y (IN REF. 2)
S -> P (IN REF. 2)
F -> S (IN REF. 7)
A (IN REF. 7)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSK-3B BINDING SITE (BY SIMILARITY).
BETA-CATENIN BINDING SITE (BY
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RGS.
GSK-3B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Smith D.I., I
of conductin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 272; DB 1;
Pred. No. 1.8e-24;
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                                             DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Liu W.;
Ln (AXIN2),
                                                                                                                                                                                                                                                                                                                                                                                 effects on embryonic
                                                                                                               LYMPHOBLAST.
DEPHOSPHORYLATED
                                                                                                                                                                                                      Z
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                                                                                                                                                                                                    ASE-3 BETA (GSK-3B)
N AND BETA-CATENIN
BETA-CATENIN.
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Best Local S
Matches 53
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Pfam; PF00615; RGS; 1.

Pfam; PF00778; DIX; 1.

PRINTS; PR01301; RGSPROTEIN.

PROSITE; PS50132; RGS; 1.

Developmental protein; Phosphorylation.

DOMAIN 81 200 RGS.

DOMAIN 327 413 GSK-3B BINDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
                                                                                         MEDLINE-20171051; PubMed-10704853;

Shimizu T., Yamanaka Y., Ryu S.-L., Hashimoto H., Yabe T., Hirata T.,
Shimizu T., Yamanaka Y., Ryu S.-L., Hashimoto H., Yabe T., Hirata T.,
Shimizu T., Yamanaka Y., Ryu S.-L., Hashimoto H., Yabe T., Hirata T.,
Shimizu T., Yamanaka Y., Ryu S.-L., Hashimoto H., Yabe T.,
"Cooperative roles of Bozozok/Dharma and Nodal-related proteins in the formation of the dorsal organizer in zebrafish.";

Mech. Dev. 91:293-303(2000)

-I- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES BETA-CATENIN PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-CATENIN AND APC BY GSK-3B (BY SIMILARITY).

-I- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
                                                                                                                                                                                                                                                                            Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Rasborinae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                         AXN2_BRARE
P57095;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
DOMAIN
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01-OCT-2000 (Rel. 40, Last annotation update)
AXIN 2 (AXIS INHIBITION PROTEIN 2).
                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                             PP2A (BY SIMILARITY).
SIMILARITY: CONTAINS 1 RGS DOMAIN.
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0; Mismatches
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Q -> R (IN REF. 2).
MISSING (IN REF. 2).
P -> S (IN REF. 2).
Q -> H (IN REF. 2).
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BETA-CATENIN BINDING SITE (BY
SIMILARITY).
POLY-HIS.
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QPGVGKQQVTKPMSVSSNTRRNEDGL -> HHGGQGPGHQT
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                          the European Bioinformatics Institute. The use by non-profit institutions as long of modified and this statement is not removed. entitles requires a license agreement (See I
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Pfam; PF00778; DIX; 1.
PROSITE; PS50132; RGS; 1.
Developmental protein; Phosphorylation.
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                                                                                                                                                                                                                                                                                                                           PP2A (BY SIMILARITY).
                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through a copyright the Swiss Institute of Bioinformatics and the EMBL
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4; Mismatches 7
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BETA-CATENIN BINDING SITE (BY
SIMILARITY).
POLY-SER.
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Matches 32
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InterPro; IPR000342;
InterPro; IPR001158;
Pfam; PF00615; RGS; 1.
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                                                                                                                            the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                    Bae Y.-K., Hibi M., Hirano T.;

"Cooperative roles of Bozozok/Dharma and Nodal-related proformation of the dorsal organizer in zebrafish.";

Mech. Dev. 91:293-303(2000).

-i- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN
BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Puteleostomi;
Eukaryota; Metazoa; Chordata; Peteleostei; Buteleostei; Ostariophysi
Actinopteryqii; Neopteryqii; Teleostei; Buteleostei; Ostariophysi
Cypriniformes; Cyprinidae; Rasborinae; Danio.
                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE=20171051; PubMed=10704853;
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Pfam; PF00778; DIX; 1.
PROSITE; PS50132; RGS; 1.
Developmental protein; Phosphorylation.
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               Pfam; PF00778; DIX; 1. PROSITE; PS50132; RGS;
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   Developmental protein; Phosphorylation.
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                                                                                                                                                                                                                                                                           CATENIN AND APC BY GSK-3B (BY SIMILARITY) SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY) PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOS PP2A (BY SIMILARITY).
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                                                                                                      AB032262; BAA92439.1;
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32; Conserv
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841 AA;
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(Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INHIBITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              841
94931 MW;
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433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57.9%;
59.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROTEIN 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 157.5;
Pred. No. 5.5e
l1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSK-3B BINDING SITE (BETA-CATENIN BINDING SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              400D0C90E72506FE CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                and Nodal-related proteins in
zebrafish.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; DB 1;
5.5e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A
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                                                                                                                                                                                                                                                                                           DEPHOSPHORYLATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 841;
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                                                                                                                                                                                                                                                                                                                                                   DOWN
                                                                                                                                                                                                                                                                                                                                      N REGULATES
OF BETA-
                                                                                                                                                                                                                                                                                                                                                                                                                           Hirata T.,
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RESULT
AXN1_RAT
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Best Local S
                           InterPro; IPR000342; -.
InterPro; IPR001158; -.
Pfam; PF00615; RGS; 1.
Pfam; PF00778; DIX; 1.
PROSITE; PS50132; RGS; 1.
Developmental protein; Pho
                                                                                                                                                                                                                                                                                                                                                                                     dependent phosphorylation of beta-catenin.;

dependent phosphorylation of beta-catenin.;

embo J. 17:1371-1384(1998).

-i- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-CATENIN AND APC BY GSK-3B (BY SIMILARITY).

-i- SUBGUNIT: INTERACTS WITH GSK-3B AND BETA-CATENIN. THE INTERACTION BETWEEN AXIN AND BETA-CATENIN OCCURS VIA THE ARMADILLO REPEATS CONTAINED IN BETA-CATENIN. TERNARY COMPLEX. ALSO BINDS TO PLAKOGLOBIN (GAMMA-CATENIN), APC, DYL AND P22A (BY SIMILARITY).

-i- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).

-i- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).

-i- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN TESTIS, THYMUS AND LUNG FOLLOWED BY CEREBRUM, CEREBELLUM, HEART, KIDNEY, SKELETAL MUSCLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-2000
01-0CT-2000
01-0CT-2000
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NON_TER
                                                                                                                                                                                         use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                            This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ikeda S., Kishida S., Yamamoto H., Murai H., Koyama S., Kikuchi "Axin, a negative regulator of the Wnt signaling pathway, forms complex with GSK-3beta and beta-catenin and promotes GSK-3beta-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
01-DCTEIN (AXIS INHIBITION PROTEIN 1) (RAXIN) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AXN1_RAT
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                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                          the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AXIN1 OK AALI.
Rattus norvegicus (Rat).
Rattus norvegicus (Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                               HSSP; P49799; 1AGR.
                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                             between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   366 NGRVPLPHIPRTINRIPKDI-HVEPEKFAAELISRLEGVLREREAQEKLEERLK 417
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                                                                                                                                                                                                                                                                                                          PP2A (BY SIMILARITY).
SIMILARITY: CONTAINS 1 RGS DOMAIN.
SIMILARITY: CONTAINS 1 DIX DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7
                                                                                                                                                                                                                                                                                                                                                             PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
                                                                                                                                                                                                                                                                                                                                                                           SPLEEN AND LIVER.
                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - Buropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                            AF017756;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32;
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351
437
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94351 MW;
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                                 Phosphorylation.
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                                                                                                                                              ALT_INIT.
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Pred. No. 3.7e-10;
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GSK-3B BINDING SITE (
BETA-CATENIN BINDING
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zeng L., Pagotto F., Zhang T., Hsu W., Vasicek T.J., Perry W.L. III, Lee J.J., Tilghman S.M., Gumbiner B.M., Costantini F.;
"The mouse Fused locus encodes Axin, an inhibitor of the Wnt signaling pathway that regulates embryonic axis formation.";
Cell 90:181-192(1997).

Cell 90:181-192(1997).

BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2000 (Rel. 40, Created)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
AXIN 1 (AXIS INHIBITION PROTEIN 1) (FUSED PROTEIN) (FRAGMENT).
AXIN1 OR AXIN OR FU.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AXN1_MOUSE 035625;
                                                                                                                                                                                                                                                               EMBL; AF009011; AAC53285.1; HSSP; P49799; 1AGR. MGD; MGI-1096327; Axin. InterPro; IPR000342; -. InterPro; IPR001158; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2000
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                                                                                                                                                             PROSITE;
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                                                                                                                  Developmental
                                                                                                                                                                                                Pfam;
                                                                                                                                                                                                                                            Pfam;
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m; PF00615; RGS; 1.
m; PF00778; DIX; 1.
SITE; PS50132; RGS; 1.
elopmental protein; Phosphorylation; Al
elopmental protein; Phosphorylation; Al
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elopmental protein; Al

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: CONTAINS 1 RGS DOMAIN. SIMILARITY: CONTAINS 1 DIX DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATENIN AND APC BY GSK-3B (BY SIMILARITY).
SUBUNIT: INTERACTS WITH GSK-3B AND BETA-CATENIN. THE INTERACTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PTM: PROBABLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NGRVPLPHIPRTYRMPKEIR-VEPQKFAEELIHRLEAVQRTREAEEKLEERLK 480
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567
893
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Pred. No. 3.5e-09;
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Best Local s
Matches 30
                             InterPro; IPR000342; -.
InterPro; IPR001158; -.
Pfam; PF00615; RGS; 1.
Pfam; PF00778; DIX; 1.
PROSITE; PS50132; RGS; 1
Developmental protein; Pl
NON_TER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-97373830; PubMed-9230313;

Zeng L., Fagotto F., Zhang T., Hsu W., Vasicek T.J., Perry W.L. III,

Lee J.J., Tilghman S.M., Gumbiner B.M., Costantini F.;

"The mouse Fused locus encodes Axin, an inhibitor of the Wnt signaling
pathway that regulates embryonic axis formation.";

Cell 90:181-192(1997).

Cell 90:181-192(1997).

-I- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES

BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARSPLIC
SEQUENCE
             NON_TER
                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercia entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2000 (Rel. 40,
01-OCT-2000 (Rel. 40,
01-OCT-2000 (Rel. 40,
AXIN 1 (AXIS INHIBITION)
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DOMAIN
                                                                                                                                   EMBL; AF009674; AAC51624.1;
HSSP; P49799; IAGR.
MIM; 603816; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          492 NGRVPLPHIPRTYRMPKEIR-VEPQKFAEELIHRLEAVQRTREAEEKLEERLK 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TERNARY COMPLEX. MAY ALSO BINDS TO PLAKOGLO APC, DVL AND PP2A.
SUBCELLULAR LOCATION: CYTOPLASMIC.
TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED.
PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND
                                                                                                                                                                                                                                                                                                      SIMILARITY: CONTAINS 1 RGS DOMAIN. SIMILARITY: CONTAINS 1 DIX DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                          CATENIN AND APC BY GSK-3B.
SUBUNIT: INTERACTS WITH GLYCOGEN SYNTHASE KINASE-3 BETA (GSK-3B)
AND BETA-CATENIN. THE INTERACTION BETWEEN AXIN AND BETA-CATENIN
OCCURS VIA THE ARMADILLO REPEATS CONTAINED IN BETA-CATENIN.
                                                                                                                                 603816;
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30; Conservative
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(Rel. 40, Last annotation update)
INHIBITION PROTEIN 1) (HAXIN) (FRAGMENT).
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630
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 248
470
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                                         1.
Phosphorylation.
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Pred. No. 3.9e
8; Mismatches
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BETA-CATENIN BINDING SITE (BY
SIMILARITY).
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GSK-3B BINDING
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70EEB53D387BD26F CRC64;
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                                                                                                                                                                                                                                                                                                                                                      DEPHOSPHORYLATED
 (BY SIMILARITY).
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Best Local
DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hedgepeth C.M., Deardorff M.A., Klein P.S.;

"Xenopus axin interacts with glycogen synthase kinase-3 beta and is expressed in the anterior midbrain.";

Mech. Dev. 80:147-151(1999).

-i- FUNCTION: INHIBITOR OF THE WMT SIGNALING PATHWAY. DOWN REGULATES BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-CATENIN AND APC BY GSK-3B (BY SIMILARITY).

-i- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).

-i- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).

-i- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).

-i- BYELOPMENTAL STAGE: WEAKLY AND UBJQUITOUSLY EXPRESSED THROUGHOUT EARLY DEVELOPMENT, AND HIGHLY EXPRESSED IN THE ANTERIOR MESSENCEPHALON ADJACENT TO THE FOREBRAIN-MIDBRAIN BOUNDARY.

-i- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as its content is in no modified and this statement is not removed. Usage by and for commer entitles requires a license agreement (See http://www.isb-sib.ch/annou or send an email to license@isb-sib.ch).
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SEQUENCE
                                                                                 DOMAIN
                                                                                                                                                                                         Pfam; PF00778; DIX; 1. PROSITE; PS50132; RGS;
                                                                                                                                                                                                                                                                                                                                       EMBL; AF097313; AAC71036.1; -. HSSP; P49799; 1AGR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE=99173782; PubMed=10072781;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2000 (Rel. 40, Created)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
AXIN (AXIS INHIBITION PROTEIN) (XAXIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9YGY0;
                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                   Ptam;
                                                                                                                                                                                                                                                                                                          InterPro; IPR000342; -.
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                                                                                                                                                                  Developmental protein; Phosphorylation.
                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=8355
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SIMILARITY: CONTAINS 1 RGS DOMAIN.
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                                                                                                                                                                                                                                                   PF00615; RGS;
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99803 WW;
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                                  RGS.
GSK-3B BINDING SITE (BY SIMILARITY).
BETA-CATENIN BINDING SITE (BY
SIMILARITY).
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Pred. No. 4.6e-09;
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  BDA152734C97191E CRC64;
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7

Query Match

Score 136.5;

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HME1_CH
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Best Local 9
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                                                                                                                    DOMAIN
DNA_BIND
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Provart N.J., Joyner A.L.; "Cloning and sequence comparison of the mouse, human, and engrailed genes reveal potential functional domains and re
                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                       PRINTS; PR00024; HOMEOBOX. PRINTS; PR00026; ENGRAILED.
                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE=93185339; PubMed=1363401;
                                                                                                                                                             DOMAIN
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                                                                                                                                                                                                     Homeobox;
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PROSITE; PS50071; HOMEOBOX_2; 1.
PROSITE; PS00033; ENGRAILED; 1.
                                                                                                                                                                                                                                                                                               InterPro; IPR001356;
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                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           regions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gallus gallus (Chicken).
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Ol-FEB-1994 (Rel. 28, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
HOMEOBOX PROTEIN ENGRAILED-1 (GG-EN-1).
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               8 PHFPRTHRLPKEMTPVEP----AAFAAELISRLEKLKLELE-SRHSLEERLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: NUCLEAR.
SIMILARITY: BELONGS TO THE ENGRAILED FAMILY OF HOMEOBOX PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genet. 13:345-358(1992).
Genet. In a LOCATION: NUCLEAR.
PSSPRTRKLKKKKTEKEDKRPRTAFTAE - - - QLQRLKAEFQANRYITEQRRQ
                                                                                                                                                                                                                                                                                   PF00046;
                                                                                                                                                                                                                                                                                                                                                   L12694; AAA53435.1; -. L12695; AAA53436.1; -.
                                                                                                                                                                                                                                                                                                                                       P02836; 1HDD.
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                                                                Similarity
                                                                                                                   DNA-binding; Developmental protein; Nuclear protein.

22 29 POLY-GLY.
36 65 PRO-RICH.
59 65 POLY-PRO.
97 104 POLY-GLY.
244 303 HOMEOBOX.
333 AA; 34515 MW; DOFIBIF917E1FBAD CRC64;
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IPR000747; -.
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RESULT 13
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Best Local
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30-MAY-2000
30-MAY-2000
                                                                                                                                                                                                                                                           YUN3_YEAST STANDARD; PRT; 539 AA.
P47084;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
HYPOTHETICAL 62.2 KDA PROTEIN IN MPP10-SAGI INTERGENIC REGION.
YJR003C OR J1415 OR YJR83.30.
Saccharomyces cerevisiae (Baker's yeast).
Saccharomyces cerevisiae, Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                               SEQUENCE FACE.

STRAIN-5288C / FY1679,

Ge Haan M., Smits P.H.M., Grivell L.A.;

de Haan M., Smits P.H.M., Grivell L.A.;

submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus subtilis.
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
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              EMBL; X87611; CAA60924.1; -. EMBL; Z49503; CAA89525.1; -.
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14.9
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KDA
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PROTEIN IN PROA-METC INTERGENIC
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Pred. No. 1;
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EMBL; L12699;
HSSP; P02836;
TRANSFAC; T020
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DNA_BIND
SEQUENCE
                                                                                                                                                                                  PROSITE;
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Q05925;
                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Logan C., Hanks M.C., Noble-Topham Provart N.J., Joyner A.L.; and sequence comparison of engrailed genes reveal potential fu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1994 (Rel. 28, Last sequence update) 01-OCT-2000 (Rel. 40, Last annotation updat HOMEOBOX PROTEIN ENGRAILED-1 (HU-EN-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1994 (Rel. 28,
01-FEB-1994 (Rel. 28,
01-OCT-2000 (Rel. 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein. seQuence 539 AA; 62214 MW;
                                                                                                                                                                                                          PRINTS; PR00024; HOMEOBOX. PRINTS; PR00026; ENGRAILED.
                                                                                                                                                                                                                                                                      MIM; 131290;
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                                                                                                                                                 DOMAIN
                                                                                                                                                          Homeobox;
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InterPro; IPR001356; -.
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               PHFPRTHRLPKEMTPVEP----AAFAAELISRLEKLKLELE-SRHSLEERLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genet. 13:345-358(1992)
PSSPRTRKLKKKKNEKEDKRPRTAFTAE---QLQRLKAEFQANRYITEQRRQ
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PS50071;
PS00033;
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199 218
224 231
302 361
391 AA; 400
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; HOMEOBOX_2; 1.
; ENGRAILED; 1.
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                                                                                                            40044 MW;
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Pred. No. 7;
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Pred. No.
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                                                                                                              30DA29BF0995956F
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Search completed: June
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Best Local Similarity 32.4
Matches 22; Conservative
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MEDLINE=97422617; PubMed=9268643;

Hanna M.C., Platts J.T., Kirkness E.F.;

Hanna M.C., Platts J.T., Kirkness E.F.;

"Identification of a gene within the tandem array of red and green color pigment genes.";

Genomics 43:384-386(1997).
-i- TISSUE SPECIFICITY: TESTIS-SPECIFIC.
-i- SIMILARITY: SOME, TO HUMAN KIAA0481.
                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               015482;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
TESTIS-SPECIFIC PROTEIN TEX28.
CXORF2 OR TEX28.
                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                      EMBL; U93720; AAB71379.1; -. MIM; 300092; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                         NCBI_TaxID=9606;
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                                                                             222 SYHSLKER 229
                                                                                               45 SRHSLEER 52
                                                                                                                                                                       2 NGQVSLPHFPRTHRLP-----KEMTPVEPAAFAAELISRLEKLKLEL------E 44
                                                                                                                                                                                                                                                                                 92; -.
410 AA; 46131 MW;
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              7, 2001, 02:10:31
                                                                                                                                                                                                                       21.9%;
                                                                                                                                                                                                    Score 59.5; DB 1; Length 410; Pred. No. 8.9; 9; Mismatches 20; Indels 1
                                                                                                                                                                                                                                                                                    8E455A761D52A660 CRC64;
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Minimum DB seq
Maximum DB seq
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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110
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272
272
272
268
264
157.64
1142.5
1142.5
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62.5
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61.5
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length: 2000000000
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2000 Compugen Ltd.
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p_invertebrate:*
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sp_vertebrate:*
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842
2590
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995
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Q9Y2T1
Q9UH84
Q9UH84
3 Q42400
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Q9W7R4
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Q34449
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                070239 rattus norv
035625 mus musculu
015169 homo sapien
09y9y0 xenopus lae
09w7r4 brachydanio
09rbi0 acinetobact
03r449 bacillus su
064113 bacteriopha
096565 junonia coe
068167 lactococcus
                                                                                                        070240 rattus norv
088566 mus musculu
099x16 mus musculu
09y2t1 homo sapien
09uh84 homo sapien
042400 gallus gall
09ptp2 xenopus lae
070239 rattus norv
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         081599 triticum ae
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30 .	29	28	27	26	25	24	23	22	21	20
56	56.5	56.5	56.5	56.5	56.5	57	57	57	57	57.5	57.5	57.5	58	58	58.5	58.5	58.5	59	59	59	59.5	59.5	59.5	59.5	59.5
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Q9UUD0	Q9XIM3	Q9USX7	087270	Q9M8W6	Q74750	Q9xuJ7	Q9V539	Q9SSL8	Q22757	Q9XII7	067124	067279	Q17652	Q9YGU2	Q9NQV6	Q9UL19	Q9PAT1	Q9RKJ4	Q9UPX6	Q9ZGQ7	Q10465	Q9WTS6	Q9NZJ2	Q43379	047954
Q9uud0 sch1zosacch	Q9xim3 arabidopsis	Q9usx7 schizosacch	O87270 bartonella	Q9m8w6 arabidopsis	Q74750 human immun	Q9xuj7 caenorhabdi	Q9v539 drosophila	Q9ssl8 arabidopsis	Q22757 caenorhabdi	Q9xii7 arabidopsis	O67124 aquifex aeo	067279 aquifex aeo	Q17652 caenorhabdi	Q9ygu2 brachydanio	. Q9nqv6 homo sapien			Q9rkj4 streptomyce		Q9zgq7 myxococcus	O O	Q9wts6 mus musculu	Q9nzj2 homo sapien	Q43379 avena sativ	047954 trypanosoma

## ALIGNMENTS

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Best Local Similarity
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INTERPRO; IPR001158; -.
PFAM; PF00615; RGS; 1.
PFAM; PF00778; DIX; 1.
PRODOM; PD001580; -; 1.
PRODOM; PD003639; -; 1.
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01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     xenopus embryos.";
Mol. Cell. Biol. 18:2867-2875(1998).
EMBL; AF017757; AAC40089.1; -.
HSSP: P49799; lagr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kikuchi A.; "Axil, a member of the Axin family, interacts with both glycogen synthase kinase 3beta and beta-catenin and inhibits axis formation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-98226558; PubMed-9566905;
Yamamoto H., Kishida S., Uochi T., Ikeda S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
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       343
838 AA;
                                                                                                                                              Conservative
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Rodentia;
                                                                                                                                                                                                                                                                                                                       92947 MW; 45B825Cl3BA07F37 CRC64;
                                                                                                                                           100.0%; Score 272; DB 1: 100.0%; Pred. No. 3e-23; tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rattus.
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INTERPRO; IPRO01158; -.
PFAM; PF00615; RGS; 1.
PFAM; PF00778; DIX; 1.
PFAM; PF00078; DIX; 1.
PRODOM; PD003539; -; 1.
PRODOM; PD003639; -; 1.
SEQUENCE 840 AA; 92934 MW; //
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Q9QXJ6;
01-MAY-2000
01-MAY-2000
01-OCT-2000
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01-NOV-1998;
01-NOV-1998;
01-OCT-2000;
                                                                                                                                                                                                                               expression pattern, interaction axis formation."; submitted (NOV-1999) to the EMBI
                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                       Zhang T., Fago
Jenkins N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE=98221239; PubMed=9554852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
[1]
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                              PFAM;
                                                                                                                                PFAM;
                                                                                                                                              EMBL; AF205889; AAF22800.1; HSSP; P49799; 1AGR. INTERPRO; IPR000342; -. INTERPRO; IPR001158; -.
                                                                                                                                                                                                                                                                                                  Zhang T., Fagotto F., Hsu W., Zeng L., Gilbert D.,
Jenkins N.A., Warburton D., Costantini F.;
"Properties of mouse Axin2 and human AXIN2: chromo:
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
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MGD; MGI:1270862; Axin2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF073788; AAC26047.1; -. HSSP; P49799; 1AGR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Science 280:596-599(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Functional interaction of an axin homolog, catenin, APC, and GSK3beta.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Behrens J., Jerchow B.-A., Wurtele M., Kuhl M., Wedlich D., Birchmeier W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AXIN2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONDUCTIN.
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Local Similarity 100.0%;
nes 54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ω
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                                                                                 PF00615; RGS; 1.
PF00778; DIX; 1.
S; PR01301; RGSPR
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3 (TrEMBLrel. 08,
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                                                          RGSPROTEIN.
A; 92896 MW;
100.0%;
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13,
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Last sequence up
Last annotation
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                     EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.
  Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                                          767D546B43C921C5 CRC64;
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272;
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11;
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Length 840;
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                                                                                                                                                                                                                                                                              embryonic
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Best Local Similarity
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                                                                                                                                                                             Q9UH84;
Q9UH84;
01-MAY-2000
01-MAY-2000
01-OCT-2000
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Q9Y2T1;
Q1-NOV-1999
01-NOV-1999
01-OCT-2000
                                 Submitted (NOV-1999) to the EMBL; AF205888; AAF22799.1; HSSP; P49799; 1AGR.
                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                    Mai M., Qian C., Yokomizo A., "Cloning of the human homolog chromosome 17q23-q24."; Genomics 55:341-344(1999).
EMBL; AF078165; AAD20976.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          expression pattern,
axis formation.";
                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                 INTERPRO; IPR000342; -.
INTERPRO; IPR001158; -.
                                                                                                   TISSUE=BRAIN, LYMPHOBLAST;
                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=99168905; PubMed=10049590; Mai M., Qian C., Yokomizo A., Smith "Cloning of the human homolog of con
                                                                                                            SEQUENCE FROM N.A.
                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                               AXIN2
                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                             PFAM; PF00615; PFAM; PF00778;
                                                                                                                                                                                                                                                                                                                                                           INTERPRO; IPRO00342; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                           343
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                                                                                                                                                                                                                                                           ANGQVSLPHFPRTHRLPKEMTPVEPATFAAELISRLEKLKLELESRHSLEERLQ
         PF00615;
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                                                                                                                                                                             (TrEMBLrel. 13, ) (TrEMBLrel. 13, ) (TrEMBLrel. 15,
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RGS;
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Primates;
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93557 MW;
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98.1%;
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Last sequence up
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Pred. No. 8.6e
0; Mismatches
                                                  EMBL/GenBank/DDBJ databases
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Last annotation update)
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; Mismatches
                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                     F7B62BED6AB4664D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                               conductin
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                                                                                                                                                                                                                777
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                                                                                   Gilbert D.,
F.;
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.6e-23;
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                                                                  2: chromosomal location
and effects on embryon:
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                                                                                            Copeland N.G.,
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                                                                   embryonic
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Matches
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Zeng L., Fagotto F., Zhang T., Hsu W., Vasicek T.J., Perr.
III Lee J.J., Tilghman S.M., Gumbiner B.M., Costantini F.

"The mouse Fused locus encodes Axin, an inhibitor of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1998
01-JAN-1998
01-OCT-2000
                                                                                                                                                                                                                                                                                                                   Q9PTP2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gallus gallus (Chicken).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
AXIN-RELATED PROTEIN.
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF009012; AAC60245
HSSP; P49799; 1AGR.
INTERPRO; IPR000342; ...
INTERPRO; IPR001158; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pathway that regulates embryonic Cell 90:181-192(1997).
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SEQUENCE 777 AA
                                            TISSUE-OVARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PFAM; PF00615; RGS; 1. PFAM; PF00778; DIX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9031;
                                                                                                                 NCBI_TaxID=8355;
                                                                                                                                      Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
  (toh K., Antipova A., Ratcliffe M.,
Dishevelled transduces a signal by
                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANGRVPLPHIPRTYRMPKDI-HVEPEKFAAELINRLEEVQKEREAEEKLEERLK 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    l Similarity
32; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
52; Conserv
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PD003639; -; 1.
PB 841 AA; 94931 MW; 400D0C90E72506FE CRC64;
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8 (TrEMBLrel. 05,
0 (TrEMBLrel. 15,
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A; 86857 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57.98;
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 157.5; DB 1
Pred. No. 4.8e-10;
1; Mismatches 10
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                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3A4943ABF430BBD3 CRC64;
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  Sokol S.;
displacing
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    from
                                                                                                                                                                                   Euteleostomi;
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                                                                                                                                                         Pipidae;
    axin-GSK3
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Best Local :
Eukaryota; Metazoa; Chordata; C
Mammalla; Eutheria; Rodentia; So
NCBI_TaxID-10090;
                                                                                                                                                                   O35625 PRELIMINARY;
O35625;
01-JAN-1998 (TrEMBLrel. 0
01-JAN-1998 (TrEMBLrel. 0
01-CCT-2000 (TrEMBLrel. 1
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INTERPRO; IPR001158; -.
PFAM; PF00615; RGS; 1.
PFAM; PF00778; DIX; 1.
PRODOM; PD001580; -; 1.
PRODOM; PD003639; -; 1.
SEQUENCE 832 AA; 92856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

MEDILINE-98151361; PubMed=9482734;

Ikeda S., Yamamoto H., Murai H., Kishida S., Kikuchi A.;

Ikeda S., Yamamoto H., Murai H., Kishida S., Kikuchi A.;

"Axin, a negative regulator of the Wnt signaling pathway, forms complex with GSK-3beta and beta-catenin and promotes GSK-3beta-dependent phosphorylation of beta-catenin.";

EMBO J. 17:1371-1384(1998).

EMBL; AF017756; AAC40066.1; -.

HSSP; P49799; LAGR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INTERPRO; IPRO01158; -. PFAM; PF00778; DIX; 1. PRINTS; PR01301; RGSPRO: SEQUENCE 706 AA; 7919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Submitted (APR-1999)
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illarity 56.6%;
Conservative
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A; 79196 MW; C3D0AF0D9540F162 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92856 MW;
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Last annotation updat
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Pred. No. 1.5e-08;
7; Mismatches 17;
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Pred. No. 2.6e-08;
3; Mismatches 14
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                                                     Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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RESULT 11
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015169;
01-JAN-1998;
01-JAN-1998;
01-OCT-2000;
 Q9YGY0;
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AXIN.
Homo sapiens (Human).
Homo sapiens (Human).
'~rvota; Metazoa; Chordata;
'~rvota; Metazoa; Primates;
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INTERPRO; IPRO01158; -.
PFAM; PF00615; RGS; 1.
PFAM; PF00778; DIX; 1.
PFAMTS; PR01301; RGSPROTEIN.
NON TEP
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INTERPRO; IPR001158; -.
PFAM; PF00615; RGS; 1.
PFAM; PF00778; DIX; 1.
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HSSP; P49799; lAGR.
                                                                                                                                                                                                                                                  pathway that regulate Cell 90:181-192(1997)
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III Lee J.J., Tilghman S.M., Gumbiner B.M., Costantini F
"The mouse Fused locus encodes Axin, an inhibitor of the
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE=97373830; PubMed=9230313;
                                                                                                                                                                                                                                                                                                                                                                                   AXIN (FRAGMENT).
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HSSP; P49799; 1
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            PRELIMINARY;
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Pred. No. 3.1e
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                                                                                                      Score 141.5; DB 4; Pred. No. 3.6e-08; Mismatches 14;
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            PRT;
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Best Local :
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INTERPRO; IPRO01158; -
PPAM; PF00615; RGS; 1.
PPAM; PF000778; DIX; 1.
PRODOM; PD001580; -; 1.
PRODOM; PD003639; -; 1.
PRODOM; PD003639; -; 1.
PRODOM; PD003639; -; 1.
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01-MAY-1999
01-OCT-2000
AXIN.
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01-NOV-1999
01-OCT-2000
                                                                                                                                                                                           Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi.
Cypriniformes; Cyprinidae; Rasborinae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-99173782; PubMed-10072781; Hedgepeth C.M., Deardorff M.A., Klein "Xenopus axin interacts with glycogen expressed in the anterior midbrain."; Mech. Dev. 80:147-151(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
PRINTS; PRO0011; EGFLAMININ.
PROSITE; PS00022; EGF_1; UNKNOWN_8.
PROSITE; PS001186; EGF_2; 7.
SEQUENCE 2590 AA; 288587 MW; 59
                                                                                                                                                             SEQUENCE FROM N.A. Mieda M., Kikuchi Y.,
                                                                                                                                                                                                                                                                        TEN-M3
                                                                                                                                                                                                                                                                                                                        Q9W7R4;
                                                                                                                                                                                                                                                                                                                                  Q9W7R4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF097313
HSSP; P49799;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xenopus laevis (African clawed
                                                                                EMBL; AB026979; BAA81892.1;
HSSP; P02468; 1KLO.
                                                                                                                        system."
                                                                                                                                  "Compartmentalized homologues of the I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xenopodinae; Xenopus.
                                                  PFAM; PF00008; EGF; 5.
                                                            INTERPRO; IPR000561; -.
                                                                                                                                                                                                                                                                                                                                                                                              362 ANGRGPLPHIPRTYHMPKDI-HVDPEKFAAELISRLEGVLRDREAEQKLEERLK
                                                                                                                                                                                                                                                                                                                                                                                                           12
                                                                                                              Dev.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AF097313; AAC71036.1; -.
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                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                     d expression
Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94459 MW;
                                                                                                                                               , Hirate Y.,
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Last sequence up
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Last sequence update)
Last annotation update)
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 136.5; DB 1
Pred. No. 1.3e-07;
                                                                                                                                      tenm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BDA152734C97191E CRC64;
                                                                                                                                     , Aoki M., C
f zebrafish
nm /odd Oz g
  597592866219148D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P.S.;
synthase kinase-3
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                                                                                                                                                                                                                                                                                                                                    A
                                                                                                                                                  Okamoto
sh ten-m3
                                                                                                                                     gene,
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  CRC64
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and ten-m4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Query Match Best Local S Matches 22

Similarity 31.0 22; Conservative

25.0%; 31.0%;

Score 68; DB Pred. No. 33; 6; Mismatches

13;

Length 2590;

19;

Indels

24;

Gaps

2

--PVEPAAFAAELISRLEKLKLE---

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RESULT 14
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Best Local (
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MEDLINE-98044033; PubMed-9384377;

Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,

Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,

Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,

Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,

Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,

Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,

Fritz C., Fujita M., Fujita Y., Funa S., Galizzi A., Galleron N.,

Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,

Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,

Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       O34449;
01-JAN-1998 (TrEMBLrel.
01-JAN-1998 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CCT-2000 (TrEMBLrel. 15, Last annotation update)
PUTATIVE 2-COMPONENT REGULATORY PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INTERPRO; IPRO01789; -.
INTERPRO; IPRO01867; -.
PFAM; PF00072; response_reg; 1.
PFAM; PF00486; trans_reg_C; 1.
SEQUENCE 226 AA; 26423 MW; B3C1E641015C74DB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Bacteriol. 181:4568-4575(1999).
EMBL; AF150928; AAF04314.1; -.
HSSF; P08402; 1800.
                                                                                                                                                                                                                                                                                                                                                 STRAIN-168
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes; Bacillus/Staphylococcus NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          034449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jones R.M., Collier L.S., Neidle E.L., Williams P.A.; "areABC genes determine the catabolism of aryl esters in Acinetobacter sp. strain ADP1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-ADP1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Firmicutes; Bacillus/Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation updat
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Pred. No. 7
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RESULT
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RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
Median N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Parro V., Pohl T.M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porvollik S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Scrokin A., Tacconi E., Takagl T., Takahashi H., Takemaru K.,
RA Sorokin A., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
RA Viari A., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
"The complete genome sequence of the gram-positive bacterium Bacillus substils.";
Subtilis.";
                                                                                                                                                                                                   Query Match
Best Local
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Best Local
                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                    Lazarevic V., Duester, Duester, Desternant D.;
Karamata D.;
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases
EMBL; AF020713; AAC13073.1; -.
SEQUENCE 251 AA; 28593 MW; BE79F500A3A0E3C8 CRC64;
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064113;
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01-AUG-1998 (TrEMBLrel.
01-AUG-1998 (TrEMBLrel.
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Submitted (NOV-1997) to the EM
EMBL; 299114; CAB139591; -.
EMBL; 299115; CAB13985.1; -.
SEQUENCE 251 AA; 28593 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., K.
Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viruses;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PUTATIVE ANTIREPRESSOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID-66797;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteriophage SPBc2
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    62
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    ATGR-SLKHFHLTRKGCDMVANKMTGAKGVLFTAQYVSKFEEMEKALKARPSL
                                                                    ANGQVSLPHFPRTHR----LPKEMTPVEPAAFAAELISRLEKLKLELESRHSL 49
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                                                                                                                                                                                               Similarity
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                                                                                                                                                                 Conservative
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13; Mismatches
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## ALIGNMENTS

Human conductin protein. 17-JUN-1999 (first entry) W93570;

W93570 standard; Protein; 840

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FIND DRY NOT THE PROPERTY OF T Tumor-suppressing protein conductin diagnosis of tumors WPI; 1999-214706/18. N-PSDB; X23370. Conductin; tumour; diagnosis; treatment; beta-catenin; anti-tumour; therapy; cytoplasmic degradation; blockade; Wnt signalling pathway; Mingless signalling pathway; Adenomatous Polyposis Coli; APC; tumour suppressor. Behrens J, Birchmeier W; 02-SEP-1997; 01-SEP-1998; 11-MAR-1999. WO9911780-A2. Homo sapiens (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX 97DE-1038205. 98WO-DE02621. . used for treatment

W29659

Human

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Best Local
  N-PSDB;
          WPI; 1999-214706/18
                                Behrens J,
                                                                          02-SEP-1997;
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                                                                                                                      11-MAR-1999
                                                                                                                                                                                                                                                                                                                                                  Conductin; tumour; diagnosis; treatment; beta-catenin; anti-tumour; therapy; cytoplasmic degradation; blockade; Wnt signalling pathway; Wingless signalling pathway; Adenomatous Polyposis Coli; APC;
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                                                                                                                                                                                       Region
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                                                     (DELB-) DELBRUECK CENT MOLEKULARE
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                                                                                                                                                                                                                                                                 /note= "Regulator of G protein signalling
    described in claim 12"
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claim 14"
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Pred. No. 2.9e-35;
Mismatches 0;
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Best Local
Nucleic acids encoding mutant and wild type Axin and oligonucleotides derived from them are useful for detecting mutations in the Axin gene and for determining whether a subject likely to develop cancer (including breast, colorectal, gastrointestinal, esophageal, carcinomas or melanomas). The wild
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention describes a novel human conductin protein which has anti-tumour activity. Detecting the presence or amount of conductin, at protein or nucleic acid levels, is used to diagnose tumours, while agents that (re)activate conductin are used for tumour therapy. Conductin binds to beta-catenin and induces its cytoplasmic degradation, resulting in blockade of the WntyWingless signalling pathway in vertebrates. Conductin also binds to Adenomatous Polyposis Coli (APC)
                                                                                                                                                                                                                                                                                                                                                                                    Axin; cancer; breast cancer; colorectal cancer;
gastrointestinal cancer; esophageal cancer; carcinoma; melanoma;
diagnosis; treatment; therapy; thyroid carcinoma; tumorigenesis;
                                                                                 Claim
                                                                                                        Newly isolated nucleic acid encoding "axis inhibition" protein (Axin) - useful for detecting, diagnosing and treating cancer
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DB; X09013.
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Pred. No. 2.9e-35;
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Best Local
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Nucleic acids encoding mutant and wild type Axin and oligonucleotides derived from them are useful for detecting mutations in the Axin gene and for determining whether a subject is likely to develop cancer (including breast, colorectal, gastrointestinal, esophageal, carcinomas or melanomas). The wild type Axin and homologues of Axin are useful for treating subjects who are likely to develop cancer (thyroid carcinomas). The nucleic acids are also useful for diagnosing cancer and for detecting mutations in cancerous cells. Wild type Axin, its antisense molecule and identified compounds form pharmaceutical compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               type Axin and homologues of Axin are useful for treating subjects who are likely to develop cancer (thyroid carcinomas). The nucleic acids are also useful for diagnosing cancer and for detecting mutations in cancerous cells. Wild type Axin, its antisense molecule and identified compounds form pharmaceutical compositions in the treatment of cancer. The compositions are also useful for treating cancer by inhibiting tumorigenesis (by inducing degradation of beta-catenin). The nucleic acid encoding Axin acts through negative regulation of the Wnt pathway in the Nieuwkoop Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Axin; cancer; breast cancer; colorectal cancer; gastrointestinal cancer; esophageal cancer; carcinoma; melanoma; diagnosis; treatment; therapy; thyroid carcinoma; tumorigenesis;
                                                                                                                                                                                                                                                                                                           Constantini F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W96264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                              Disclosure; Figure 11;
                                                                                                                                                                                                          Newly isolated nucleic acid encoding "axis inhibition" (Axin) - useful for detecting, diagnosing and treating
                                                                                                                                                                                                                                                                           WPI; 1999-120510/10.
                                                                                                                                                                                                                                                                                                                                                                          10-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                         09-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9902179-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        beta-catenin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human axin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W96264 standard; Protein; 900 AA.
                                                                                                                                                                                                                                                                                                                                          (UYCO ) UNIV COLUMBIA NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         544 rvrmeeegedgemp----sgpmashklpsvpawhhfppryvdmgcsglrdaheenpesil 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44 DDHLSRVLKTPGCQSPGVGRYSPRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QIREDEEKEGSEQALSSRDGAPVQHPLALLPS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dehvqrvmrtpgcqspgpghrspds 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            992 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                          97us-0890865
                                                                                                                                                                                                                                                                                                                                                                                                         98WO-US14414
                                                                                                                                                                                                                                                                                                           Zeng
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                                                                                                                                                                              95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 139.5; DB 2
Pred. No. 2.4e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83
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                                                                                                                                                                                                              protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21;
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Matches 33
                                                            Query Match
Best Local S
Matches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in the treatment of cancer. The compositions are also useful for treating cancer by inhibiting tumorigenesis (by inducing degradation of beta-catenin). The nucleic acid encoding Axin acts through negative regulation of the Wnt pathway in the Nieuwkoop Center.
                                                                                                                                                                                                                                                                                                                                                                                     Steroid; hormone; receptor; osteosarcoma; superfamily
                                                                                                                                                                                                                                                                                                                                                                                                        Steroid hormone receptor (NUCI).
                                                                                                                                                                                                                                                                                                                                                                                                                            13-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                R41875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                               GB2265376-A
                                                                                                                                                                                                                                                                                                                                                                   Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R41875 standard; Protein; 441 AA.
                                                                                                            Sequence
                                                                                                                               The steroid hormone receptor (designated NUCI) is identify and evaluate chemical entities that bind
                                                                                                                                                            Claim 5; Page 39-40; 62pp;
                                                                                                                                                                                New human steroid hormone receptor NUCI - evaluate ligands binding to the receptor
                                                                                                                                                                                                               N-PDSB;
                                                                                                                                                                                                                                            Rodan GA,
                                                                                                                                                                                                                                                               (MERI ) MERCK & CO INC
                                                                                                                                                                                                                                                                                    24-MAR-1992;
                                                                                                                                                                                                                                                                                                        23-MAR-1993;
                                                                                                                                                                                                                                                                                                                            29-SEP-1993
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                               QIREDEEKEGSEQALSSRDGAPVOH--PLALLPSGSYEE-----DPOTILDDHLSRVLKT 53
  PGCQSPGVGRYSPRSR 69
                     evreeeekeevaea----egapelnggpqhalpsssytdlsrsssppslldq-----lq
                                                                                                                                                                                                                        1993-305586/39.
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                                                                     Similarity
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                                                             Conservative
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                                                                     19.0%;
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                                                                                                                                                                                                                                             Schmidt A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10;
                                                            ; Pred. No. 3.8; 10; Mismatches
                                                                                                                                                             English
                                                                     Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 113.5; DB 2
Pred. No. 3.1e-05;
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                                                                     No. 3
                                                                                                                                                                                                                                             Vogel RL;
                                                                                 DB
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to it
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RESULT
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R89214
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Best Local 9
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                                                                                       07-JUL-1999
                             Nuclear receptor agonist; antagonist; identification; PPAR; peroxisome proliferator activated receptor.
                                                                                                              Y05472;
                                                                                                                                  Y05472 standard;
                                                                                                                                                                                                                                                                                                                                                         A novel human peroxisome proliferator activated receptor (PPAR), designated hNUC1B (R89214), is expressed from a cDNA clone (T10583) isolated from a human kidney cDNA library. hNUC1B is a member of the PPAR family and can be used to screen NUC protein inhibitors.
                                                               Human PPAR-delta protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 44; Page 29-31; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Screening methods for identifying NUC protein inhibitors - as potential agents for the treatment of hyperlipidemia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1996-087756/09.
N-PSDB; T10583.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hNUC1B; peroxisome proliferator activated receptor; hypercholesterolemia; hyperlipoproteinemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-APR-1996 (first entry)
         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                         hypercholesteremia and hyperlipoproteinemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mukherjee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (LIGA-) LIGAND PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9601430-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peroxisome proliferator activated receptor hNUC1B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R89214 standard;
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                                                                                                                                                                                                                                                         1 QIREDEEKEGSEQALSSRDGAPVQH--PLALLPSGSYEE-----DPQTILDDHLSRVLKT 53
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                                                                                                                                                                                                                                    evreeeekeevaea----egapelnggpqhalpsssytdlsrsssppslldq-----lq
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23; Conservative
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                                                                                                                                                                                                                                                                                                                                        441 AA;
                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94US-0270635
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                                                                                                                                  Protein;
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                                                                                                                                                                                                                                                                                         19.0%;
                                                                                                                                                                                                               69
                                                                                                                                                                                         75
                                                                                                                                  441
                                                                                                                                                                                                                                                                                 10;
                                                                                                                                                                                                                                                                               Score 68.5; DB Pred. No. 3.8; 10; Mismatches
                                                                                                                                  B
                                                                                                                                                                                                                                                                                                     DB 17;
                                                                                                                                                                                                                                                                                 26;
                                                                                                                                                                                                                                                                                                     Length 441;
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RESULT
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Best Local Similarity
Matches 23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        agonists and antagonists comprises measuring fluorescent resonance transfer between fluorescent-labelled nuclear receptors and co-activators. The method can be used for identifying agonists and antagonist of nuclear receptors.
                                                                                                                                                                            antimitotic factor; mitosis.
                                                                                                                                                                                   Human; MIN1; cell cycle; G2/M border; progression; cdc2 kinase; yeas functional complementation; weel; mikl; mutant; cancer; development;
                                                                                                                                                                                                                   Human cell cycle protein min1.
                  N-PSDB; T05406.
                             WPI; 1995-399339/51.
                                                (SHKJ ) SHINGIJUTSU JIGYODAN
                                                                     05-APR-1994;
                                                                                         05-APR-1994;
                                                                                                             24-OCT-1995
                                                                                                                                  JP07274971-A
                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                        08-AUG-1996 (first entry)
                                                                                                                                                                                                                                                             R77417;
                                                                                                                                                                                                                                                                                R77417 standard; Protein; 1132 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence is the human peroxisome receptor-delta (PPAR-delta).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 10a;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying nuclear receptor agonists
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-263998/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cummings RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MERI ) MERCK & CO INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                  60 mgcdgascgslnmecr
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                                                                                                                                                                                                                                                                                                                                                                           10 evreeeekeevaea----egapelnggpqhalpsssytdlsrsssppslldq-----lq 59
                                                                                                                                                                                                                                                                                                                                                                                       1 QIREDEEKEGSEQALSSRDGAPVQH--PLALLPSGSYEE-----DPQTILDDHLSRVLKT 53
                                                                                                                                                                                                                                                                                                    8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention relates to a method for identifying nuclear receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       441
                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                      94JP-0093033.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA;
                                                                                         94JP-0093033.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Moller
                                                                                                                                                                                                                                                                                                                                                                                                                    10;
                                                                                                                                                                                                                                                                                                                                                                                                                              Score 68.5;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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Human derived cell cycle gene encoding an anti:mitotic factor -

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RESULT W29659
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AC W296

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Query Match 18.9%; Sometimes Sent Local Similarity 32.9%; Properties 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local Similarity
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1033 vktpqcqhvspgm 1045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This is the amino acid sequence of the human MINI gene product. The protein has a mol. wt. about 129 kD. The gene is expressed at the G2/M border of the cell cycle and can inactivate theil cycle progression protein cdc2 kinase. The gene was isolated by functional complementation of a yeast weel/miki mutant strain. The gene and protein can be used in the determination of cancer cell development and as an antimitotic
                                                                                                                                                                                                                                                                                          New isolated nucleic acids and secreted proteins - obtained from human adult ovary, human foetal kidney, human foetal brain and human adult brain cDNA libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W29659 standard; Protein; 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 4; 5pp; Japanese
                                                                                                                                    Sequence
                                                                                                                                                                                      The sequence is that of a novel, isolated secreted protein.
                                                                                                                                                                                                                                        Disclosure; Page 67-68; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-413686/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-JAN-1998;
09-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9830695-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               secreted protein; BP202_3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens BP202_3 clone secreted protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-FEB-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in the control of the G2/M phase of the cell cycle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Agostino MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GEMY ) GENETICS INST INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      976 qfleqlpkddhddffst---tplqhqrillpsfqgseddddilpnmdknpttpssvifpl 1032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51 LKTPGCQ--SPGV 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QIREDEEKEGSEQALSSRDGAPVOHPLALLPSGSYEEDPQTILDDH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J, Jacobs K,
Spaulding V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1132 AA;
                                                                                                                                    397 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-0004684.
97US-0780814.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lavallie ER,
Treacy M;
  Score 68; DB;
Pred. No. 3.9;
10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 68.5;
Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            мсСоу ЈМ,
                      DВ
3.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 16;
                                                    19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26;
     23;
                                                    Length 397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Merberg
     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1132;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----LSRV 50
     18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15;
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     4
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B 5

11 SEQALSSRDGAPVQHPLALLPSGSYEEDPQTILDDHLSRVLKTPGCQSPGVG--RYSPRS 68

seq--sasesapedqp-----dreedpragaed--pkaekspgadskglgckrgspka

184

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RESULT 10
W44865
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                                                                                    밁
                                                                                                            telomere length or modulates telomerase activity. Its amino acid sequence was deduced from a cDNA clone (see V19480) obtained from a cDNA clone (see V19480) obtained from a cDNA clone (see V19480) obtained from a cDNA clone (see W19480) obtained from the constitution of the constitution of the vitro telomerase of the constitution in methods for reconstituting in vitro telomerase or other enzymatic activities that maintain telomeres and regulate telomere length. These methods have application in screens for therapeutic agents, and for diagnostic tests. In addition, peptides corresponding to TPC2 or TPC3 proteins can also be used to regulate telomere length and telomerase activity in mammalian cells. Immunogenic peptides and proteins of the invention can also be used in therapeutic immunisation and vaccination procedures. Antibodies that specifically bind to TPC2 or TPC3 proteins can be used in screening, diagnosing and monitoring diseases and other conditions, such as cancer, pregancy or fertility.
Matches
              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                    This polypeptide comprises human TPC3, a protein that regulates
                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 6A-C; 86pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; V19480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Adams RR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ·13-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diagnosis; vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TPC3; telomere length;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human TPC3 telomere length and telomerase regulatory protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-AUG-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W44865;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W44865 standard; Protein; 382 AA.
                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        telomerase activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human TPC2, TPC3 and TR genes - regulate telomere length or modulate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1998-207373/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GERO-) GERON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         238 qmrefleqlpkddhddffst---tplqhqrillpsfqdsedddilpnmdknpttpssv1 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     295 fplvktpqcqhvspgm 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QIREDEE---KEGSEQALSSRDGAPVQHPLALLPSGSYEEDPQTILDDH------L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Andrews WH,
                                                                                    382 AA;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96WO-US14679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96WO-US14679
                17.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          telomerase; human; cancer; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Feng J,
9;
              Score 63.5;
Pred. No. 13;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Villeponteau
                                DB
                                  19;
17;
                                Length
 Indels
                                    382;
 13;
 Gaps
 4.
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RESULT
Y57950
ID Y5
XX Y
AC Y5
XX Y
DT 23
DT 23
DT 23
CX HU
XX HU
XX HU
XW HU
KW AT
KW AT
KW GK
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                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-SEP-1995;
05-JAN-1996;
13-SEP-1996;
                                                                                                                                                                                                                                                                                                                                           This sequence is the human TPC3 protein, which is contained within the recombinant mammalian host cell of the invention. The invention provides methods and reagents for regulating telomerale length and modulating telomerase activity in mammalian cells as well as for detecting, diagnosing, and treating related diseases and conditions as cancer, pregnancy, or fertility in humans and other mammals.
            Human; transmembrane protein; HTMPN; diagnosis; immunospecific; antiproliferative; neuroprotective; immune disorder; reproductive disorder; mooth muscle disorder; neurological disorder; gastrointestinal disorder; developmental disorder;
                                                                        Human transmembrane protein HTMPN-74.
                                                                                                  23-MAR-2000
                                                                                                                                                 Y57950 standard;
                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA encoding proteins TPC2 and TPC3 - uslength or modulating telomerase activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-152104/13.
N-PSDB; X01534.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Adams RR, Andrews WH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-SEP-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TPC2; TPC3; human; telomere length regulation; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W73959;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W73959 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GERO-) GERON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human TPC3 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fertility; diagnosis; therapy.
                                                                                                                                                                                                            236 seq--sasesapedqp-----dreedpragaed--pkaekspgadskglgckrgspka 284
                                                                                                                                                                          12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11
                                                                                                                                                                                                                                   11 SEQALSSRDGAPVQHPLALLPSGSYEEDPQTILDDHLSRVLKTPGCQSPGVG--RYSPRS 68
  proliferative
                                                                                                                                                                                                                                                             Similarity 35.(
21; Conservative
                                                                                                                                                                                                                                                                                                                         434 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Fig 6; 59pp; English.
                                                                                                 (first entry)
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96US-0583808.
96US-0710249.
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                                                                                                                                                 Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein;
   disorder.
                                                                                                                                                                                                                                                                       17.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Feng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               434
                                                                                                                                                   605
                                                                                                                                                                                                                                                            score 63.5; D
Pred. No. 15;
9; Mismatches
                                                                                                                                                                                                                                                             9;
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                                                                                                                                                   A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Villeponteau
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      useful for regulating telomere
                                                                                                                                                                                                                                                                                     DΒ
                                                                                                                                                                                                                                                            17;
                                                                                                                                                                                                                                                                                     20;
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                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pregnancy;
                                                                                                                                                                                                                                                                                     434;
                                                                                                                                                                                                                                                             13;
                                                                                                                                                                                                                                                            Gaps
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RESULT
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Best Local S
Matches 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-MAY-1998;
02-JUL-1998;
02-OCT-1998;
24-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                           neuroprotective activities. The human transmembrane proteins, polynucleotides encoding them and other compositions and methods from the present invention, can be used for the diagnosis, treatment or prevention of immune, reproductive, smooth muscle, neurological, gastrointestinal, developmental and cell proliferative disorders. The HTMPN's can be used to treat or prevent disorders associated with a decreased expression or activity of HTMPN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             proteins, polynucleotides, vectors, host cells and antibodies used to diagnose, treat or prevent immune, reproductive, smooth muscle, neurological, gastrointestinal, developmental and cell proliferative disorders -
                                                                      cytoplasmic
                                                                                   merozoite; diarrhoea; protozoacide;
                                                                                                            GP900;
                                                                                                                                     Cryptosporidium parvum Iowa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     256698 to 256776 encode Y57877 to Y57955 which represent human transmembrane proteins designated HTMPN-1 to HTMPN-79, respectively. The transmembrane protein have immunospecific, antiproliferative and neuroprotective activities. The human transmembrane proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo
                      US6071518-A
                                            Cryptosporidium
                                                                                               competitive inhibition; attachment;
                                                                                                                                                               28-OCT-2000
                                                                                                                                                                                     в11732;
                                                                                                                                                                                                              B11732 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 172-174; 229pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-072605/06.
N-PSDB; Z56771.
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                                                                                                                                                                                                                                                                         161 reeeeeeeeeemekeevekqdveeeeellpvngsqeeakpqvrdfsltsssqtpg
                                                                                                                                                                                                                                       13
                                                                                                                                                                                                                                                                                         3 REDEEKEGSEQALSSR--DGAPVQHPLALLP-SGSYEEDPQTILDDHLSRVLKTPG 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sapiens
                                                                                                             Iowa
                                                                                                                                                                                                                                                                                                                           l Similarity 33.9
19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INCYTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lal
                                                                                                                                                                                                                                                                                                                                                                                        605 AA;
                                                                         domain.
                                                                                                            isolate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patterson
                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-0109869
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98US-0102954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-US11904
                                               parvum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hillman
                                                                                               glycoprotein; antibody; cryptosporidiosis;
on; attachment; invasion; ligand binding; s;
                                                                                                                                                                                                                                                                                                                           17.6%; Score 63.5; 33.9%; Pred. No. 23; tive 10; Mismatches
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                                                                                                                                                                                                              1042
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gorgone GA,
                                                                                                                                     isolate GP900, domain
                                                                                                                                                                                                              AA
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                                                                                   invasion; domain 5;
                                                                                     domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kaser MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Guegler KJ,
                                                                                                                                                                                                                                                                                                                                                    DB 21;
                                                                                                                                                                                                                                                                                                                            24;
                                                                                     transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Baughn MR;
                                                                                                                                                                                                                                                                                                                                                    Length 605;
                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                      domain;
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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GC GP900 antibody production, and to a method of cryptosporidiosis treatment CC or prophylaxis comprising administration of anti-GP900 antibodies to an competitively inhibit sporozoite or merozoite attachment or invasion, and care also useful for the generation of anti-GP900 fragments are able to competitively inhibit sporozoite or merozoite attachment or invasion, and care also useful for the generation of anti-GP900 antibodies. The cc antibodies also inhibit sporozoite or merozoite attachment/invasion and cd additionally inhibit the binding of GP900 ligands to GP900. GP900 cc proteins, fragments and antibodies may therefore be used to treat or prevent cryptosporidiosis. Infection with Cryptosporidium is a common cc use of diarrhoea in humans and causes life-threatening diarrhoea in cc immunocompromised persons. Cryptosporidiosis can be contracted from cc contaminated municipal water supplies (e.g., public swimming pools). It is also a cause of disease in animals, resulting in financial losses in ca agriculture. GP900 fragments, fusion proteins and antibodies may also be used for the diagnosis of Cryptosporidium parvum infections, and for the cused for the diagnosis of Cryptosporidium parvum Iowa containts of the Cryptosporidium parvum Iowa containts of the Cryptosporidium parvum Iowa containts of contains a putative transmembrane domain and a cc of GP900, which contains a putative transmembrane domain and a
                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local Similarity
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01-JUN-1993;
29-MAY-1992;
03-APR-1995;
             Cryptosporidium parvum Iowa isolate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to the GP900 glycoprotein of the protozoan Cryptosporidium parvum, DNA encoding it, GP900 fragments, and fusion proteins comprising GP900 fragments. The invention also relates to the administration of GP900 or fragments thereof to a host to elicit anti-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New GP900 protein fragments and fusion proteins of Cryptosporidium parvum, useful for detecting the presence of the parasite, and diagnosing or treating Cryptosporidium infections by competitive inhibition of the function of GP900 -
                                                     28-OCT-2000 (first entry)
                                                                                                                               B11726 standard; Protein; 1837 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cytoplasmic domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 3; Column 73-80; 59pp; English.
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                                                                                                                                                                                                                                                                                                                            KEGSEQALSSRDGAPVQHPLALLPSGSYEEDPQT----
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92US-0891301.
95US-0415751.
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Pred. No. 59;
8; Mismatches
                 GP900
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                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1042;
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57 QSPGVGRYSPRS

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1706 aapkkggvipes 1717

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                                                                                                                                                                                                    Cryptosportidium parvum, DNA encoding it, GP9900 fragments, and fusion CC cryptosportidium parvum, DNA encoding it, GP9900 fragments, and fusion CC administration of GP900 or fragments thereof to a host to ellicit anti-CC GP900 antibody production, and to a method of cryptosporidiosis treatment CC or prophylaxis comprising administration of anti-GP900 antibodies to an individual cryptosporidium parvum GP900 and GP900 fragments are able to CC competitively inhibit sporozoite or merozoite attachment or invasion, and CC are also useful for the generation of anti-GP900 antibodies. The CC antibodies also inhibit sporozoite or merozoite attachment or invasion and CC anditionally inhibit the binding of GP900 ligands to GP900. GP900 GP900 proteins, fragments and antibodies may therefore be used to treat or prevent cryptosporidosis. Infection with Cryptosporidium is a common CC cause of diarrhoea in humans and causes life-threatening diarrhoea in immunocompromised persons. Cryptosporidiosis can be contracted from CC contaminated municipal water supplies (e.g., public swimming pools). It is also a cause of disease in animals, resulting in financial losses in agriculture. GP900 fragments, fusion proteins and antibodies may also be used for the diagnosis of Cryptosporidium parvum infections, and for the CC detection of the parasite in the environment. The present sequence crepresents the GP900 protein of the Iowa isolate of Cryptosporidium
                                                                     Matches
                                                                                                      Query Match
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01-JUN-1993;
29-MAY-1992;
03-APR-1995;
 1652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New GP900 protein fragments and fusion proteins of Cryptosporidium parvum, useful for detecting the presence of the parasite, and diagnosing or treating Cryptosporidium infections by competitive inhibition of the function of GP900 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GP900; Iowa isolate; glycoprotein; antibody; cryptosporidiosis; competitive inhibition; attachment; invasion; ligand binding; s
                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to the GP900 glycoprotein of the protozoan Cryptosporidium parvum, DNA encoding it, GP900 fragments, and fu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim
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                                 8 KEGSEQALSSRDGAPVQHPLALLPSGSYEEDPQT----
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)В; А61846, А61847.
kagsqskssdesgnpid-----
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                                                                     Conservative
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93US-0071880.
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                                                                                      17.48;
29.28;
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Score 62.5; DB 21;
Pred. No. 1.2e+02;
Pred. No. 1.2e+02;
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                                    -----ILDDHLSRVLKT-PGC 56
                                                                                                      Length 1837;
                                                                       Indels
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GRESULT ID SECOND TO SECON
05-MAR 1999
09-MAR 1999
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23-MAR 1999
25-MAR 1999
25-MAR 1999
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11-JUN 1999
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99US-0121825
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99US-0144085

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99US-0144085

99US-0144332

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99US-014591

99US-0148319

99US-0148684

99US-0149426
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                                                                     Query Match 17.2%;
Best Local Similarity 36.0%;
Matches 18; Conservative
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99US-0161359
                                                                     Score 62; DB 21;
Pred. No. 15;
9; Mismatches 19
                                                                       19;
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Search completed: June Job time: 5660 sec

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Scoring table:
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Maximum DB
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62
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Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-476-900A-6
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US-08-726-320-4
US-08-928-361B-30
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32.521 Million cell updates/sec
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Sequence 5, Appil
Sequence 5, Appil
Sequence 13, Appil
Sequence 15, Appil
Sequence 29, Appil
Sequence 29, Appil
Sequence 9, Appil
Sequence 9, Appil
Sequence 9, Appil
Sequence 28, Appil
Sequence 6, Appil
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US-08-710-249-4
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	22
54	54.5	54.5	54.5	55.5	55.5	56	56	56	56	56	56.5	56.5	56.5	56.5	56.5	56.5	56.5
15.0	15.1	15.1	15.1	15.4	15.4	15.6	15.6	15.6	15.6	15.6	15.7	15.7	15.7	15.7	15.7	15.7	15./
993	222	222	206	242	242	1199	1162	432	432	432	711	711	471	471	459	449	449
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US-09-060-410-4	5185431-4	US-09-040-483-3	5185431-1	US-09-206-537-2	US-08-845-998-2	US-09-208-742-2	US-08-728-323A-2	US-08-480-912-8	US-08-488-382A-8	US-08-522-166-8	US-08-465-473B-7	US-08-235-838-7	PCT-US94-02539-31	US-08-657-392-31	US-08-673-312-2	PCT-US94-02539-2	US-08-65/-392-2
Sequence 4, Appl	Patent No. 518543	Sequence :	Patent No. 5	Sequence :	Sequence :	Sequence :	Sequence :	Sequence (	Sequence (	Sequence (	Sequence 7	Sequence :	Sequence :	Sequence :	Sequence :	Sequence 2	sequence .
۰, A	518	<ol><li>Appl</li></ol>	518	2, A	2, A	2, A	2, A	8, A	ø, ≽	8, A	7, A	7, A	31,	31,	2, A	2, A	, ,
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## ALIGNMENTS

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TYPE: amino a TOPOLOGY: lin  
; MOLECULE TYPE: US-08-710-249-4
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GENERAL INFORMATI
                                                                                                                                                                                                                                CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/583,808
FILING DATE: 05-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/003,492
FILING DATE: 08-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REGISTRATION NUMBER: 32,944
                                                                                                                              TELEFAX: (415) 576-03
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 434 amino acid
                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Methods and Reagents for Regulating TITLE OF INVENTION: Telomere Length and Telomerase Activity NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Andrews, William H. APPLICANT: Adams, Robert R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Villepontea APPLICANT: Feng, Junii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: Two Embarca
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/0 FILING DATE: 13-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                     TELEPHONE:
                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
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                                                             amino acid
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                                                                                434 amino acids
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                                           linear
                                                                                                                                                  576-0300
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; Sequence 5, Application US/08928361B
; Patent No. 6071518
                                RESULT 3
US-08-928-361B-5
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: F10ppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,361B
FILING DATE: 12-SEP-1997
                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1042 amino acids
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APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: PETERS, VERNY, JONES & BIKSA
STREET: 385 Sherman Avenue, Suite 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 650-324-1677
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                                                                                                        911 AAPKKGGVIPES 922
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                                                                                                                                       57 QSPGVGRYSPRS 68
                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Verny, Hana
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94306-1840
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Palo Alto
STATE: CA
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                                                                                                                                                                             KAGSQSKSSDESGNPID----
                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
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                                                                                                                                                                                                                                                                 17.48; 29.28;
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35.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPECIES INFECTIONS
                                                                                                                                                                          -PSTNMPYDPKTGKLIDPESGIAIDNSVSGVFATVPGT 910
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Pred. No. 18;
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                                                                                                                                                                                                                                                                                  Length 1042;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application Patent No. 6025480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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COUNTRY: USA
ZIP: 94306-1840
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: PLOPS/MS-DOS
MEDIUM TYPE: PC-DOS/MS-DOS
MEDIUM TYPE: P
                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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                                                                                                                                                                                                                                           TITLE OF INVENTION: TITLE OF INVENTION:
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                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                               APPLICANT: Massague, Joan APPLICANT: Lee, Mong-hong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 1837 amino acids
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ADDRESSEE: PETERS, VERNY, JONES & BIKSA STREET: 385 Sherman Avenue, Suite 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1652 KAGSQSKSSDESGNPID-----
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APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57 QSPGVGRYSPRS 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Verny, Hana REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION: NUMBER: US/08/928,361B FILING DATE: 12-SEP-1997
                                                                                                       STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME:
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                                                                                                                                       ADDRESSEE:
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: CA
                                                                       New York
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                                       New York
                                                                                                       E: Cooper & Dunham
1185 Avenue of the Americas
United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               650-324-1678
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                                                                                                                                                                                                                                           ISOLATED NUCLEIC ACID MOLECULES ENCODING p75KIP2, A CYCLIN-DEPENDENT KINASE INHIBITOR AND USES SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17.4%; 29.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS, THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM SPECIES INFECTIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carolyn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30,518
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Pred. No. 40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

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Patent No. 6025480
GENERAL INFORMATION:
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Best Local Similarity
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FILING DATE:
CLASSIFICATION: 435
ATTORNEY_AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 28,678
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acids
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1747/47418
                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/415,655
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein HYPOTHETICAL: NO
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Massague, Joan APPLICANT: Lee, Mong-hong
                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 278-0400
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                                                                                                                                                                                                                                                               COUNTRY: UI
                                                                                                                                                                                                                                                                                                       STREET: 1185 AV
CITY: New York
STATE: New York
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STRANDEDNESS: not rele
TOPOLOGY: not relevant
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                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 EDEEKEGSE---QALSSRDGAPVQHPLALLPSGSYEEDPQTILDDHLSRVLKTPGCQS-- 58
                                                                                                                                                                                                                                                                                                                                               E: Cooper & Dunham
1185 Avenue of the Americas
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                                                                                                                                                                                                                                                                                    United States of America
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US-08-415-655-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 17.2
Best Local Similarity 30.7
Matches 23; Conservative
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                                                               TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 278-0400
                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1747/47418
                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/415,655
                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 10036
COMPUTER READABLE FORM:
                MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  332 VAPGVGAVEQTPRKR 346
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STRANDEDNESS: not
                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: New York
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                                              amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                New York
: United States of America
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1185 Avenue of the Americas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lee, Mong-hong
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                                   linear
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             protein
                                                                                                                                                                                                                                                                                                                                                                           Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ISOLĀTED NUCLEIC ACID MOLECULES ENCODING P75KIP2, A CYCLIN-DEPENDENT KINASE INHIBITOR AND USES
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Query Match Best Local Similarity

17.2%; 30.7%;

Score 62; Pred. No.

DB . 8;

Length 348;

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US-08-476-900A-29
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; MOLECULE TYPE: protein
US-08-404-531B-29
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APPLICANT: Joseph Bryan, Lydia Aguilar Bryan, Daniel Nelson TITLE OF INVENTION: Sequence Encoding Mammalian Sulfonylurea Receptor Patent No. 6031150

TITLE OF INVENTION: and Method of Detecting Persistent Hyperinsulinem: TITLE OF INVENTION: Infancy
                                                                                                                           Sequence 29, Application US/08476900A Patent No. 6031150
                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 18; Conserv
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GENERAL INFORMATION:
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                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Joseph Bryan, Lydia Aguilar Bryan, Daniel Nelson, Pamela APPLICANT: Thomas, Gilbert Cote, and Robert Gagel TITLE OF INVENTION: Sequence Encoding Mammalian Sulfonylurea Recept
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
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NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                    948 KASEPSQGLPRAMSSRDG------LILDEEEEEEEAAESEEDDNLSSVL 990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Beardell, Lori Y.
REGISTRATION NUMBER: 34,293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 1 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: One Liberty CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: No. 5863724ris
STREET: One Liberty Place 46th. Floor
                                                                                                                                                                                                                                                                                3 REDEEKEGSEQALSSRDGAPVQHPLALLPSGSYEEDPQTILDDHLSRVL 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Floppy disk
  and Method of Detecting Persistent Hyperinsulinemic Hypoglycem Infancy
                                                                                                                                                                                                                                                                                                                                                         16.4%;
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                                                                                                                                                                                                                                                                                                                                    Score 59; DB
Pred. No. 84;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BYLR-0003
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                                                                                                                                                                                                                                                                                                                                                            Patent No. 6054313
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 29, Appragrammer No. 6054313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,546A
                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                CLASSIFICATION: 800 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Joseph I APPLICANT: Thomas,
                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 07-JUN-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                     STREET: One L.
FILING DATE:
                                                                     APPLICATION NUMBER: US/08 FILING DATE: 07-JUNE-1995
                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                           ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz ADDRESSEE: No. 6054313ris
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                  APPLICATION NUMBER:
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REFERENCE/DOCKET NUMBER:
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STREET: One Liberty Place 46th. Floor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 REDEEKEGSEQALSSRDGAPVQHPLALLPSGSYEEDPQTILDDHLSRVL 51
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215-568-3439
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Thomas, Gilbert Cote, and Robert Gagel
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15-MARCH-1995
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36.7%;
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                08/404,531
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CLASSIFICATION: 800 ATTORNEY/AGENT INFORMATION:

Beardell, Lori

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Query Match
Best Local Similarity
Thes 18; Conserve
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Best Local Similarity
Watches 18; Conserve
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                                                                                                       US-08-404-531B-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 5863724
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
ADDRESSEE: No. 5863724ris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 9, Application US/08404531B Patent No. 5863724
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                                                                                                                                                                                                      TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO:
                                                                                                                  TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Joseph Bryan, Lydia Aguilar Bryan, Daniel Nelson, Pamela APPLICANT: Thomas, Gilbert Cote, and Robert Gagel TITLE OF INVENTION: Sequence Encoding Mammalian Sulfonylurea Receptor
                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 1582 amino aci
                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 215-568-3100
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NAME: Beardell, Lori Y.
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: BY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: One Libert CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/404,531B FILING DATE: 15-MAR-1995
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One Liberty Place 46th, Floor
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                 Conservative
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36.7%;
                                  16.48;
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                                Score 59;
Pred. No.
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Pred. No. 84;
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                 Mismatches
                                                  DB 2; Length 1582;
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                 18;
                Indels
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                                                             APPLICANT: JOSEPH Bryan,
APPLICANT: Thomas, Gilbe
APPLICANT: Thomas, Gilbe
TITLE OF INVENTION: Sequ
Patent No. 6054313
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                        RESULT
                                                                                                                                                        Patent No. 6054313
GENERAL INFORMATION:
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: an TITLE OF INVENTION: IN NUMBER OF SEQUENCES: 4
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                       948 KASEPSQGLPRAMSSRDG---
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 STREET:
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ADDRESSEE: No. 6031150ris
STREET: One Liberty Place 46th. Floor
                                                                                                                                                                                                                                                                                                                                                        Local Similarity 36.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Beardell, Lori Y.
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 07-JUN
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                             ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz ADDRESSEE: No. 6054313r1s
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6031150
: One Liberty Place 46th. Floor Philadelphia
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                                                                                                                                  Joseph Bryan, Lydia Aguilar Bryan, Daniel Nelson, Pamela
Thomas, Gilbert Cote, and Robert Gagel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-JUN-1995
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49
                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and Method of Detecting Persistent Hyperinsulinemic Hypogly
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                                                                                                                                                                                                                                                                                       ---LLLDEEEEEEEAAESEEDDNLSSVL 990
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                                                                                                                                                                                                                                                                                                                                                        Score 59; DB Pred. No. 91; 7; Mismatches
                                                                                                                    Encoding
                                                                                                                    Mammalian
                                                                                                                                                                                                                                                                                                                                                                                        DB 3; Length 1582;
                                                                                                                                                                                                                                                                                                                                                          18;
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                                                                                                                    Sulfonylurea Receptor
                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                          6
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US-08-726-320-5
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Best Local Similarity 36.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/08726320 Patent No. 6171815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/726,320 FILING DATE: Filed Herewith PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 31..
CITY: Palo Alto
STATE: CA
                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: SCORRESPONDENCE ADDRESS: Incyte Ph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Coleman, Roger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                          NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM CO
OPERATING SYSTEM:
SOFTWARE: FastSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE:
                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
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)GY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                 IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Floppy disk
   NUMBER:
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AF-0001 US
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Pred. No. 91;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 3; Length 1582;
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                                                                                             TELEX: 248345
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 567 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 16
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR., GERALD M.
REGISTRATION NUMBER: 28,977
                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
              HYPOTHETICAL:
                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
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LIBRARY: GenBa
CLONE: 784874
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 948 KASEPSQGLPRAMSSRDG------LILDEEEEEEEAAESEEDDNLSSVL 990
                                                                TYPE: AMINO STRANDEDNESS:
                                                                                                                                                          OPERATING SYSTEM:
SOFTWARE: PatentI
                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: UPFILING DATE: 19930121
                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 22042
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: si
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                                                                                  AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Falls Church
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CALVERT, JAI .. CALVERT, JAI .. WITTER, RICHARD L.
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                                                  linear
                                                                                                                                                                                                                                                                                                                                                               PatentIn Release #1.0, Version #1.25
              : protein
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RECOMBINANTS EXPRESSING THE ENVELOPE GLYCOPROTEIN OF
AVIAN RETICULOENDOTHELIOSIS RETROVIRUS
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COUNTRY: USA
ZIP: 19103
ZOMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA PC-DOS/MS-DOS
SOFTWARE: PATENTIA PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/404,531B
FILING DATE: 15-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Beardell, Lori Y.
NAME: Beardell, Lori Y.
NAME: Beardell, Lori Y.
NAME: BEARTION NUMBER: BYLR-0003
TELEPHONE: 215-568-3100
TELEPHONE: 215-568-3100
TELEPHONE: 215-568-3439
INFORMATION FOR SED ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 1498 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: protein
US-08-404-531B-28
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Search completed: June 7, 2001, 02:02:11 Job time: 5404 sec
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US-08-404-531B-28
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Patent No. 5863724
GENERAL INFORMATION:
APPLICANT: Joseph Bryan, Lydia Aguilar Bryan, Daniel Nelson, Pamela APPLICANT: Thomas, Gilbert Cote, and Robert Gagel
TITLE OF INVENTION: Sequence Encoding Mammalian Sulfonylurea Receptor
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Best Local Similarity 37.5%;
Matches 15; Conservative
                                                                                                                                                                                                           Query Match 16.1%;
Best Local Similarity 39.1%;
Matches 18; Conservative
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NUMBER OF SEQUENCES: 49
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ADDRESSEE: No. 5863724ris
STREET: One Liberty Place 46th. Floor
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                                                                                                                                              6 EEKEGSEQALSSRDGAPVQHPLALLPSGSYEEDPQTILDDHLSRVL 51
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Pred. No. 30;
6; Mismatches 19; Indels
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Pred. No. 1.1e+02;
6; Mismatches 16; Indels
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OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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brahma associated	hypothetical prote	hypothetical prote	env polyprotein -	collagenase 3 (EC	retrovirus-related	proline-rich prote	hypothetical prote	immediate-early ph	hypothetical prote	heterocyst pattern	3-methyl-2-oxobuta				

## ALIGNMENTS

A:Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Mesidues: 1-832 <IKE>
A;Cross-references: EMBL:AF017756; NID:g2982197; PIDN:AAC40066.1; PID:g2982198
A;Note: GSK-3beta interacting protein
C;Keywords: phosphoprotein; signal transduction C;Species: Rattus norvegicus (Norway rat)
C;Date: 05-Nov-1999 #sequence\_revision 05-Nov-1999 #text\_change
C;Accession: T08422
R;Ikeda, S.; Yamamoto, H.; Murai, H.; Kishida, S.; Kikuchi, A.
EMBO J. 17, 1371-1384, 1998
A;Title: Axin, a negative regulator of the Wnt signaling pathway A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-838 <YAM>
A;Residues: 1-838 KYAM>
A;Cross-references: EMBL:AP017757; NID:g3080758; PIDN:AAC40089.1; PID:g3080759
A;Note: interacts with GSK-3beta and beta-catenin
C;Keywords: phosphoprotein; signal transduction R;Yamamoto, H.; Kishida, S.; Uochi, T.; Ikeda, S.; Koyama, S.; Asashima, M.; Kikuchi, Mol. Cell. Biol. 18, 2867-2875, 1998
A;Title: Axil, a member of the Axin family, interacts with both glycogen synthase kin A;Reference number: Z16414; MUID:98226558
A;Accession: T08423 Axin homolog Axil - rat
N;Alternate names: Axil
C;Species: Rattus norvegicus (Norway rat)
C;Date: 05-Nov-1999 \*sequence\_revision 05
C;Accession: T08423 A; Reference number: Z16413; A; Accession: T08422 negative regulator axin [imported] - rat N; Alternate names: rAxin  $\label{eq:names}$ 밁 δÃ 밁 õ Query Match Best Local : Matches 457 VGRYSPRSR 465 61 VGRYSPRSR 69 ch 100.0%; L Similarity 100.0%; 69; Conservative 0 regulator of the Wnt signaling pathway, forms a complex wit 3; MUID:98151361 0; Score 360; DB 2; Pred. No. 3.9e-32; ); Mismatches 0; 05-Nov-1999 #text\_change 21-Jul-2000 Length 838; Indels 21-Jul-2000 0, Gaps 0

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A;Molecule type: mRNA
A;Residues: 1-745,'V',747-793 <RES>
A;Cross-references: GB:L26489; NID:g432275; PIDN:AAA37643.1; PID:g432276 C;Comment: This subtilisin-like endoproteinase removes paired basic resicentics:
C;Genetics:
                                                                                                                                                                                                                                                                                                                               C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 18-Jun-1999
C;Accession: A23679; I49677
R;Hatsuzawa, K.; Hosaka, M.; Nakagawa, T.; Nagase, M.; Shoda, A.; Murakami, K.; Nakagawa, J. Biol. Chem. 265, 22075-22078, 1990
A;Title: Structure and expression of mouse furin, a yeast Kex2-related protease. Lack A;Reference number: A23679; MUID:91093035
A;Accession: A23679
                                                                                                                                                   A;Cross-references: GB:X54056; NID:g50996; PIDN:CAA37988.1; PID:g50997 R;Creemers, J.J.W.; Roebroek, A.A.J.; van den Ouweland, A.A.M.; van Dui Mol. Biol. 11, 127-138, 1992 A;Title: Cloning and functional expression of a 4.3 kbp mouse fur cDNA. A;Reference number: 149677 A;Accession: 149677
                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-793 <HAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: protein A; Residues: 226-244 < MO2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Momoi, H.; Yamada, H.; Ueguchi, C.; Mizuno, Gene 134, 119-122, 1993
A;Title: Sequence of a fission yeast gene enc A;Reference number: JT0764; MUID:94063505
A;Accession: JT0764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N; Alternate names: kexin homolog; paired-basic endopeptidase; prohormone-processing
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A;Accession: PN0161
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A; Residues: 1-409 < MOM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;Species: Schizosaccharomyces pombe;Date: 30-Sep-1993 #sequence_revision 20-Aug-1994
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-206 <BUL>
                                                               A; Reference number: A64300; MUID: 96337999 A; Accession: H64410
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hypothetical protein homolog MJ0888 - Methanococcus jannaschii C; Species: Methanococcus jannaschii C; Species: Methanococcus jannaschii C; Species: Methanococcus jannaschii C; Species: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000 C; Accession: H64410 R; Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G. Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Grson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996
A; Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O. A; Title: Complete genome sequence of the methanogenic archaeon, Methanococcus in the sequence of the methanococcus in the sequence of the methanogenic archaeon, Methanococcus in the sequence of the methanogenic archaeon, Methanococcus in the sequence of the methanococcus in the sequence of the sequence of the methanococcus in the sequence of the s
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Mol. Endocrinol. 6, 1634-1641, 1992
A;Title: Identification of a new member of the steroid hormone receptor superfamily
A;Reference number: A45360; MUID:93078797
A;Accession: A45360
                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
H64410
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A;Note: sequence extracted from NCBI backbone (NCBIP:118801)
C;Superfamily: unassigned erbA-related proteins; erbA transforming protein homology
C;Keywords: DNA binding; steroid hormone receptor; transcription regulation; zinc fin
F;72-359/Domain: erbA transforming protein homology <ERBA>
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C;Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 31-Oct-1997
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10 EVREEEEKEEVAEA----EGAPELNGGPQHALPSSSYTDLSRSSSPPSLLDQ-----LQ 59
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30.3%; Pred. No. 5.4;
Live 10; Mismatches
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Pred. No. 5.6;
3; Mismatches
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A:Cross-references: GB:U67532; GB:L77117; NID:g2826344; PIDN:AAB98892.1; PID:g1591566; C:Genetics:
A:Map position: REV819507-818887
C:Superfamily: glyoxalase
                                                                                                      A; Molecule type: DNA
A; Residues: 1-563 <KLE>
A; Residues: 1-563 <KLE>
A; Residues: 1-563 <KLE>
A; Residues: 1-563 <KLE>
C; Cyserfamily: fumarate reductase flavoprotein; 3-oxosteroid 1-dehydrogenase homology;
C; Keywords: FAD; flavoprotein; oxidoreductase
F; 4-265/Domain: fumarate reductase flavoprotein homology <FRE>
                                                                                                                                                                                                                                                                      A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaec A;Reference number: A69250; MUID:98049343
A;Accession: A69335
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C;Accession: T38487

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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-409 <BRO>
A;Residues: 1-409 <BRO>
A;Cross-references: EMBL:297210; PIDN:CAB10129.1; GSPDB:GN00066; SPDB:SPAC29A4.02c
A;Experimental source: strain 972h-; cosmid c29A4
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                                                                                                                                                                                                                                                  A; Status: preliminary; nucleic acid sequence not shown;
                                                                                                                                                                                                                                                                                                                                                                                     R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Glll, S.; Kirkness, E.F. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weldman, J.F.; McDonald, L. Nature 390, 364-370, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 11-Jun-1999 C;Accession: A69335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                succinate dehydrogenase (EC 1.3.99.1) flavoprotein - Archaeoglobus fulgidus
C; Species: Archaeoglobus fulgidus
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A; Introns: 73/1
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Pred. No. 9.3;
L1; Mismatches
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Score 66;
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Query Match
Best Local Similarity
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R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Go; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holr Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987
A;Accession: C70648
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A. Accession: S13106
                                                                                                                                                                                                                                                                                                                                       probable nuoJ protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: C70648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;144-382/Domain: subtilisin homology <SBT>
F;715-735/Domain: transmembrane #status predicted <TMM>
F;736-793/Domain: intracellular #status predicted <INT>
F;153,194,368/Active site: Asp, His, Ser #status predicted
F;387,440,553/Binding site: carbohydrate (Asn) (covalent)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Superfamily: kexin; subtilisin homology
C;Keywords: glycoprotein; hydrolase; serine proteinase;
F;1-26/Domain: signal sequence #status predicted <SIG>F;27-793/Product: furin #status predicted <WAT>F;27-714/Domain: extracellular #status predicted <EXT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Date: 31-Dec-1992 #sequence_revision
C;Accession: S13106
A; Molecule type: DNA
A; Residues: 1-262 <COL>
A; Cross-references: GB: Z83867; GB: ALL23456;
A; Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:X55660; NID:g56171; PIDN:CAA39193.1; C;Comment: This subtilisin-like endoproteinase removes paired
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N; Alternate names: kexin homolog; paired-basic endopeptidase; prohormone-processing
C; Species: Rattus norvegicus (Norway rat)
                                                                                                   A; Status: preliminary; nucleic acid sequence not shown; translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Residues: 1-793 <MIS>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GDGLAIAYRNGIPLKDMEFFQFHPTGLVPSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19;
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                           NID: g3261695;
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                              PIDN:CAB06285.1; PID:e29093
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A;Note: sequence extracted from NCBI backbone (NCBIN:111148, NCBIP:111150)
C;Keywords: surface antigen
                                                                                                                                                                                                                                                                                       A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-907 <HAL>
                                                                                                                                                                                                                                                                                                                                        Mol. Biochem. Parasitol. 53, 105-112, 1992
A;Title: Mimicry of elastin repetitive motifs by Theileria annulata sporozoite surface A;Reference number: A45560; MUID:92365719
A;Accession: A45560
                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 20-Mar-1998 C;Accession: A45560
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A45560
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sporozoite surface antigen SPAG-1 - Theileria annulata
C;Species: Theileria annulata
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A;Experimental source: BAC clone B14D6; strain OR74A
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                                                                                                                                             Matches
                                                                                                                                                              Query Match
Best Local
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les 17; Conserv
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                                                                                                       4 EDEEKEGSEQALSSRD--GAPVQHP-----
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                                   QTILDDHLSRVLKTPGCQSPGVG 62
                                                                   DDEEEEEDDKSTSSKNGKGSPKAQPGVSSSSTSSASPTSPTTTLSQTGLGPSGSHAQQDP 179
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he Protein Sequence
----VGVPGVGVPGVG 192
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Database, P
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Pred. No. 14;
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                                                                                                                                           Mismatches
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base, May 2000
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A;Status: Tall13
A;Status: A novel multi-domain mucin-like glycoprotein A;Recession: T31113
A;Status: A novel multi-domain mucin-like glycoprotein A;Recession: T31113
                                                                              cyclin cdk inhibitor p57 - mouse
N;Alternate names: CDI p57; cyclin-cyclin-dependent kinase inhibitor C;Species: Mus musculus (house mouse)
C;Date: 09-Mar_1996 #sequence_revision 09-Mar-1996 #text_change 05-Nc
                                                                                                                                                                 RESULT
149262
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R;Lee, M.H.; Reynisdottir, I.; Massague, Genes Dev. 9, 639-649, 1995
A;Title: Cloning of p57KIP2, a cyclin-de
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A;Residues: 1-1832 <BAR>
A;Cross-references: EMBL;AF068065; NID:g4063041; PID:g4063042; PIDN:AAC98153.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mucin-like glycoprotein 900 - Cryptosporidium parvum
C;Species: Cryptosporidium parvum
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999
                                                             C; Accession: I49262
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A;Experimental source: serotype D, strain UW-3/Cx
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession:
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C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998
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A; Residues: 1-619 <ARN>
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of p57KIP2, a cyclin-dependent kinase inhibitor with unique domain

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OM protein - protein search, using sw model
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8 anabaena sp
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	P10645 homo sapien	P80698 bacillus su	P49596 caenorhabdi	P79766 gallus gall	P13089 glycine max	Q9y2k6 homo sapien	018927 equus cabal	P05059 bos taurus	P28549 macropus eu	P41245 mus musculu	Q01484 homo sapien	Q09429 rattus norv

## ALIGNMENTS

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MBL; AF017757; AAC40089.1; SSP; P49799; 1AGR. nterPro; IPR001342; nterPro; IPR00158; fam; PF00615; RGS; 1. fam; PF00778; DIX; 1. ROSITE; PS50132; RGS; 1. ROSITE; PS50132; RGS; 1. evelopmental protein; Phosphorylation. evelopmental protein; Phosphorylation. OMAIN 81 200 RGS. OMAIN 327 413 GSK-3B BINDING SITE (BY SIMILA	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).	- SUMCELLULAR LOCATION: CYTOPLASMIC. SUBCELLULAR LOCATION: CYTOPLASMIC. TISSUE SPECIFICITY: EXPRESSED IN LU - PTM: PROBABLY PHOSPHORYLATED BY GSK PP2A SIMILARITY: CONTAINS 1 RGS DOMAIN SIMILARITY: CONTAINS 1 DIX DOMAIN.	MOI. Cell. Biol. 18:2867-2875(1998).  MOI. Cell. Biol. 18:2867-2875(1998).  -!- FUNCTION: INHIBITOR OF THE WAT SIGNALING PATHWAY. DOWN REGULATES BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA- CATENIN AND APC BY GSK-3B (BY SIMILARITY).  -!- SUBUNIT: INTERACTS WITH GLYCOGEN SYNTHASE KINASE-3 BETA (GSK-3B) AND BETA-CATENIN. THE INTERACTION BETWEEN AXIN AND BETA-CATENIN OCCURS VIA THE ANNADILLO REPEATS CONTAINED IN BETA-CATENIN.	[1] SEQUENCE FROM N.A. SEQUENCE FROM N.A. TISSUE=Brain; MEDLINE=98226558; PubMed=9566905; Yamamoto H., Kishida S., Uochi T., Ikeda S., Koyama S., Asashima M., Kikuchi A.; "Axil, a member of the Axin family, interacts with both glycogen synthase kinase 3beta and beta-catenin and inhibits axis formation of	AXIN2. AXIN2.  Rattus norvegicus (Rat).  Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  NCBI_TaxID=10116;	01-0CT-2000 (Rel. 40, Created) 01-0CT-2000 (Rel. 40, Last sequence update) 01-0CT-2000 (Rel. 40, Last annotation update) 01-0CT-2000 (Rel. 40, Last annotation update) AXIN 2 (AXIS INHIBITION PROTEIN 2) (CONDUCTIN) (AXIN-LIKE PROTEIN)	T 1  RAT  RAT  C70240  STANDARD; PRT; 838 AA.

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Best Local
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"Properties of mouse Axin2 and human AXIN2 expression pattern, interaction with Axin axis formation.";
Submitted '.....
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088566; Q9QXJ6;
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01-0CT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
AXIN 2 (AXIS INHIBITION PROTEIN 2) (CONDUCTIN) (AXIN-LIKE PROTEIN)
                             the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by an
entitles requires a license agreement (See http://www.isb-
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                  Behrens J., Jerchow B.-A., Wuertele M., Grimm J., Asbrand C., Wirtz R., Kuehl M., Wedlich D., Birchmeier W.; "Functional interaction of an axin homolog, conductin, with b catenin, APC, and GSK3beta."; Science 280:596-599(1998).
                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE-98221239; PubMed-9554852;
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AAC26047.1;
AAF22800.1;
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838
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Rodentia;
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Sciurognathi; Muridae;
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No. 8.3e-32;
matches 0;
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                                          long as its content is i moved. Usage by and for (See http://www.isb-sib.ch
                                                                                                                                                                                                                                                                                                    Gilbert D.,
F.;
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RESULT 3
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Q9Y2T1; Q9UH
01-OCT-2000
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SEQUENCE
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01-OCT-2000 (Rel. 40, Last annotation update)
AXIN 2 (AXIS INHIBITION PROTEIN 2) (CONDUCTIN) (AXIN-LIKE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pfam; pF00615; RGS; 1.
pfam; pF00778; DIX; 1.
pRINTS; PR01301; RGSPROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGD; MGI:1270862; Axin2.
HSSP; P49799; 1AGR.
                 SEQUENCE FROM N.A.

TISSUE-Brain, and Lymphoblast;
Zhang T., Fagotto F., Hsu W., Zeng L., Gilbert D.,
Jenkins N.A., Warburton D., Costantini F.;
"Properties of mouse Axin2 and human AXIN2: chromos
expression pattern, interaction with Axin and effec
                                                                                                                                                               Mai M., Qian C., Yokomizo A., Smith "Cloning of the human homolog of corchromosome 17q23-q24.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                             axis formation.",
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                                                                                                                                                                                                                                                     Homo sapiens (Human)
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           OCCURS VIA THE ARMADILLO REPEATS CONTAINED IN BETA-CATENIN
TERNARY COMPLEX (BY SIMILARITY).
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59; Conservative
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Primates;
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BETA-CATENIN BINDING SITE (BY
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Pred. No. 8.3e-32;
Mismatches 0;
                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                PRT;
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DE AXIN 2
GN AXIN2.
OS Brachy
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RP SEQUEN
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                                                                                 Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Futeleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi
Cypriniformes; Cyprinidae; Rasborinae; Danio.
NCBI_TaxID-7955;
                                                                                                                                                                                                                                 AXN2_BRARE
P57095;
          SEQUENCE FROM N.A.
MEDLINE=20171051; PubMed=10704853;
Shimizu T., Yamanaka Y., Ryu S.-L.
Bae Y.-K., Hibi M., Hirano T.;
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InterPro; IPR001158; -.
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SIMILARITY: CONTAINS 1 RGS DOMAIN.
SIMILARITY: CONTAINS 1 DIX DOMAIN.
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ental protein; Phosphorylation.
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(Rel. 40, Last sequence update)
(Rel. 40, Last annotation updat
INHIBITION PROTEIN 2).
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Pred. No. 9.7e-29;
4; Mismatches 3;
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BETA-CATENIN BINDING SITE (BY
SIMILARITY).
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DEPHOSPHORYLATED
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Best Local Similarity
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Q1-OCT-2000 (Rel. 40, Created)
01-OCT-2000 (Rel. 40, Last seq
01-OCT-2000 (Rel. 40, Last ann
01-OCT-2000 (Rel. 40, DROTEIN)
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SEQUENCE
Hedgepeth C.M., Deardorff M.A., Klein P.S.;
Hedgepeth C.M., Deardorff M.A., Klein P.S.;
"Xenopus axin interacts with glycogen synthase kinase-3 be expressed in the anterior midbrain.";
Mech. Dev. 80:147-151(1999).
Hech. Dev. 80:147-151(1999).

-i- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION CATENIN AND APC BY GSK-3B (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       formation of the dorsal organizer in zebrafish.";
Mech. Dev. 91:293-303(2000).
-i- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
CATENIN AND APC BY GSK-3B (BY SIMILARITY).
-i- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
-i- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AB032263; BAA92440.1; HSSP; P49799; lAGR.
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                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-99173782; PubMed-10072781;
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                                                                                                                                                                                                              Xenopus laevis (African clawed frog)
Eukaryota; Metazoa; Chordata; Crania
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InterPro; IPR001158; -.
                                                                                                                                                                  NCBI_TaxID=8355;
                                                                                                                                                                                    Kenopodinae;
                                                                                                                                                                                                  Amphibia; Batrachia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50132; RGS; Developmental protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 VGRYSPRSR
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SIMILARITY: CONTAINS 1 RGS DOMAIN.
SIMILARITY: CONTAINS 1 DIX DOMAIN.
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329
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415
467
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                                                                                                                                                                                                      Anura; Mesobatrachia;
                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation updat
PROTEIN) (XAXIN).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 217.5; DB 1
Pred. No. 3.1e-16;
9; Mismatches 11
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BETA-CATENIN BINDING SITE (BY
SIMILARITY).
POLY-SER.
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                                                                                                                                                                                                                   Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46E5ADA6DE2240CC CRC64;
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                                                                                                                                                                                                                                                                                   update)
                                                                                                                                                                                                                     Vertebrata; Euteleostomi;
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                                                                                                                                                                                                      Pipoidea;
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Best Local
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HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LT 6
BRARE
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SEQUENCE
                                                                                                                                                                                                                             MEDLINE-20171051; PubMed=10704853; MEDLINE-20171051; PubMed=10704853; MEDLINE-20171051; PubMed=10704853;
                                                                                                                            Shimizu T., Yamanaka Y., Ryu S.-L., H
Bae Y.-K., Hibi M., Hirano T.;
"Cooperative roles of Bozozok/Dharma
formation of the dorsal organizer in
Mech. Dev. 91:293-303(2000).
                                                                                                                                                                                                                                                                                                                                                             Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Rasborinae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2000 (Rel. 40, Created)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
AXIN 1 (AXIS INHIBITION PROTEIN 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000342;
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P57094;
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BEYELOPMENTAL STACE: WEAKLY AND UBLOUITOUSLY EXPRESSED THROUGHOUT EARLY DEVELOPMENT, AND HIGHLY EXPRESSED IN THE ANYERIOR MESENCEPHALON ADJACENT TO THE FOREBRAIN-MIDBRAIN BOUNDARY.

PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PP2A (BY SIMILARITY).
SIMILARITY: CONTAINS 1 RGS DOMAIN.
SIMILARITY: CONTAINS 1 DIX DOMAIN.
FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION CATENIN AND APC BY GSK-3B (BY SIMILARITY). SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY). PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DHLSRVLKTPGCQSPGVGRYSPRSR 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EEEGDDGDVSSGPSV-ISHK---LPSGPPMHHFNSRYSETGCVGMQIRDAHEENPESILD 474
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EHVQRVMKTPGCQSPGTGRHSPKSR 499
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ental protein; Phosphorylation.
88 211 RGS.
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842 /
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94459 MW;
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BETA-CATENIN BINDING SITE
SIMILARITY).
DIX.
DIX.
BDA152734C97191E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 158; DB 1; Pred. No. 1.1e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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                                                                                                                                                                                                                                           Hashimoto H., Yabe T., Hirata T.,
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                                                                                                                                                               and Nodal-re
zebrafish.";
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                                                                                                                                                                                          Nodal-related
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INDING SITE (BY
                DEPHOSPHORYLATED
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                                                                                                                                                                                        proteins
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Best Local (
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AXIN (AXIS INHIBITION PROTEIN).
AXIN OR AXN.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AXN_CHICK
042400;
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pfam; pr00778; DIX; 1.
pR0SITE; ps50132; RGS; 1.
Developmental protein; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gallus gallus (Chicken).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AB032262; BAA92439.1; -. HSSP; P49799; 1AGR.
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InterPro;
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                    DOMAIN
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MEDLINE=97373830; PubMed=9230313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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SIMILARITY: CONTAINS 1 RGS DOMAIN.
SIMILARITY: CONTAINS 1 DIX DOMAIN.
                                                                                                                                                                                                                                                                                                                                                    LINE=97373830; PubMed=923V313;
g.L., Fagotto F., Zhang T., Hau W., Vasicek T.J., Perr J.J., Tilghman S.M., Gumbiner B.M., Costantini F.;
g. T., Tilghman S.M., Gumbiner B.M., an inhibitor of the mouse Fused locus encodes Axin, an inhibitor of the mouse Fused locus encodes Axin, an inhibitor of the
                                                                                              PP2A (BY SIMILARITY).
SIMILARITY: CONTAINS 1 RGS DOMAIN.
SIMILARITY: CONTAINS 1 DIX DOMAIN.
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94351 MW;
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Pred. No. 1e-0
10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DIX
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BETA-CATENIN BINDING SITE (BY
SIMILARITY).
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No. 1e-08;
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                                                                                                                                                                                                                                                                                                         DOWN
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SEQUENCE
                                                                                                                                                              dependent phosphorylation of beta-catenin.";

EMBO J. 17:1371-1384(1998).

-I- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-CATENIN AND APC BY GSK-3B (BY SYMILARITY).

-I- SUBUNIT: INTERACTS WITH GSK-3B AND BETA-CATENIN. THE INTERACTION BETWEEN AXIN AND BETA-CATENIN OCCURS VIA THE ARMADILLO REPEATS CONTAINED IN BETA-CATENIN. TERNARY COMPLEX. ALSO BINDS TO PLAKOGLOBIN (GAWAA-CATENIN), APC, DVL AND PP2A (BY SYMILARITY).

-I- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).

-I- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN TESTIS, THYMUS AND LUNG FOLLOWED BY CEREBRUM, CEREBELLUM, HEART, KIDNEY, SKELETAL MUSCLE, SPECIFION AND LUNG FOLLOWED BY CEREBRUM, CEREBELLUM, HEART, KIDNEY, SKELETAL MUSCLE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2000 (Rel. 40, Created)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
AXIN 1 PROTEIN (AXIS INHIBITION PROTEIN 1) (RAXIN) (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ikeda S., Kishida S., Yamamoto H., Murai H., Koyama S., Kikuchi "Axin, a negative regulator of the Wnt signaling pathway, forms complex with GSK-3beta and beta-catenin and promotes GSK-3beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an
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Ikeda S., Kishida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID-10116;
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BETA-CATENIN BINDING
SIMILARITY).
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O1-0CT-2000 (Rel. 40, Created)
O1-0CT-2000 (Rel. 40, Last sequence update)
O1-0CT-2000 (Rel. 40, Last annotation update)
O1-0CT-2000 (Rel. 40, Last annotation update)
AXIN 1 (AXIS INHIBITION PROTEIN 1) (FUSED PROTEIN) (FRAGMENT)
AXIN OR FU.
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                                                                                                                                                                                                                                                                                                                                  Zeng L., Fagotto F., Zhang T., Hsu W., Vasicek T.J., Perry W.L. III, Lee J.J., Tilghman S.M., Gumbiner B.M., Costantini F.; "The mouse Fused locus encodes Axin, an inhibitor of the Wnt signaling pathway that regulates embryonic axis formation."; Cell 90:181-192(1997).

Cell 90:181-192(1997).

FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
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InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=97373830; PubMed=9230313;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
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Mammalia; Eutheria;
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HSSP; P49799; 1AGR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 QIREDEEKEGSEQALSSRDGAPVQHPLALLPS------GSYEEDPQTIL 43
                                                                CATENIN AND APC BY GSK-3B (BY SIMILARITY).

SUBUNIT: INTERACTS WITH GSK-3B AND BETA-CATENIN. THE INTERACTION BETWEEN AXIN AND BETA-CATENIN OCCURS VIA THE ARMADILLO REPEATS CONTAINED IN BETA-CATENIN. TERNARY COMPLEX. ALSO BINDS TO PLAKOGLOBIN (GAMMA-CATENIN), APC, DUL AND PP2A (BY SIMILARITY).

SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).

ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE PRODUCED BY ALTERNATIVE SPLICING.

TISSUE SPECIFICITY: EXPRESSED IN EMBRYONIC STEM CELLS.
DEVELOPMENTAL STAGE: WIDELY EXPRESSED AT ELO.5 TO E16.5 DAY.
DEVELOPMENTAL STAGE: WIDELY EXPRESSED AT ELO.5 TO E16.5 DAY.
  SIMILARITY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PF00615; RGS; 1.
PF00778; DIX; 1.
TE; PS50132; RGS;
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IPR001158; -.
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893 AA;
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  RGS
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GSK-3B BINDING SITE.
BETA-CATENIN BINDING
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  DOMAIN.
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015169;

01-0CT-2000 (Rel. 40, Cres

01-0CT-2000 (Rel. 40, Last

01-0CT-2000 (Rel. 40, Last

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101-0CT-2010 (Rel. 40, Last)

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InterPro; IPR001158; -.
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                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

MEDLINE=97373830; PubMed=9230313;

MEDLINE=97373830; PubMed=9230313;

Zeng L., Fagotto F., Zhang T., Hsu W., Vasicek T.J., Perry W.L. III,

Zeng L., Tilghman S.M., Gumbiner B.M., Costantini F.;

Lee J.J., Tilghman S.M., Gumbiner B.M., Costantino of the Wnt signaling

"The mouse Fused locus encodes Axin, an inhibitor of the Wnt signaling

pathway that regulates embryonic axis formation.";

Cell 90:181-192(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
     - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
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                                                                BETA-CATEMIN. AND APC BY GSK-3B.
CATEMIN AND APC BY GSK-3B.
CATEMIN AND APC BY GSK-3B.
SUBUNIT: INTERACTS WITH GLYCOGEN SYNTHASE KINASE-3 BETA (GSK-3B)
SUBUNIT: INTERACTS WITH GLYCOGEN SYNTHASE KINASE-3 BETA-CATEMIN
AND BETA-CATEMIN. THE INTERACTION BETWEEN AXIN AND BETA-CATEMIN.
OCCURS VIA THE ARMADILLO REPEATS CONTAINED IN BETA-CATEMIN.
OCCURS VIA THE ARMADILLO REPEATS CONTAINED IN BETA-CATEMIN.),
APC, DVL AND PP2A.
SUBCELLULAR LOCATION:
TISSUE SPECIFICITY: UI
                                                                                                                                                                                                                     FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGI:1096327; Axin.
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PS50132; RGS;
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GSK-3B BINDING SITE (BY SIMILARITY).
BETA-CATENIN BINDING SITE (BY
SIMILARITY).
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v; 70EEB53D387BD26F CRC64;
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SEQUENCE
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-!- SIMILARITY: CONTAINS 1 DIX DOMAIN.
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                                                                                                                                                                                                               PROSITE;
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        Momoi H., Yamada H., Ueguchi C., Mizuno T.; "Sequence of a fission yeast gene encoding homology to eukaryotic elongation factor-1 gene 134:119-122(1993).
                                                                                                                                                              Schizosaccharomycetales;
Schizosaccharomyces.
                                                                                                                                                                        Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                           Schizosaccharomyces pombe (Fission yeast)
                                                                                                                                                                                                       TEF3 OR SPAC29A4.02C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                             MEDLINE=94063505;
                                                                                                                         STRAIN=972;
                                                                                                                                                     NCBI_TaxID=4896;
                                        STRAIN=972;
                                                   SEQUENCE FROM N.A.
                                                                                                                                  SEQUENCE FROM N.A., AND SEQUENCE
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 CELLULAR COMPONENTS
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                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
33; Conserv
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Ps50132; RGS; 1.
Phosphorylation.
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99803 I
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Pred.
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BETA-CATENIN BINDING SITE (BY
SIMILARITY).
DIX.
                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         EE5F990B11FC7B3B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                      OF 226-244
                                                                                                                                                                                                                                                                                                                                                                                                                113.5;
No. 8.
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                                                                                 a protein with extensive gamma.";
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SUBUNIT: EF-1 IS COMPOSED OF FOUR SUBUNITS: ALPHA, BETA,

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FURI_MOUSE

STANDARD;

PRT;

793 AA.

C P23188;

C 01-NOV-1991 (Rel. 20, Created)

T 01-NOV-1991 (Rel. 20, Last sequence update)

T 01-NOV-1991 (Rel. 20, Last annotation update)

T 30-MAY-2000 (Rel. 39, Last annotation update)

PEURIN PRECURSOR (EC 3.4.21.75) (PAIRED BASIC AMI

ECLEAVING ENZYME) (PACE) (DIBASIC PROCESSING ENZYME)

FUR OR PCSK3.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hatsuzawa K., Hosaka M., Nakagawa T., Nagase M., Shoda A.,
Murakami K., Nakayama K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Elongation factor; Protein biosynthesis
CONFLICT 246 246 R -> A (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; D14606; BAA03456.1; -. EMBL; 297210; CAB10129.1; -.
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or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                        TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                       J. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Structure and expression of mouse furin, a protesse Lack of processing of coexpressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE-91093035; PubMed-2266110;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; JT0764; JT0764.
InterPro; IPR000521; -.
InterPro; IPR001662; -.
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12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PS50040; EF1G; 1.
                                                                                                                                                                                                                                                                                                                                                                                                     Chem. 265:22075-22078(1990)
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45786 MW; A49CB947A9F66DF0 CRC64;
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1.2;
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Query Match
Best Local S
Matches 20
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InterPro; IPR000209; -.

InterPro; IPR002844; -.

Pfam; PF001483; P; 1.

PRINTS; PR00723; SUBTILISIN.
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EMBL; L26489; PIR; A23679; K
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ACT_SITE
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TRANSMEM
ACT_SITE
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PROPEP
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                                                                   SEQUENCE
                                                                              CONFLICT
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                                                                                                                                                                                                      DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEROPS; S08.071;
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                                                                                                                                                               CARBOHYD
                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                                                                                                                      Hydrolase;
                                                                                                                                                                                                                                                                                                                                      ymogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE SPECIFICITY: SEEMS TO BE EXPRESSED UBIQUITOUSLY.

DOMAIN: CONTAINS A HOMO B DOMAIN, ALSO KNOWN AS P OR MIDDLE DOMAIN

AND A SUBTILISIN-LIKE CATALYTIC DOMAIN. ESSENTIAL DOMAINS FOR

CATALYTIC ACTIVITY.

DOMAIN: CONTAINS A CYTOPLASMIC DOMAIN RESPONSIBLE FOR ITS TGN

LOCALIZATION AND RECYCLING FROM THE CELL SURFACE.

DOMAIN: THE PROPEPTIDE IS AUTOCATALYTICALLY REMOVED THROUGH AN

INTRAMOLECULAR CLEAVAGE PROBABLY IN THE ENDOPLASMIC RETICULUM

(ER). IN THE TGN THE SECOND CLEAVAGE IN THE PROPEPTIDE COULD LEAD

TO THE ACTIVATION OF FURIN.

SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8; ALSO KNOWN AS THE

SUBTILASE FAMILY. HIGH SIMILARITY WITH OTHER FURIN-LIKE ENZYMES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANS GOLGI NETWORK. PROPEPTIDE CLEAVAGE IS A PREREQUISITE FOR EXIT OF FURLN MOLECULES OUT OF THE ENDOPLASHIC RETICULUM (ER). SECOND CLEAVAGE IN THE PROPEPTIDE OCCUR IN THE TRANS GOLGI NETWORK (TGN), WHICH IS FOLLOWED BY THE RELEASE OF THE PROPEPTIDE BOUND TO FURIN AND THE ACTIVATION OF FURIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESPECTIVE PRECURSORS.
COFACTOR: CALCIUM-DEPENDENT (BY SIMILARITY).
ENZYME REGULATION: COULD BE INHIBITED BY THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              European Bioinformatics Institute. The by non-profit institutions as long
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778
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            19.7%;
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                                                                                                                                                                                                                                                                                                                                                      Transmembrane; Glycoprotein; Signal;
              Score 71;
Pred. No.
                                                                                                                                N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
CLEAVAGE (SECOND AUTO-).
CLEAVAGE (FIRST AUTO-).
                                                                CELL SURFACE SIGNAL.
TRANS GOLGI NETWORK SIGNAL.
CELL ATTACHMENT SITE (POTENTIAL).
M -> V (IN REF. 2).
55121C3DE2E1A42D CRC64;
                                                                                                                                                                                                                              CHARGE RELAY
                                                                                                                                                                                                                                                          CHARGE
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BY SIMILARITY.
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E RELAY SYSTEM
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Similarity

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EQTCSRQSQSSRESRPQQQPPALRPEVEMEPRLQAGLASHLPEVLAGLSC 721 EKEGSEQALSSRDGAPVQHPLALLPSGSYEEDPQTILDDHLSRVLKTPGC

56

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RESULT 13
PPAS_HUMAN
                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
01-OCT-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR BETA (PPAR-BETA)
(PPAR-DELTA) (NUCLEAR HORMONE RECEPTOR 1) (NUC1) (NUC1).
PPARB OR NRIC2 OR PPARD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-93078797; PubMed-1333051;
MEDLINE-93078797; RubMed-1333051;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                               Receptor: Transcription regulation; Activator; DNA-Nuclear protein; Zinc-finger; Multigene family.
DNA_BIND 74 138 NUCLEAR RECEPTOR-TYPE.
DNA_FING 74 94 C4-TYPE.
ZN_FING 74 94 C4-TYPE.
ZN_FING 11 133 C4-TYPE.
DOMAIN 254 441 AA; 49903 MW; 94FBBZA4B465Z1E8 CRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as its content is in no way use by non-profit institutions as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       acids."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       superfamily that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rodan G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
Eukaryota; Metazoa; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPAS_HUMAN
                                                                                                                                                                                                                                      Pfam; PF00104; hormone_rec; 1. pfam; PF00105; zf-c4; 1. PRINTS; PR00047; STROIDFINGER. PRINTS; PR00398; STRDHORMONER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Identification of a new member of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia; Eutheria; Primates;
                                                                                                                                                                                    PRINTS; PRO1290; PROXISOMPABR.
PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000536; -.
InterPro; IPR001628; -.
InterPro; IPR001723; -.
                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P03377
MIM; 600409;
                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; L07592; AAA36469.1;
                                                                                                                                                                                                                      PRINTS;
                                                                                                                                                                                                                                                                                                          InterPro; IPR003074; -.
InterPro; IPR003075; -.
                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; A45360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: RECEPTOR THAT BIND PEROXISOME PROLIFERATORS SUCH AS HYPOLIPIDEMIC DRUGS AND FATTY ACIDS. ONCE ACTIVATED BY A LIGAND, THE RECEPTOR BINDS TO A PROMOTER ELEMENT IN THE GENE FOR ACYL-COA OXIDASE AND ACTIVATES ITS TRANSCRIPTION. IT THEREFORE CONTROLS THE PEROXISOMAL BETA-OXIDATION PATHWAY OF FATTY ACIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT: HETERODIMER WITH THE RETINOID X RECEPTOR. SUBCELLULAR LOCATION: NUCLEAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NR1 SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Endocrinol. 6:1634-1641(1992)
                                                                                                                                                                                                                                                                                                                                                                                                             P03372; 1HCQ.
                                                                                                                                                                                                    PR01288; PROXISOMEPAR. PR01290; PROXISOMPABR.
                                                                                                                                                                                                                                                                                                                                                                                                                                A45360.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         is activated
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 19.0%;
30.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
 Score 68.5; D
Pred. No. 3.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a peroxisome
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                 Вď
                   1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shinar D
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                                                                     SIMILARITY)
CRC64;
                   Length 441
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Best Local
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L_RAT
FURL_RAT STAN
P23377;
01-NOV-1991 (Rel. 2
01-NOV-1991 (Rel. 2
01-OCT-2000 (Rel. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997
01-NOV-1997
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-96337999; pubMede-8688087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,

Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,

Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,

Sutton G.G., Blake J.A., Fitzgerald L.M., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Scott J.L., Geoghagen N.S.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q58298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             METJA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MJ0888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL
                                                                                                                                                                                                                                                                            Hypothetical protein.
SEQUENCE 206 AA; 23229 MW; AC2C59FF1E80840E CRC64;
                                                                                                                                                                                                                                                                                                           InterPro; IPR001279; -
Pfam; PF00753; lactamase_B;
                                                                                                                                                                                                                                                                                                                                       EMBL; U67532; AAB98892.1; TIGR; MJ0888; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SCIENCE 273:1058-1073(1996).
-i- SIMILARITY: WEAK, TO B.SUBTILIS YQGX AND TO M.JANNASCHII MJ0296.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=2190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Archaea; Euryarchaeota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Methanococcus jannaschii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ¥888_METJA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Complete genome sequence jannaschii.";
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                                                                                           15
                                                                                                                                                       QIREDEEKEGSEQALSSRDGAPVQH--PLALLPSGSYEE-----DPQTILDDHLSRVLKT 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGCDGASCGSLNMECR 75
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                                                                                                                                      23;
                                                                                                                                                                                                    19;
                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 35, Last annotation update)
                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROTEIN MJ0888.
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                                                              STANDARD;
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40,
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Last
                                   Created)
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                                                                                                                                                                                                      10;
    sequence update) annotation updat
                                                                                                                                                                                                                   Score 68; DB Pred. No. 1.4;
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                                                                 PRT;
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                                                                                                                                                                                                                                 1; Length 206
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Nucleic acids res. 18:6719-6719(1990).

IN FUNCTION: FURIN IS LIKELY TO REPRESENT THE UBIQUITOUS ENDOPROTEASE ACTIVITY WITHIN CONSTITUTIVE SECRETORY PATHWAYS AND CAPABLE OF CLEAVAGE AT THE RX(K/R)R CONSENSUS MOTIF.

ICATALYTIC ACTIVITY: RELEASE OF MATURE POTEINS FROM THEIR PROPROTEINS BY CLEAVAGE OF ARG-YAA-ARG-|-ZAA BONDS, WHERE XAA CAN BE ANY AMINO ACID AND YAA IS ARG OR LYS. RELEASES ALBUMIN, COMPLEMENT COMPONENT C3 AND VON WILLEBRAND FACTOR FROM THEIR COMPLEMENT COMPONENT C3 AND VON WILLEBRAND FACTOR FROM THEIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-WISTAR; TISSUE-Liver;
MEDLINE-91067492; PubMed-2251148;
                                                                                                                                          PRINTS; PR00723; SUBTILISIN.
PROSITE; PS00136; SUBTILASE_HIS; 1.
PROSITE; PS00137; SUBTILASE_HIS; 1.
PROSITE; PS00138; SUBTILASE_SER; 1.
Hydrolase; Serine protease; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content use by non-profit institutions are long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <del>+</del> <del>+</del>
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                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000209; ...
InterPro; IPR002884; ...
Pfam; PF01483; P; 1.
Pfam; PF00082; Pept1das
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; Q99405;
MEROPS; S08.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; x55660; CAA39193.1;
PIR; S13106; KXRTF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <del>-</del>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROPEPTIDE.

SUBCELLULAR LOCATION: SEEMS TO BE LOCALIZED INTRACELLULARLY TO THE TRANS GOLGI NETWORK. PROPEPTIDE CLEAVAGE IS A PREREQUISITE FOR EXIT OF FURIN MOLECULES OUT OF THE ENDOPLASMIC RETICULUM (ER). SECOND CLEAVAGE IN THE PROPEPTIDE OCCUR IN THE TRANS GOLGI NETWORK (TON), WHICH IS FOLLOWED BY THE RELEASE OF THE PROPEPTIDE BOUND TO FURIN AND THE ACTIVATION OF FURIN.

TISSUE SPECIFICITY: SEEMS TO BE EXPRESSED UBIQUITOUSLY.

DEVELOPMENTAL STAGE: EXPRESSED AT E7 DAY IN ENDODERM AND MESODERM, UNIFORMLY EXPRESSED UNTIL E10, WHEN EXPRESSION IS HIGHER IN HEART OF THE PROPERTY OF THE P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATALYTIC ACTIVITY.

CONTAINS A CYTOPLASMIC DOMAIN RESPONSIBLE FOR ITS TGN DOMAIN: CONTAINS A CYTOPLASMIC DOMAIN RESPONSIBLE FOR ITS TGN LOCALIZATION AND RECYCLING FROM THE CELL SURFACE.

PTM: THE PROPEPTIDE IS AUTOCATALYTICALLY REMOVED THROUGH AN INTRAMOLECULAR CLEAVAGE PROBABLY IN THE ENDOPLASMIC RETICULUM (ER). IN THE TGN THE SECOND CLEAVAGE IN THE PROPEPTIDE COULD ITO THE ACTIVATION OF FURIN.

SIMILARITY: BELONGS TO PEPTIDASE FAMILY SB; ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESPECTIVE PRECURSORS.

COFACTOR: CALCIUM-DEPENDENT (BY SIMILARITY).

ENZYME REGULATION: COULD BE INHIBITED BY THE NOT SECONDLY CLEAVED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBTILASE FAMILY. HIGH SIMILARITY WITH OTHER FURIN-LIKE ENZYMES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN: CONTAINS A HOMO B DOMAIN, ALSO KNOWN AS P OR MIDDLE DOMAIN AND A SUBTILISIN-LIKE CATALYTIC DOMAIN. ESSENTIAL DOMAINS FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AND LIVER PRIMORDIA. IN MID-AND LATE-GESTATIONAL STAGES, WIDELY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXPRESSED
                                                                                                      Calcium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .071; -
          25
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                                                                                                                                                                                                                                                                                                                                                                                                Peptidase_S8; 1.
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O42400 gallus gall
O70239 rattus norv
O35625 mus musculu
O15169 homo sapien
O9ptp2 xenopus lae
O918w3 gallus gall
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O2576 archaeoglob
O90v8 leishmania
O93464 carassius a
P95172 mycobacteri
O99577 neurospora
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Query Match 100.0%; Best Local Similarity 100.0%; Matches 69; Conservative (

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INTERPRO; IPR001342; -.
INTERPRO; IPR001158; -.
PFAM; PF00615; RGS; 1.
PFAM; PF00778; DIX; 1.
PRODOM; PD001580; -; 1.
PRODOM; PD003639; -; 1.
SEQUENCE 840 AA; 92934
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Science 280:596-599(1998).
EMBL; AF073788; AAC26047.1; -.
HSSP; P49799; laGR.
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                                                                                                                                                  Zhang T., Fagotto F., Hsu W., Zeng L., Gilbert D., Copeland N.G., Jenkins N.A., Warburton D., Costantini F.; "Properties of mouse Axin2 and human AXIN2: chromosomal location, expression pattern, interaction with Axin and effects on embryonianic formation".
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Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
                                 axis formation.";
Submitted (NOV-1999) to the
EMBL; AF205889; AAF22800.1;
HSSP; P49799; lAGR.
                                                                                                                                                                                                                                SEQUENCE FROM N.A. Zhang T., Fagotto F., Jenkins N.A., Warburt
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Sciurognathi;
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thi; Muridae; Murinae; Mus
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Homo sapiens (Human).
Eukaryota; Metazoa; (
Mammalia; Eutheria; I
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Q9UH84;
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PFAM; PF00615; RGS; 1.
PFAM; PF00778; DIX; 1.
PRINTS; PR01301; RGSPROTEIN.
SEQUENCE 840 AA; 92896 MW;
Q9Y2T1
Q9Y2T1;
01-NOV-1999
01-NOV-1999
01-OCT-2000
CONDUCTIN.
                                                                                                                                                                                                                                                                           Zhang T., Fagotto F., Hsu W., Zeng L., Gilbe Jenkins N.A., Warburton D., Costantini F.;
"Properties of mouse Axin2 and human AXIN2: expression pattern, interaction with Axin an axis formation.";
submitted (NOV-1999) to the EMBL/GenBank/DDE EMBL; AF205888; AAF22799.1;
HSSP; P49799, 1AGR.
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PFAM; PF00778; DIX; 1.
PRINTS; PR01301; RGSPRC
SEQUENCE 777 AA; 868
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69; Conserv
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62; Conservative
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Metazoa; Chordata; C
Metazoa; Primates; C
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pred. No. 5.5e-34;
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Best Local S
Matches 34
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Matches 62
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"Cloning of the human homolog of
chromosome 17g23-g24.";
Genomics 55:341-344(1999).
EMBL; AF078165; AAD20976.1; -
HSSP; P49799; lAGR
                                                                                                                                                                                                                                            INTERPRO; IPRO00342; -.
INTERPRO; IPRO01158; -.
PRAM; PF00615; RGS; 1.
PFAM; PF00778; DIX; 1.
PRODOM; PD003639; -; 1.
PRODOM; PD003639; -; 1.
SEQUENCE 842 AA; 94459 MW; 1
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INTERPRO; IPR001158; -.
PFAM; PF00615; RG; 1.
PFAM; PF00778; DIX; 1.
SEQUENCE 843 AA; 9355;
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Q9YGYO;
Q1-MAY-1999
Q1-MAY-1999
Q1-QCT-2000
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                   Hedgepeth C.M., Deardorff M.A., Klein P.S.;
"Xenopus axin interacts with glycogen synthase kinase-3
expressed in the anterior midbrain.";
Mech. Dev. 80:147-151(199).
EMBL; AF097313; AAC71036.1; -.
HSSP; P49799; IAGR.
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Eukaryota; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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DHLSRVLKTPGCQSPGVGRYSPRSR 69
                                            EEEGDDGDVSSGPSV-ISHK---LPSGPPMHHFNSRYSETGCVGMQIRDAHEENPESILD 474
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                                                                                                                                    Conservative
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Pred. No. 1.1e-30;
Pred. No. 1.3e-30;
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Pred. No. 3e-10;
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Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Linhogauria: Ayes; Neognathae; Galliformes; Phasianidae; Phasiani
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        Ikeda S., Yamamoto H., Murai H., Kishida S., Kikuchi A.; "Axin, a negative regulator of the Wnt signaling pathway, complex with GSK-3beta and beta-catenin and promotes GSK-dependent phosphorylation of beta-catenin."; EMBO J. 17:1371-1384(1998).

EMBL; AF017756; AAC40066.1; -.
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01-OCT-2000
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Zeng L., Fagotto F., Zhang T., Hsu W., Vasicek T.J., Perr
III Lee J.J., Tilghman S.M., Gumbiner B.M., Costantini F.
"The mouse Fused locus encodes Axin, an inhibitor of the
pathway that regulates embryonic axis formation.";
Cell 90:181-122(1997).
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                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERPRO; IPR000342; -.
INTERPRO; IPR001158; -.
PFAM; PF00615; RGS; 1.
PFAM; PF00778; DIX; 1.
                                                                                      SEQUENCE FROM N.A. MEDLINE=98151361; PubMed=9482734;
                                                                                                                        NCBI_TaxID-10116
                                                                                                                                                           Rattus norvegicus (Rat).
                                                                                                                                                                       RAXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF009012; AAC60245.1; HSSP; P49799; 1AGR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                      459
                                                                                                                                                                                                                                                                                                                                   403
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                                                                                                                                                                                                                                                                                                                                                3 REDEEK------EGSEQALSSRDGAPVQHPLALLPSG---
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                                                                                                                                                                                                                                                                                     REAEEKLEERLKRVRAEEEGEDADISSGPSV-ISHK---MPSAQPFHHFAPRYSEMGCAG
                                                                                                                                                                                                                                                                                                                                                                                          Similarity
IPR000342;
                                                                                                                                                                                Gremblrel.
Gremblrel.
Gremblrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel.
                                                                                                                                    Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                         94931 MW;
                                                                                                                                                                                                                                                                                                                                                                                          40.68;
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Pred. No. 7.7e-09;
4; Mismatches 14
                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                     Murinae; Rattus.
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Best Local Similarity
Matches 30; Conserv
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Best Local :
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01-JAN-1998
01-OCT-2000
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PRODOM; PD003639; -; 1.
SEQUENCE 832 AA; 92856 MW;
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035625;
015169;
015169;
01-JAN-1998
01-JAN-1998
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AXIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pathway that regulates embryonic Cell 90:181-192(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97373830; PubMed=9230313; MEDLINE=97373830; PubMed=9230313; Zeng L., Fagotto F., Zhang T., Hsu W., Vasicek T.J., Perr III Lee J.J., Tilghman S.M., Gumbiner B.M., Costantini F. "The mouse Fused locus encodes Axin, an inhibitor of the pathway that regulates embryonic axis formation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PFAM; PF00615; RGS; PFAM; PF00778; DIX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF009011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        476 DEHVQRVMRTPGCQSPGPGHRSPDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR01301; RGSPROTEIN.
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                                                                                                                                                                                                                                                                                                     1 QIREDEEKEGSEQALSSRDGAPVQHPLALLPS----
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                                                                                                                                                                                                                                                            RVRMEEEGEDGEMP----SGPMASHKLPSVPAWHHFPPRYVDMGCSGLRDAHEENPESIL
                                                                                                                                                                          P49799;
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8 (TrEMBLrel. 05,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             992 AA; 109917 MW;
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  (TrEMBLrel.
                                                                    PRELIMINARY;
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35.3%; Pred. No. 4.4e-08;
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      05,
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Pred. No. 5.
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Sciurognathi; Muridae; Murinae; Mus
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                                                                        PRT;
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         sequence update)
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les 20;
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on update)
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                                                                                                                                                                                                                                                                                                                                                                                                         992;
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Best Local
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Best Local S
Matches 28
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Zeng L., Fagotto F., Zhang T., Hsu W., Vasicek T.J., Perry W.L.,
III Lee J.J., Tilghman S.M., Gumbiner B.M., Costantini F.;
"The mouse Fused locus encodes Axin, an inhibitor of the Wnt signaling pathway that regulates embryonic axis formation.";
Cell 90:181-192(1997).
EMBL; AF009674; AAC51624:1; -.
HSSP; P49799; IAGR.
                                                                                            Submitted (APR-1999) to the EMB Submitted (APR-1999) to the EMB EMBL; AF140243; AAF22574.1; -. INTERPRO; IPR000342; -. INTERPRO; IPR001158; -. PPAM; PR00778; DIX; 1. PRINTS; PR01301; RGSPROTEIN. PRINTS; PR01301; RGSPROTEIN. SEQUENCE 706 AA; 79196 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AXIN
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                          O9PTP2; PRELIMINARY;
O9PTP2; TEMBLEE1. 13,
O1-MAY-2000 (TrEMBLEE1. 13,
O1-JUN-2000 (TrEMBLEE1. 14,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INTERPRO; IPRO00342; ...
INTERPRO; IPRO01158; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR01301; RGSPROTEIN
                                                                                                                                                                                              TISSUE-OVARY;
Itoh K., Antipova A., Ratcliffe M.,
                                                                                                                                                                                                                                                                           Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                               AXIN-RELATED PROTEIN.
                                                                                                                                                                               complex.";
                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                     NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                   Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 440 REAEEKLEERLKRYRMEEEGEDGDPSSGPPGPC-HKLPPAPAWHHFPPRLCWTWACAGLR 498
                                                                                                                                                                                                                                                                                                                                                                                                                                   499 DAHEENPESILDEHVQRVLRTTGRQSPGPGHRSPDS
                                                                                                                                                                                            "Dishevelled transduces a signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                 33 GSYEEDPQTILDDHLSRVLKTPGCQSPGVGRYSPRS 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 REDEEK-----
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33;
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                                      28;
                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             900 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                    Conservative
                                                                                                                                                                                                                                                                  Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99803 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----EGSEQALSSRDGAPVQHPLALLPS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31.5%;
                                                 31.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 113.5; 1
Pred. No. 5.5e
10; Mismatches
                                                                                                                                                                                                                                                                                                                             Created)
Last sequence update)
Last annotation update)
                                      Score 112.5;
Pred. No. 5.5e
13; Mismatches
                                                                                                                                                                      EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EE5F990B11FC7B3B
                                                                                                   C3D0AF0D9540F162 CRC64;
                                                                                                                                                                                                Sokol S.;
displacing GSK3 from axin-GSK3
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                                                                  DB 13;
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Best Local Similarity 32.4
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9JL71
Q9JL71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         O918W3;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-20267232; PubMed-10809235;
Takada I., Yu R.T., Xu H.E., Lambe
                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                       01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
TEASHIRT 2 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Evans R.M., Umesono K.;
"Alteration of a single amino acid in activated receptor-alpha (PPAR alpha) phenotype.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q918W3
                                                                                                                                                                                                                                                                                                                      TSH2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MO1. Endocrinol. 14:733-740(2000).
EMBL; AF163810; AAF80480.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Archosauria; Aves;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                          NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID-9031;
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                                                                                                                                    "Vertebrate orthologues of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                teashirt."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SQSPFVQRKGKFQP 421
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                                                                Dev. 91:445-448(2000).
AF207880; AAF64095.1;
                       1098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          443 AA;
                                                                                                                                                          Core N., Boned A.,
1098 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                     1098
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chordata; Craniata; Vertebrata; Euteleostomi;
Neognathae; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50108 MW;
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121367 MW;
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                                                                                                                                                                                                                                                                                                                                                            Created)
Last sequence update)
Last annotation update)
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Pred. No. 3.2;
12; Mismatches
                                                                  .•
                                                                                                                                  Kerridge S.,
e Drosophila
                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EB6E0C39554C76CD CRC64;
42BA01C7DB2BAFEB CRC64;
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                                                                                                                                  patterning
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KC STRAIN=VC-16 / DSM 4304 / ATCC 49558;

RX MEDLINE=98049343; PubMed=9389475;

RA Klenk H.-P. Clayton R.A., Tomb J.-F., White O., Nelson K.E.,

RA Klenk H.-P. Clayton R.A., Gwinn M., Hickey E.K., Peterson J.D.,

RA Kichardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,

RA Richardson D.L., Cherlavage A.R., Graham D.E., Kyrpides N.C.,

RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,

RA Feterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,

RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,

RA Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,

Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,

A Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.
  RESULT Q900V8
Q900V8
AC Q90
DT 01:
DT 01:
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Best Local S
Matches 19
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O29576:
01-JAN-1998 (TrEMBLrel. 0
01-JAN-1998 (TrEMBLrel. 0
01-MAY-2000 (TrEMBLrel. 1
Q9U0V8 PRELIMINARY; PRT; 679 AA.
Q9U0V8:
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
HYPOTHETICAL 73.8 KDA PROTEIN.
L7836.04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Archaeoglobus fulgidus.
Archaea; Euryarchaeota; Archaeoglobales;
Archaeoglobus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein. SEQUENCE 563 AA; 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PFAM; PF00890; FAD_binding_2; 1.
PROSITE; PS00037; MYB_1; UNKNOWN_1.
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TIGR; AF0681; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               reducing archaeon Archaeoglobu Nature 390:364-370(1997). EMBL; AE001057; AAB90557.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The complete genome sequence of the hyperthermophilic, sulphate-
reducing archaeon Archaeoglobus fulgidus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AF0681
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=2234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INTERPRO; IPR000464; -.
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                                                                                                                                                                                                                                                                                                        LLNKNGERFMKRYAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSEQALSSRDGAPVQ------HPLALLPSGSYEEDPQTILDDHLSRVLKTPGCQSPG-- 60
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                                                                                                                                                                                                                                                                                                                                                        -----VGRYSP 66
                                                                                                                                                                                                                                                                                                                                                                                                              GDGLAIAYRNGIPLKDMEFFQFHPTGLVPSG--
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25.3%;
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05, Last sequence update)
13, Last annotation update)
1, FLAVOPROTEIN SUBUNIT A (SDHA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 66; DB Pred. No. 12; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 67.5;
Pred. No. 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7F2BE92DFD242311 CRC64;
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12;
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OS Leishmania major.
OC EURATYOCA: Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OC NCBL_TAXID-5664;
OX NCBL_TAXID-5664;
RN [1]
RP SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RP STARIM-FRIEDLIN;
RA Oliver K., Harris D., Ivens A.C., Lawson D., Quail M.,
RA Cliver K., Harris D., Ivens A.C., Lawson D., Quail M.,
RA SIDJUBNOE FROM N.A.
SUBMITTED CONTROL NO.
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN-FRIEDLIN;
RA Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
RC STRAIN-FRIEDLIN;
RA Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
RC STRAIN-FRIEDLIN;
RA Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
RC STRAIN-FRIEDLIN;
RA Genome Res. 8:135-145(1998).
DR RHEL, All17263; CAB55379.1; -.
RM Hypothetical map of the Leishmania major Friedlin genome.";
RT "A physical map of the Leishmania major Friedlin genome.";
RT "A physical map of the Leishmania major Friedlin genome.";
RT "A physical map of the Leishmania major Friedlin genome.";
RT "A physical map of the Leishmania major Friedlin genome.";
RT "Hypothetical protein.
SEQUENCE 679 AA; 73834 MW; 1FCDF361BD81243E CRC64;
SQ SEQUENCE 679 AA; 73834 MW; 1FCDF361BD81243E CRC64;
SQ SEQUENCE 679 AA; 73834 MW; 1FCDF361BD81243E CRC64;
SQ SEQUENCE 679 AA; 73834 MW; 1FCDF361BD81243E CRC64;
SQ SEQUENCE 679 AA; 73834 MW; 1FCDF361BD81243E CRC64;
SQ SEQUENCE 679 AA; 73834 MW; 1FCDF361BD81243E CRC64;
SQ SEQUENCE 679 AA; 73834 MW; 1FCDF361BD81243E CRC64;
SQ SEQUENCE 679 AA; 73834 MW; 1FCDF361BD81243E CRC64;
SQ SEQUENCE 679 AA; 73834 MW; 1FCDF361BD81243E CRC64;
SQ SEQUENCE 679 AA; 73834 MW; 1FCDF361BD81243E CRC64;
SQ SEQUENCE 679 AA; 73834 MW; 1FCDF361BD81243E CRC64;
SQ SEQUENCE 679 AA; 73834 MW; 1FCDF361BD81243E CRC64;
SQ SEQUENCE 679 AA; 73834 MW; 1FCDF361BD81243E CRC64;
SQ SEQUENCE 679 AA; 73834 MW; 1FCDF361BD81243E CRC64;
SQ SEQUENCE 679 AA; 73834 MW; 1FCDF361BD81243E CRC64;
SQ SEQUENCE 679 AA; 73834 MW; 1FCDF361BD81243E CRC64;
SQ SEQUENCE FROM N.A.
SQ SEQ
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Result
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Listing first 45 summaries
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Perfect score:
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                                                                                                                                                                                                                                                                              Score
55.55.55
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1: /SIDS2/gcgdata/geneseq/geneseqp/AA1980.DAT:*
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276
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W93569
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Simian immunodefic
Arabidopsis thalia
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Arabidopsis thalia
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## ALIGNMENTS

PPT definition of the period o Conductin; tumour; diagnosis; treatment; beta-catenin; anti-tumour; therapy; cytoplasmic degradation; blockade; Wnt signalling pathway; Wingless signalling pathway; Adenomatous Polyposis Coli; APC; tumour suppressor. W93570; Tumor-suppressing protein conductin diagnosis of tumors 17-JUN-1999 (first entry) WPI; 1999-214706/18. N-PSDB; X23370. Behrens J, Birchmeier 02-SEP-1997; 01-SEP-1998; 11-MAR-1999. W09911780-A2. Homo sapiens. Human conductin protein. W93570 standard; Protein; 840 (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN 97DE-1038205. 98WO-DE02621. Σ ₹ used for treatment and

B.t. neutral prote

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                               Conductin; tumour; diagnosis; treatment; beta-catenin; anti-tumour; therapy; cytoplasmic degradation; blockade; Wnt signalling pathway; Wingless signalling pathway; Adenomatous Polyposis Coli; APC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W93569;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W93569 standard; Protein; 840 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
            Tumor-suppressing protein conductin diagnosis of tumors
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                                            X23369.
                                                                                                DELBRUECK CENT MOLEKULARE MEDIZIN MAX
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                                                                           Σ
                                                                                                                                                                                                                                   "Beta-catenin
claim 14"
                                                                                                                                                                                                                                                                  "GSK 3-beta binding region as described claim 13"
                                                                                                                                                                                                       "Dishevilled claim 15"
                                                                                                                                                                                                                                                                                                "Regulator of G protein signalling domain as described in claim 12"
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Pred. No. 2.7e-29;
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RESULT
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Oligonucleotides derived from them are useful for detecting contrations in the Axin gene and for determining whether a subject is contrations in the Axin gene and for determining whether a subject is contractal, carelope cancer (including breast, colorectal, castrointestinal, esophageal, carcinomas or melanomas). The wild compare the provided care also useful for diagnosing cancer and for detecting acids are also useful for diagnosing cancer and for detecting mutations in cancerous cells. Wild type Axin, its antisense molecule and identified compounds form pharmaceutical compositions in the treatment of cancer. The compositions are also useful for treating cancer by inhibiting tumorigenesis (by inducing degradation of beta-catenin). The nucleic acid encoding Axin acts through
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Matches 51
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                                                                                                                                                                                                                                         Newly isolated nucleic acid encoding "axis inhibition" (Axin) - useful for detecting, diagnosing and treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        beta-catenin.
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gastrointestinal cancer; esophageal cancer; car
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Pred. No. 2.7e-29;
Mismatches 0;
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inoma; tumorigenesis;
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                                                                                                                                                                                                likely to develop cancer (including breast, colorectal, gastrointestinal, esophageal, carcinomas or melanomas). The wild type Axin and homologues of Axin are useful for treating subjects who are likely to develop cancer (thyroid carcinomas). The nucleic acids are also useful for diagnosing cancer and for detecting mutations in cancerous cells. Wild type Axin, its antisense molecule and identified compounds form pharmaceutical compositions in the treatment of cancer. The compositions are also useful for treating cancer by inhibiting tumorigenesis (by inducing degradation of beta-catenin). The nucleic acid encoding Axin acts through negative regulation of the Wnt pathway in the Nieuwkoop Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids encoding mutant and wild type Axin and oligonucleotides derived from them are useful for detecting mutations in the Axin gene and for determining whether a subject is
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                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Axin) -
                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                isolated nucleic acid encoding "axis inhibition" protein ) - useful for detecting, diagnosing and treating cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34;
         34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              900 AA;
                                                                                                                                                     992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
         Conservative
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                                    68.8%;
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                              Score 190; DB 20
Pred. No. 2e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 191; DB 20;
Pred. No. 1.3e-17;
9; Mismatches 8
         Mismatches
                                                                DB 20;
         8
                                                                Length 992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 900;
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Indels .
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      Gaps
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                                                           condered arrangement of R groups (defining as side chains), excluding condered arrangement of R groups (defining as side chains), excluding condered arrangement of R groups (tables given in the specification).

(I), and related enzymes, are used to produce a wide range of terpenoids (e.g. cyclic, acylic, optionally hydroxylated), useful e.g. as controlled the result of signal transduction pathways, precursors of signal transduction pathways, precursors of steroid hormones and bile acids, as photoreceptors and as co-factor side chains. Some synthases with little or no catalytic activity (and nucleic acids encoding them) are used as controls in the analysis of products formed by enzymatic synthesis; as nutrient supplements; for affinity purification of isoprenoids; or to develop immunological reagents or nucleic acids for monitoring expression of terpene synthase or nucleic acids for monitoring expression of terpene synthase or nucleic acids for monitoring expression of terpene synthase or nucleic acids for monitoring expression of terpene synthase or nucleic acids for monitoring expression of terpene synthase or nucleic acids for monitoring expression of terpene synthase or nucleic acids for monitoring expression of terpene synthase or nucleic acids for monitoring expression of terpene synthase or nucleic acids for monitoring expression of terpene synthases or nucleic acids for monitoring expression of terpene synthases or nucleic acids for monitoring expression of terpene synthases.

20 may produce novel terpene products. A38910 to A38938 and Y90831 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-SEP-1998;
22-APR-1999;
23-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthase; protein co-ordinate data; active site; modification; terpenoid; 3-dimensional coordinate; alpha carbon atom; plant; terpene synthase; isoprenoid; breeding programme; fragrance; flavour; pheromone; defensive agent; plyment; antitumour; steroid hormone; signal transduction pathway; bile acid; affinity purification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Castor bean casbene synthase protein sequence SEQ ID NO:42
                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes an isolated terpene synthase (I) comprising a region with at least 20% identity to region 265-535 of a 548 amino acid (aa) sequence (Ia), given in ¥90831. (I) contains nine alpha-carbon atoms (alphaC) that have interatomic distances, between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chappell J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ricinus communis.
                                                                                                                                                                                                                                                                                                                                                                                                                each other, within tabulated ranges, have a centre point (within a sphere of radius 2.3 Angstrom ) within tabulated ranges, and have an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 106; Page 406-407; 450pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel terpene synthase enzymes, useful for producing terpene hydrocarbons, e.g. fragrances or antitumor agents, are derived known enzymes by specific amino acid alterations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             photoreceptor; enzymatic synthesis; nutrient supplement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .mmunological reagent.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Manna KR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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99US-0150262.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              English.
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Best Local Similarity
                                                                                                                                        The present sequence is the Pol protein from the simian immunodeficiency virus found in the red capped mangabey and designated SIVrcm. This virus is related to the HIV viruses that cause AIDS in humans. Knowing the sequence of the Pol protein and its gene is useful as it enables screening for the virus to take place in humans and animals (there is a possibility that this virus undergoes cross-species transmission), allows vaccines to be produced and aids research into the origin of these viruses. This latter is important if an AIDS vaccine is to be found.
                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                  New polypeptide, useful for producing antibodies and for diagnosis simian viral infection in humans comprises complete genome of new simian immunodeficiency virus isolate -
                                                                                                                                                                                                                                                                                                                                     WPI; 2000-423454/36.
N-PSDB; A51008.
B01775, B01776.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-DEC-1998;
                                                                                                                                                                                                                                                            Disclosure; Page 152-156; 173pp; English.
                                                                                                                                                                                                                                                                                                                                                                                         Lu CY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Simian immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Red capped monkey; simian immunodeficiency virus; SIV; SIVrcm; vaccination; Pol protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Simian immunodeficiency virus SIVrcm Pol protein #I.
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                                                                                                                                                                                                                                                                                                                                                                                                    Hahn BH,
                                                                                                                                                                                                                                                                                                                                                                                                                             (UABR-) UAB RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200034529-A1.
936 latnklqnqiskiqnfrvyyregrdqlwrgpakliwkgegavviqeetgdlkvvprrkak 995
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              LTLGHFKEQLSKKGNYRYYFKKASDEFACG------AVFEEIWDDETVLPMYEGR 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14;
                                                                                                                                                                                                                                                                                                                                                                                                     Shaw GM, Gao F,
                                                                                                                    1018 AA;
                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                20.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                    Marx PA,
                                                                Score 56.5;
Pred. No. 43;
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                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                    Smith SM, Georges-Courbot MC;
                                                                            DB 21;
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                                                                            Length 1018;
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05-MAR-1999

09-MAR-1999

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25-MAR-1999

29-MAR-1999

01-APR-1999

06-APR-1999

16-APR-1999

16-APR-1999

16-APR-1999
14-JUN-1999;
16-JUN-1999;
16-JUN-1999;
17-JUN-1999;
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06-MAY-1999;
06-MAY-1999;
07-MAY-1999;
                                   10-JUN-1999
                                          08-JUN-1999;
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07-JUN-1999;
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03-JUN-1999;
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27-MAY-1999;
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24-MAY-1999;
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18-MAY-1999;
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04-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein identification; signal transduction pathway; metabolic hybridisation assay; genetic mapping; gene expression control;
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                                                                          99US-0134941.

99US-0135124.

99US-0135353.

99US-0135629.

99US-0136021.

99US-0136782.

99US-0137722.

99US-0137722.

99US-0137728.
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990S-0132487.
990S-0132863.
990S-0134256.
990S-0134218.
990S-0134219.
990S-0134221.
99US-0139119.
99US-0139452.
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99US-0132048.
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99US-0123180.
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l Similarity 33.1
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99US-015929.
99US-0160767.
99US-0160814.
99US-0161360.
                                             20.1%;
                                    Score 55.5; D
Pred. No. 13;
8; Mismatches
                                    8;
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RESULT G13111

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99US-0139455.
99US-0139456.
99US-0139460.
99US-0139461.
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09-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-FEB-2000;
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                                                                                                                                                          127
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99US-0161361
                                                                                   Protein;
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RESULT G13110 ID G1 XX AC G1 XX DT 17 XX DE Ar

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Matches 13
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04-OCT-1999;
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                                                                                               G45799;
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                                                            Arabidopsis thaliana protein fragment SEQ ID NO: 57544.
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                                                                              18-OCT-2000
                                                                                                                                                            130
                                                                                                                                                          10
                                                                                                                                                                                           ch 20.1%;
l similarity 33.3%;
l3; Conservative
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RESULT 11
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22-SEP-1999;
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                                                         Neutral protease; npr gene; alkaline protease; apr gene; insecticidal toxic protein; ITP; crystal protein; delta endotoxin; insecticide; bioinsecticide; biological control agent.
                                                                                B.t. neutral protease
                                                                                                        W04271;
                                    W09630526-A2
                                              Bacillus thuringiensis var. kurstaki strain
                                                                                            15-DEC-1996
             29-MAR-1996;
                        03-OCT-1996.
                                                                                                                                                                                                                                                                                                                                                                       -OCT-199
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                                                                                                                                                                     Local Similarity es 16; Conserv
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                                                                                                                                                                     20.1%;
milarity 31.4%;
Conservative
                                                                                            (first entry)
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 95US-0415823.
             96WO-US04310.
                                                                                                                                                                       Score 55.5; DI Pred. No. 56; 7; Mismatches
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                                                 EG2371 (NRRL B-18209)
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RESULT 12
G43722
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disabled Bacillus thuringiensis apr and npr genes - encoding neutral and alkaline protease incapable of degrading insecticidal toxic protein (ITP), therefore increasing ITP prodn. and stability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1996-455371/45
N-PSDB; T38353.
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29-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein identification; signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana protein fragment SEQ ID NO: 54682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                 25-FEB-2000;
                                                                                                                                                                                                                                                                                                                                       06-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                               termination sequence.
21-APR-1999;
23-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 KGNYRYYFKKASDEFACGAVFEEIWDDETVLPM---YEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               l Similarity
15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ΨP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         566 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                 2000EP-0301439
                     990S-0126264
990S-0126785
990S-0127462
990S-0128234
990S-0128714
990S-0128714
990S-0130077
990S-0130077
990S-0130449
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99US-0125788
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99US-0123180.
      9908-0130510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; score 54.5; DI
; pred. No. 39;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB
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23-APR-1999 30-APR-1999 30-APR-1999 06-MAY-1999 06-MAY-1999 11-MAY-1999 11-MAY-1999 11-MAY-1999 11-MAY-1999 12-MAY-1999 12-MAY-1999 12-MAY-1999 13-JUN-1999 16-JUN-1999 19-JUL-1999
99US-0131449 99US-0131449 99US-0132486 99US-0132486 99US-0132486 99US-0132486 99US-0134266 99US-0134219 99US-0134219 99US-0134219 99US-0134219 99US-0134219 99US-0134219 99US-013523 99US-013523 99US-013622 99US-013622 99US-013622 99US-013622 99US-013622 99US-0139452 99US-0139452 99US-0139452 99US-0139452 99US-0139452 99US-0139452 99US-0139452 99US-0139452 99US-0139452 99US-0139452 99US-0139452 99US-0139452 99US-0139453 99US-0140625 99US-0140625 99US-0142977 99US-0142977 99US-0142977 99US-0142977 99US-014362 99US-014362 99US-014362 99US-014362 99US-014362 99US-014362 99US-014362 99US-014362 99US-014333 99US-0144333 99US-0144333 99US-0144333 99US-0144333 99US-0144333 99US-0144333 99US-0144333 99US-0144333 99US-0144333 99US-0144333 99US-0144333 99US-0144333
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99US-014484. 99US-014484. 99US-014484. 99US-0145086. 99US-0145086. 99US-0145089. 99US-0145126. 99US-0145126. 99US-0145128. 99US-0145218. 99US-0145218. 99US-0145218. 99US-0145218. 99US-0145218. 99US-0145218. 99US-0146388. 99US-0147303. 99US-0147303. 99US-0147303. 99US-0147303. 99US-0147303. 99US-0147303. 99US-0147303. 99US-014726. 99US-014726. 99US-014726. 99US-014726. 99US-014927. 99US-014927. 99US-015066. 99US-015066. 99US-015066. 99US-015066. 99US-015066. 99US-015066. 99US-015108. 99US-015108. 99US-0151303. 99US-0159333. 99US-01593331.

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RESULT
G43721
B
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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18-OCT-1999;
21-OCT-1999;
21-OCT-1999;
21-OCT-1999;
21-OCT-1999;
21-OCT-1999;
21-OCT-1999;
22-OCT-1999;
22-OCT-1999;
22-OCT-1999;
25-OCT-1999;
25-OCT-1999;
26-OCT-1999;
26-OCT-1999;
26-OCT-1999;
26-OCT-1999;
28-OCT-1999;
25-FEB-1999

05-MAR-1999

09-MAR-1999

23-MAR-1999

25-MAR-1999

25-MAR-1999

01-APR-1999

06-APR-1999

16-APR-1999

21-APR-1999

23-APR-1999

24-APR-1999

30-APR-1999

30-APR-1999

05-MAY-1999

06-MAY-1999
                                                                                                                                                                                                                                                                                                                                  G43721;
                                                                                                                                                                                                                                                                                                                                                   G43721 standard;
                                                                                                                                                                                                                                                           Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                             Arabidopsis thaliana protein fragment SEQ ID NO:
                                                                                                                                                                                                         06-SEP-2000
                                                                                                                                                                                                                                           Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                 18-OCT-2000
                                                                                                                                                                                         25-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                            13
                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 19.7%;
l Similarity 34.8%;
16; Conservative
                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                          2000EP-0301439
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990S-0160741
990S-0160767
990S-0160776
990S-0160814
990S-0160981
990S-0160981
990S-0160981
990S-0161404
990S-0161406
990S-0161406
990S-0161405
990S-0161405
990S-0161360
990S-0161361
990S-0161361
990S-0161361
990S-0161992
990S-0161992
990S-0161993
990S-0161993
990S-0121825.
990S-0123548.
990S-0125788.
990S-0125785.
990S-0126785.
990S-0127462.
990S-0128734.
990S-0128734.
990S-0130077.
990S-0130049.
990S-0130449.
990S-0132485.
990S-0132485.
                                                                                                                                                                                                                                                                                                                                                    Protein; 615 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 54.5; DI Pred. No. 42; 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB
                                                                                                                                                                                                                                                                                                                                                                                                                                   14;
                                                                                                                                                                                                                                                                                                  54681.
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24-MAY-1999;
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01-JUN-1999;
03-JUN-1999;
04-JUN-1999;
07-JUN-1999;
08-JUN-1999;
10-JUN-1999;
10-JUN-1999;
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14-MAY-1999;
18-MAY-1999;
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07-MAY-1999;
11-MAY-1999;
14-MAY-1999;
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11-JUL-1999
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18-JUN-1999;
18-JUN-1999;
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27-MAY-1999;
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18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
      19-JUL-1999
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       99US-0132487
99US-0134286
99US-0134218
99US-0134219
99US-0134211
99US-0134701
99US-0134711
99US-0134711
99US-0134711
99US-0134941
199US-0136021
99US-0136021
99US-0136021
99US-0136021
99US-0137528
99US-0137528
99US-0137528
99US-0139452
99US-0139452
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99US-0139453
99US-0139453
99US-0139451
99US-0139461
99US-0140833
99US-0140833
99US-0140833
99US-0144333
99US-0144331
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99US-0144334
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В
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Best Local S
Matches 16
25-FEB-1999

05-MAR-1999

09-MAR-1999

23-MAR-1999

25-MAR-1999

01-APR-1999

01-APR-1999

01-APR-1999

16-APR-1999

16-APR-1999

23-APR-1999

24-MAY-1999

11-MAY-1999

11-MAY-1999

11-MAY-1999

11-MAY-1999

11-MAY-1999
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22-0CT-1999
22-0CT-1999
22-0CT-1999
25-0CT-1999
25-0CT-1999
26-0CT-1999
26-0CT-1999
26-0CT-1999
28-0CT-1999
28-0CT-1999
28-0CT-1999
28-0CT-1999
29-0CT-1999
                                                                                                                                                                                                                                                                                                                                                       G43720;
                                                                                                                                                                                                                                                                                                                                                                       G43720
                                                                                                                                                                                                                                                                                                Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                                           25-FEB-2000;
                                                                                                                                                                                                                                           06-SEP-2000
                                                                                                                                                                                                                                                          EP1033405-A2
                                                                                                                                                                                                                                                                         Arabidopsis thaliana
                                                                                                                                                                                                                                                                                         termination
                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana protein fragment SEQ
                                                                                                                                                                                                                                                                                                                                        18-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                             14
                                                                                                                                                                                                                                                                                                                                                                      standard; Protein; 699
                                                                                                                                                                                                                                                                                                                                                                                                                                             16; Conservative
                                                                                                                                                                                                                                                                                         sequence
                                                                                                                                                                                                                                                                                                                                       (first
                                                                                                                                                                                                                           2000EP-0301439
99US-0121825
99US-0123548
99US-0125788
99US-0126785
99US-0126785
99US-0128734
99US-0128734
99US-0128734
99US-0128734
99US-0130077
99US-0130510
99US-0130510
99US-01312048
99US-0132048
99US-0132484
99US-0132484
99US-0132486
99US-0132486
99US-0132486
99US-0132486
99US-0132863
99US-0134218
99US-0134218
99US-0134218
99US-0134218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            990S-0160815

990S-0160981

990S-0160989

990S-0161408

990S-0161405

990S-0161406

990S-0161360

990S-0161360

990S-0161920

990S-0161920

990S-0161921

990S-0161921
                                                                                                                                                                                                                                                                                                                                       entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     19.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 54.5; DI
; Pred. No. 44;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                       B
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                                                                                                                                                                                                                                                                                                                         IJ
                                                                                                                                                                                                                                                                                                                         NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                             14;
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                                                                                                                                                                                                                                                                                                                         54680.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                             615;
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22-JUL-1999
23-JUL-1999
23-JUL-1999
23-JUL-1999
26-JUL-1999
27-JUL-1999
27-JUL-1999
28-JUL-1999
28-JUL-1999
29-AUG-1999
20-AUG-1999
20-AUG-1999
20-AUG-1999
20-AUG-1999
20-AUG-1999
20-AUG-1999
21-AUG-1999
21-AUG

990S-0145192.
990S-0145218.
990S-0145218.
990S-0145218.
990S-0145213.
990S-0145213.
990S-0146386.
990S-0146388.
990S-0146388.
990S-0146388.
990S-0147302.
990S-0147302.
990S-0147303.
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990S-0147313.
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990S-0148311.
990S-0148311.
990S-0148312.
990S-0148313.
990S-0149368.
990S-015066.
990S-015066.
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990S-0150753.
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990S-015076.
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99US-0145192 99US-0145192 99US-01452145 99US-0145218 99US-0145224 99US-0145276 99US-0145913 99US-0145913	99US-0144335 99US-0144632 99US-0144884 99US-0145086 99US-0145086 99US-0145086 99US-0145087	99US-0143542 99US-0143624 99US-0144065 99US-0144085 99US-0144085 99US-0144325 99US-0144331 99US-0144333 99US-0144333 99US-0144333	99US-0139463 99US-0139750 99US-01398763 99US-0139899 99US-0140553 99US-0140553 99US-0140823 99US-0140823 99US-0141287 99US-0142154 99US-0142154 99US-0142154 99US-01421590 99US-0142803 99US-0142803	99US-0138540 99US-0139119 99US-0139452 99US-0139453 99US-0139454 99US-0139454 99US-0139454 99US-0139457 99US-0139457 99US-0139458 99US-0139459 99US-0139459 99US-0139461	99US-0134768 99US-0134941 99US-0135124 99US-0135533 99US-0136629 99US-0136392 99US-0136782 99US-0137222 99US-0137528 99US-0137528 99US-0137502 99US-0137502
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RESULT 15
R20599
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Best Local Similarity 25.5
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 19.7%; Score 54.5; DB 21; Length 699; Best Local Similarity 34.8%; Pred. No. 51; Matches 16; Conservative 5; Mismatches 14; Indels 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-OCT-1999;
26-OCT-1999;
26-OCT-1999;
28-OCT-1999;
28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
                                                                                                                              The amino acid sequence is that of a polymerase from the ROD HIV-2 isolate, it is encoded by nucleotides 1829-4936. See also R20596-R20596-R20508 and R22745-R22749.
                                                                                                                                                                                              Peptide(s) corresp. to HIV-2 amino acid sequences - used in diagnosis in vaccines and in prodn. of antibodies for diagnosis
                                                                                                                                                                                                                                                                                                                                                                                 US5079342-A.
                                                                                                        Sequence
                                                                                                                                                                         Disclosure; Page 13; 30pp; English.
                                                                                                                                                                                                                                 WPI; 1992-041067/05.
N-PSDB; Q20616.
                                                                                                                                                                                                                                                                  Alizon M, Montagnier L,
                                                                                                                                                                                                                                                                                         (INSP ) INST PASTEUR.
                                                                                                                                                                                                                                                                                                               11-FEB-1987;
                                                                                                                                                                                                                                                                                                                                                            07-JAN-1992.
                                                                                                                                                                                                                                                                                                                                                                                                       Human immunodeficiency virus-2 ROD isolate.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 ROD HIV-2 polymerase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-MAY-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R20599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R20599 standard; Protein; 1036 AA.
                                                                                                                                                                                                                                                                                                                                      11-FEB-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          || ::| ||:: :|:
961 sklkdfrvyfregtdqlwkgpgellwkgegavlvkvgtdikiiprrkakil 1011
                 1036 AA;
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990S-0161360.
990S-0161361.
990S-0161920.
990S-0161992.
990S-0161993.
990S-0162142.
                                                19.6%; Score 54; DB 13; Length 1036; 25.5%; Pred. No. 96; tive 12; Mismatches 16; Indels 1
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Search completed: June Job time: 5661 sec

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Perfect score:
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2: /cgn2_6/ptodata/2/laa/5B_COMB.pep:*

3: /cgn2_6/ptodata/2/laa/6A_COMB.pep:*

4: /cgn2_6/ptodata/2/laa/6B_COMB.pep:*

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US-08-993-118-10
US-08-993-118-10
US-08-993-118-10
US-08-993-118-10
US-08-993-124-2
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US-09-286-891-2
US-08-432-016-3
US-08-854-585-2
PCT-US95-05512-2
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US-07-687-4668-2
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Sequence 6, Appli
Sequence 28, Appli
Sequence 2, Appli
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                                                  FEATURE:
                                                          MOLECULE TYPE:
                 LOCATION: 1..1055
OTHER INFORMATION:
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                                     NAME/KEY:
                                                                   TOPOLOGY:
                                                                            STRANDEDNESS:
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                                                                                      amino acid
                                                                                                                                                                                                                                                                                                                                                 California
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ALIGNMENTS

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Sequence 5. Application US/08659251
Patent No. 5883081
GENERAL INFORMATION:
APPLICANT: Kraus, Guenter
APPLICANT: Kraus, Guenter
APPLICANT: Repeschia, Eric
APPLICANT: Poeschia, Eric
APPLICANT: Poeschia, Eric
TITLE OF INVENTION: Isolation of No. 5883081el HIV-2 Proviruses
NUMBER OF SEQUENCES: 50
CORRESSONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarceadero Center, Eighth Floor
CITY: San Francisco
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/O8/659,251
FILING DATE: AS-JUL-1995
APPLICATION NUMBER: US/O8/659,251
FILING DATE: MOMBER: US/O8/659,251
FILING DATE: MOMBE
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US-08-415-823-4
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                                                                               Sequence 4, Application US/08415823 patent No. 5759538 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                  Matches
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: The Regents of the University of California TITLE OF INVENTION: Isolation of Novel HIV-2 Proviruses NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 980 SKLKNFRVYFREGRDQLWKGPGELLWKGDGAVIVKVGTDIKIVPRRKAKII 1030
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LENGTH: 1055 amino aci
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NAME: Berliner, Robert
REGISTRATION NUMBER: 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: (213) 977-1001
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APPLICANT: Tan, Yuping TITLE OF INVENTION: BACTITLE OF INVENTION: PROTITLE OF INVENTION: PROTITURE OF INVENTION:
                                                     APPLICANT:
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OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                 Local Similarity
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LOCATION: 1..1055
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25.5%;
     BACILLUS THURINGIENSIS APT AND NPT PROTEASE GENES AND ALKALINE PROTEASE DEFICIENT AND NEUTRAL PROTEASE DEFICIENT B.T. STRAINS
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Pred. No.
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Pred. No.
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; TOPOLOGY: 1:
; MOLECULE TYPE:
US-08-415-823-4
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US-09-086-662-4
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PIBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATION NUMBER: US/08/415,823
APPLICATION NUMBER: US/08/415,823
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INFORMATION FOR SEQ ID NO:
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                           INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 566 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
TITLE OF INVENTION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Panitch Schwarze Jacobs & Nadel, P.C. ADDRESSEE: A.S. Nadel STREET: 1601 Market Street, 36th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                           CITY: Philadelphia
                                                                                  APPLICATION NUMBER: FILING DATE:
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                       COUNTRY:
STRANDEDNESS:
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1601 Market Street,
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PROTEASE GENES AND ALKALINE PROTEASE DEFICIENT AND NEUTRAL
PROTEASE DEFICIENT B.T. STRAINS
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Pred. No. 11
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; TOPOLOGY: linear; MOLECULE TYPE: pro US-09-086-662-4
                                                                                                                                                                                                         ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-465-167A-24
RESULT 6
US-08-993-118-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 5
US-08-465-167A-24
                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,167A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 08/103,623
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 15; Conserv
                                                                                                                             Matches
                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Fikes, John D.
APPLICANT: Livingston, Brian D.
APPLICANT: Sette, Alessandro D.
                                                                                                                                                                                                                                                                                                         TELEFAX: 415-576-0300 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Sidney, John C.
TITLE OF INVENTION: INMUNOGENIC PEPTIDES (as amended)
                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
                                                            212 EEIWEELSVMEVYDGR 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                             34 EEIWDDETVLPMYEGR 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72 KGDYKLGEKSAQDSFKVKQVKKDAVTDSTVVRMQQVYEG 110
                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: San Francisco
STATE: CA
                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Parmelee, Steven W. REGISTRATION NUMBER: 31,9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                        TELEPHONE:
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                                                                                                                                                                                                                                                                         amino acid
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                                                                                                                                                                                                                                                                                                                                           415-576-0300
                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                          206-467-9600
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                                                                                                                                                                                                                                                          single
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38.5%;
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Pred. No. 11;
                                                                                                                                            Score 53; I
                                                                                                                             Mismatches
                                                                                                                                                           DB 1; Length 309;
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Query Match
Best Local Similarity
"---has 8; Conserv:
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US-08-845-528C-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 10,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/8.
APPLICATION NUMBER: 25, 1997
FILING DATE: April 25, 1997
ATTORNEY/AGENT INFORMATION:
NAME: MATY Anne Schofield
                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: LUTELECOMMUNICATION INFORMATION: TELEPHONE: (212) 688-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,118
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MEDIUM TYPE: Diskett
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TITLE OF INVENTION:
                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    212 EEIWEELSVMEVYDGR 227
                                                           STREET: 805 Third Avenue CITY: New York City
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34 EEIWDDETVLPMYEGR 49
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STRANDEDNESS: sing
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OPERATING SYSTEM:
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STATE: New York
COUNTRY: U
ZIP: 10022
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                     ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10022
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805 Third Avenue
                                                                                                                                                                                                                                                                                     BOON-FALLEUR, Thierry
IVENTION: ISOLATED NUCLEIC ACID MOLECULE CODING FOR TUMOR
IVENTION: REJECTION ANTIGEN PRECURSOR MAGE-C1 AND USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DE SMET, Charles;
BOON-FALLEUR, Thierry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LUCAS, SO
DE SMET,
                                                                                                                                                                                                                                                                                                                                                                                               LUCAS, Sophie;
DE SMET, Charles;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SS: single stranded
linear
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                                                                                                                                                                     Felfe & Lynch
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50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ISOLATED NUCLEIC ACID MOLECULE CODING FOR TUMOR
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25, 1997
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Pred. No. 8.9;
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; TOPOLOGY: 11; MOLECULE TYPE: US-08-971-244-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08971244 Patent No. 5891719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                      TELEFAX: (650) 343-43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Cohen, Lucy
APPLICANT: Baeuerle, Patrick
TITLE OF INVENTION: IKAP Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 2
                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 1332 amino acids
                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: LUD 5455
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Mary Anne Schofield
REGISTRATION NUMBER: 36,669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/845,528C
FILING DATE: April 25, 1997
CLASSIFICATION: 4335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19.2%;
Local Similarity 50.0%;
hes 8; Conserva++...
                                                TYPE: amino acid
                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: HILLSBOROUGH
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34 EEIWDDETVLPMYEGR 49
                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM FS,
OPERATING SYSTEM:
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STRANDEDNESS: single stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE:
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                 protein
                                                                                                                      343-4342
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                                                                                                                                                                                      36,627
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                                                                                                                  US-08-432-016-3
                                                                                                                                  RESULT
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                                                                                Sequence 3, Application US/08432016 Patent No. 5968768
                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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Best Local
                                                                 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                 APPLICANT:
APPLICANT:
APPLICANT:
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LENGTH: 1332 amino acids
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TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-4342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/286,891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Cohen, Lucy
APPLICANT: Baeuerle, Patrick
TITLE OF INVENTION: IKAP Proteins, Nucleic Acids and Methods
 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                 321 QLWTVGNYHWYLKQSLSFSTCGKSKIVSLMWDPVT 355
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                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                   TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY:
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                                                                                                                                                                                                               9 QLSKKGNYRYYFKKASDEFACG--AVFEEIWDDET 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 QLSKKGNYRYYFKKASDEFACG -- AVFEEIWDDET 41
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T: 75 DENISE DRIVE
HILLSBOROUGH
: CALLFORNIA
                                                                                                                                                                                                                                                                                                                                                                               amino acid
HAYNES, BARTON F. ARUFFO, ALEJANDRO PATEL, DHAVALKUMAR BOWEN, MICHAEL A.
                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                  linear
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Pred. No. 53;
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MARQUARDT,

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US-08-684-594-3
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Patent No. 599817
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Best Local Similarity
Matches 16; Conserv
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NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/432,016 FILING DATE: 01-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 08/333,350
FILING DATE: 02-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 816-4000 TELEFAX: (703) 816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/143,903
FILING DATE: 02-NOV-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
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                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                    FITLE OF INVENTION: CD6 LIGAND
                                                                                                                                                                                                                    APPLICANT:
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                                                  STATE: VIRGINIA COUNTRY: U.S.A. ZIP: 22201-4714
                                                                                                                                                                                                                                                                                                                                                                                                     52 YKDRLSLSENYTLSIKNARISDEKRFVCMLVTEDDVSEEPTVVKVFK 98
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TOPOLOGY: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: WILSON, MARY J. REGISTRATION NUMBER: 32,955 REFERENCE/DOCKET NUMBER: 15
                                                                                                 STREET: 1100 NOI
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM:
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                                                                                                                 E: NIXON & VANDERHYE P.C.
1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                     ARUFFO,
                                                                                                                                                                                                      MARQUARDT,
                                                                                                                                                                                                                  PATEL, DHAVALKUMAR
BOWEN, MICHAEL A.
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SYSTEM: PC-DOS/MS-DOS
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IBM PC compatible
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Query Match
Best Local Similarity
Matches 16; Conserve
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-684-594-3
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LENGTH: 477 amin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION: APPLICANT: Tonks,
                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,585
               ATTORNEY/AGENT INFORMATION:
NAME: BOTUN, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 276
                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Density Enhanced Protein Tyrosine Phosphatase NUMBER OF SEQUENCES: 6
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REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703),816-4000
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NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
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APPLICATION NUMBER:
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CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
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                                                                                      APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52 YKDRLSLSENYTLSIKNARISDEKRFVCMLVTEDDVSEEPTVVKVFK 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/432,016 FILING DATE: 01-MAY-1995
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                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                 STREET: 233 S
CITY: Chicago
                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, Suite 6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 FKEQLSKKGNYRYYFKKA--SDE--FACGAVFE-EIWDDETVLPMYE 47
                                                                                                                                                                                                                                                                                                60606
                                                                                                                                                                                                                                                                                                                              Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tonks, Nicholas K. and
                                                                                                                                                                                                                                                                                                               United States of America
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PatentIn Release #1.0, Version #1.30
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                                                                                                           US/08/237,940
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Pred. No. 1
                 27866/31954
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RESULT 1
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Best Local Similarity
Thes 12; Conserv
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Best Local Similarity
""tches 12; Conserv
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;Patent No. 5223423
; APPLICANT: FRANCHINI, GENOVEFFA;WONG-STAAL, FLOSSIE;
;GALLO, ROBERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application PC/TUS9505512
GENERAL INFORMATION:
APPLICANT: Tooks, Nicholas K. and stman, Arne
TITLE OF INVENTION: Density Enhanced Protein Tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 312-474-0448 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                             TELEFAX: 312-474-0448
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 137 amino aci
                                                                                                                    1017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05512
FILING DATE:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
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CITY: Chicago
STATE: Illinoi
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARD: DE+CALT-
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                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Borun, Michael F. REGISTRATION NUMBER: 25,447 REFERENCE/DOCKET NUMBER: 27
                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
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Pred. No.
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Pred. No.
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/331,212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO:4:
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Best Local Similarity
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Kevin L. Bastian
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 415-543-9600
                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                      TYPE:
                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 34 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US FILING DATE: 19910418 CLASSIFICATION: 536
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                                                                                Local
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KEYLNGKSNLE-KFKKDADSFICGLMPE 308
                                                                l Similarity 46.4
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Bastian, Kevin L.
34,774
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California
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Pred. No. 2
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Result
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Copyright (c) 1993 - 2000 Com
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## ALIGNMENTS

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R; Ikeda, S.; Yamamoto, H.; Murai, H.; Kishida, S.; Kikuchi, EMBO J. 17, 1371-1384, 1998
A;Title: Axin, a negative regulator of the Wnt signaling pat A; Reference number: Z16413; MUID:98151361
A; Accession: T08422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
T08422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Rattus norvegicus (Norway rat)
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jul-2000
C;Accession: T08423
R;Yamamoto, H.; Kishida, S.; Uochi, T.; Ikeda, S.; Koyama, S.; Asashima, M.; Kikuchi, Mol. Cell. Biol. 18, 2867-2875, 1998
A;Itle: Axil, a member of the Axin family, interacts with both glycogen synthase kin A;Reference number: Z16414; MUID:98226558
A;Reference number: Z16414; MUID:98226558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:AF017757; NID:g3080758; PIDN:AAC40089.1; PID:g3080759 A;Note: interacts with GSK-3beta and beta-catenin C;Keywords: phosphoprotein; signal transduction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
T08423
                                                                                                                            A; Note: GSK-3beta interacting protein C; Keywords: phosphoprotein; signal tr
                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-832 <IKE>
A; Cross-references: EMBL: AF017756; NID: g2982197;
                                                                                                                                                                                                                                                                                                                                                                                             N;Alternate names: rAxin
C;Species: Rattus norvegicus (Norway rat)
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jul-2000
C;Accession: T08422
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A;Molecule type: mRNA
A;Residues: 1-838 <YAM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   h 100.0%; Score 276; DB 2; Similarity 100.0%; Pred. No. 1.9e-26; S1; Conservative 0; Mismatches 0;
68.8%; Scr
64.7%; Pr
ative 10;
                           Score 190; DB 2;
Pred. No. 1e-15;
                                                                                                                                                                                                                                                    from GB/EMBL/DDBJ
                                                                                                                            transduction
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                                                                                                                                                                               PIDN:AAC40066.1; PID:g2982198
                                                     Length 832;
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Mismatches

8

Indels

0

Gaps

0

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segment polarity protein dishevelled - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 24-Sep-1998
C;Accession: A49840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: dsh
A;Cross·references: FlyBase:FBgn0000499
C;Superfamily: GLGF domain homology
F;258-333/Domain: GLGF domain homology <GLG2>
                                                                                                                                                                                                                                                                                                                                                       A;Map position: 3q27
C;Superfamily: GLGF domain homology
F;255-331/Domain: GLGF domain homology <GLG4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Date: 24-Jan-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jul-2000 C;Accession: JC5763 P.R.; Jonssen, M.; Smith, K.; Dorrington, S.M.; Kaklamanis, R;Bul, T.D.; Beier, D.R.; Jonssen, M.; Smith, K.; Dorrington, S.M.; Kaklamanis, Biochem. Biophys. Res. Commun. 239, 510-516, 1997 A;Title: CDNA cloning of a human dishevelled DVL-3 gene, mapping to 3q27, and ex A;Reference number: JC5763; MUID:98008870 A;Accession: JC5763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    dishevelled protein 3 - human
C;Species: Homo sapiens (man)
C;Date: 24-Jan-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jul-2000
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C;Genetics:
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A;Molecule type: mRNA
A;Residues: 1-623 <KLI>
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dishevelled homolog
C; Species: Xenopus ]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
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A; Residues: 1-716 <BUI>
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                                                                         RESULT
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VTLGQFKELLTKKGSYRYYFKKVSDEFDCGVVFEEVREDEAILPVFEEKII 825
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                                                                                                                                    TLADFKGVL-QRPSYKFFFKSMDDDF--GVVKEEISDDNAKLPCFNGRVV
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    African clawed frog
evis (African clawed frog)
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                                                                                                                                                                                                                                                              34.6%;
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                                                                                                                                                                                                                                        Score 95.5; DB 2;
Pred. No. 0.00052;
1; Mismatches 16;
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         A; Molecule type:
A; Residues: 1-863
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ferrichrome-iron receptor 1 - Synechocystis sp. (strain PCC 6803)

N;Alternate names: protein sll1409

C;Species: Synechocystis sp.
A;Variety: PCC 6803

C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000

C;Accession: S74447

R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Nakaneko, T.; Sato, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada DNA Res. 3, 109-136, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             dihydrofolate reductase (EC 1.5.1.3) - bovine C;Species: Bos primigenius taurus (cattle) C;Date: 15-Oct-1982 #sequence_revision 15-Oct-1982 C;Accession: A00388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: Xdsh
C;Superfamily: GLGF domain homology
F;260-336/Domain: GLGF domain homology <GLG4>
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A;Molecule type: mRNA
A;Residues: 1-736 <SOK>
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F;3-125/Domain: type I dihydrofolate reductase homology <DFR>
F;30,34,64,70/Binding site: substrate (Glu, Phe, Asn, Arg) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Lai, P.H.; Pan, Y.C.E.; Gleisner, J.M.; Peterson, D.L.; WILLIAMS, Biochemistry 21, 3284-3294, 1982
A;Title: Structure of dihydrofolate reductase: primary sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:U31552; NID:g945109; PIDN:AAB00688.1; PID:g945110 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Experimental source: liver C; Superfamily: type I dihydrofolate reductase; type I dihydrofolate
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                                                                                                       DNA Res. 3, 109-13
A; Title: Sequence
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                                      A; Reference number: S74322; MUID:97061201
A; Accession: S74447
                A; Status: nucleic acid sequence not shown;
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Accession: I51691
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Similarity 34.1%;
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                                                                                                         analysis of the genome of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Y.C.E.; Gleisner, J.M.; Peterson, D.L.; Williams, K.R.; Blakley,
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R;Bentley, D.

R;Bentley, D.

R;Bentley to the EMBL Data Library, September 1995

A;Description: The sequence of C. elegans cosmid K09F5.

A;Reference number: Z18544

A;Recession: T16600

A;Recession: T16600

A;Recession: Preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-1616 <ABEND

A;Residues: 1-1616 <ABEND

A;Residues: 1-1616 <ABEND

A;Residues: SI-1616 <ABEND
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A:Introns: 33/3; 124/1; 265/1; 298/2; 328/3
C:Superfamily: Caenorhabditis elegans hypothetical protein C37A5
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Genetics:
                                          A;Map position: X
A;Introns: 291/3; 386/3; 1448/3; 1531/1
C;Superfamily: vitellogenin
                                                                                                                                                                                                             C;Genetics:
A;Gene: CESP:vit-1
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C;Species: Caenorhabditis elegans

C;Date: 20-Sep-1999 #sequence_rev

C;Accession: T16600
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
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A;Start codon: GTG
C;Superfamily: ferrichrome-iron receptor 1;
C;Keywords: iron transport
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membrane transport protein (glnQ) homolog MG303 - Mycoplasma genitalium C;Species: Mycoplasma genitalium C;Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 07-Dec-1999
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submitted to the EMBL Data Library, May 1998
A; Description: Mig-5, a gene that controls cell fate A; Reference number: Z22326
A; Accession: T43171
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-666 <GUO>
A; Cross references: EMBL:AF063244; PIDN:AAC16434.1
C; Genetics:
A; Gene: mig-5
                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein T05C12.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T24507
R;Burton, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cytoplasmic signaling transducer - C;Species: Caenorhabditis elegans C;Date: 11-Jan-2000 #sequence_revis C;Accession: T43171
                                                                                                                                                         A;Gene: CESP:T05C12.6
A;Map position: 2
A;Introns: 13/3; 63/2; 114/3; 140/1; 299/2; 340/2; 449/1; 624/1
                                                                                                                                                                                                          A;Cross-references: EMBL:266500; PIDN:CAA91307.1; A;Experimental source: clone T05C12 C;Genetics:
                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-672 <WIL>
                                                                                                                                                                                                                                                                                             submitted to the EMBL Data Library, October 1995
A;Reference number: Z19901
A;Accession: T24507
A;Status; preliminary; translated from GB/EMBL/DI
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2 TLGHFKEQLSKKGNYRYYFKK 22
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37 TLGNFKNSFTKRG-YKYYAKE 56
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Pred. No.
                                                                                     Score 57.5;
Pred. No. 27;
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C; Accession: S68700
R; Kuramochi, S.; Matsuda, S.;
FEBS Lett. 378, 7-14, 1996
A; Title: Molecular cloning an
A; Reference number: S68700; M
A; Accession: S68700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Genetic code: $C; Superfamily: ur C; Superfamily: ur C; Keywords: ATP; F; 90-288/Domain: F; 107-114/Region
T-kininogen I precursor - rat
N;Alternate names: 73K protein; LMW k
N;Contains: bradykinin; T-kinin
C;Species: Rattus norvegicus (Norway
C;Date: 17-Mar-1987 #sequence_revisio
                                                                                                                                                                                                                                                                                                                                                                                                                                            F;29-1238/Product: HPTP beta-like tyrosine phosphatase #status predicted F;267-347/Domain: fibronectin type III repeat homology <3FR> F;267-347/Domain: protein-tyrosine-phosphatase homology <PTP> F;966-1188/Domain: protein-tyrosine-phosphatase homology <PTP> F;1140/Active site: Cys (phosphocysteine intermediate) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:D45212; NID:g1208432; PIDN:BAA08146.1; PID:g1208433 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; nucleic acid sequence not shown A;Molecule type: mRNA A;Residues: 1-1238 <KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: The minimal gene complement of Mycoplasma genitalium A;Reference number: A64200; MUID:96026346 A;Accession: E64233
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R;Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.;
M.; Fuhrmann, J.; Nguyen, D.; Otterback, T.R.; Saudek,
                                                                                                                                                                                                                                                                                                                                                                                                                F;1140/Active site: Cys (phosphocysteine intermediate) *scalus prodicted F;1146/Binding site: substrate phosphate (Arg) *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Keywords: phosphoprotein
F;1-28/Domain: signal sequence #status predicted <SIG>
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                                                                           LMW kininogen
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Pred. No.
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                                                                                                     C; Genetics:
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A;Molecule type: mRNA
A;Residues: 330-420,'r',422-429,'P' <KAN>
R;Anderson, K.P.; Croyle, M.L.; Lingrel, J.B.
Gene 81, 119-128, 1989
A;Title: Primary structure of a gene encoding
A;Reference number: JQ0027; MUID:90034172
A;Accession: JQ0027
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Jpn. J. Cancer Res. 81, 63-68, 1990
A;Title: Identification of a protein increasing
A;Reference number: PL0193; MUID:90216390
A;Accession: PL0193
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A;Title: Differing expression patterns and A;Reference number: A92625; MUID:87137443
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A;Residues: 1-430 <FUR>
A;Cross-references: GB:M11883; NID:g205084; PIDN:AAA41489.1; PID:g205085
A;Cross-references: GB:M11883; NID:g205084; PIDN:AAA41489.1; NIS:g205085
A;Cross-references: GB:M11883; NID:g205085
A;Cross-refer
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A;Title: Primary structures of the mRNAs encoding the rat precursors for bradykinin
A;Introns: 65/3; 102/3; 130/1; 187/3; 223/2; 252/1; 309/3; 345/3; 374/3; C;Superfamily: kininogen; cystatin homology C;Keywords: acute phase; bradykinin; cysteine proteinase inhibitor; dupli F;1-18/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: protein
A; Residues: 376.430 (ENZ)
R; Sierra, F; Walter, R.; Vautravers, P.; Guigo
Arch. Biochem. Biophys. 322, 333-338, 1995
A; Title: Identification of several isoforms of
A; Reference number: S68034; MUID: 96032652
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A;Title: Purification and characterization of two kinds of log.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Experimental source: strain Sprague-Dawley
R;Kageyama, R.; Kitamura, N.; Ohkubo, H.; Nakanishi, S.
J. Biol. Chem. 262, 2345-2351, 1987
A;Title: Differing utilization of homologous transcription initiation A;Reference number: A25488; MUID:87137465
A;Accession: B25488
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A;Accession: A28526
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A;Title: Purification and characterization of :
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A; Residues: 375-430 <KIT>
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                                                                                                                                                                                                                                              d of an Arg or Lys, it is probably not released from
C;Comment: The T-kininogens are produced in response
                                                                                                                                                                                                                                                                                     C;Comment: T-kininogens contain T-kinin (I-S-bradykinin), a novel kinin isolated afte d of an Arg or Lys, it is probably not released from its precursor by either tissue o
                                                                                                                                                                                                                                                                                                                                                                                   ceding bradykinin.
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A; Residues: 'E', 20-48; 376-430 <ENJ>
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A; Residues: 340-430 <SIE>
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A; Residues: 1-48 < KAG>
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A; Residues: 1-60, 'E', 62-113, 'R', 115-165, 'F', 167-178, 'TKI', 182-211, 'F', 213-256, 'S', 258
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F:19-430/Product: T-kininogen I *status experimental <MAT>
F;19-130/Domain: cystatin homology <CYI>
F:141-252/Domain: cystatin homology <CY2>
F:263-374/Domain: cystatin homology <CY3>
F:263-374/Domain: cystatin homology <CY3>
F:378-386/Product: bradykinin *status predicted <BDY>
F:19/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) *status predicted F:19/Modified site: pyrrolidone carboxylic acid (Gln) (covalent) *status predicted F:83.126.168.204.325/Binding site: carbohydrate (Asn) (covalent) *status predicted F:83-94.107-125.141-144.205-217.228-247.263-266.327-339.350-369/Disulfide bonds: *status
                                                                                                                                                                                                                                                                                                                                                                                                C;Superfamily: pol polyprotein
C;Keywords: AIDS; aspartic proteinase; endonuclease; hydrolase; immunodeficiency; nucleof;85-183/product: retropepsin #status predicted <RTP>
F;109/Active site: Asp (shared with dimeric partner) #status predicted
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R;Tristem, M.; Hill, F.; Karpas, A.
J. Gen. Virol. 72, 721-724, 1991

A;Title: Nucleotide sequence of a Guinea-Bissau-derived human immunodeficiency virus typ A;Reference number: A38475; MUID:91170959
Search completed: June Job time: 5038 sec
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A;Residues: 1-1034 <TRI>
A;Rosidues: readthrough of the terminator TGA may occur between codons ATT for 564-Ile and C;Comment: The cleavage sites of this polyprotein have not been determined.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pol polyprotein - human immunodeficiency virus type 2 (isolate CAM2/Guinea-Bissau) N;Contains: endonuclease (EC 3.1.-.-); retropepsin (EC 3.4.23.16); RNA-directed DNA polycyspecies: human immunodeficiency virus type 2, HIV-2
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Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 31-Jan-1997
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4 rattus norv
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bacillus su
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OB8566; O9QXJ6;
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                                                                                          use by non-profit institutions as lon-
modified and this statement is not removi
entitles requires a license agreement (S)
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                            Zhang T., Fagotto F., Hsu W., Zeng L., Jenkins N.A., Warburton D., Costantini "Properties of mouse Axin2 and human AX expression pattern, interaction with Ax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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[2]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98221239; PubMed=9554852;
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catenin, APC, and GSK3beta.";
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                                                                                                                                                                                                                            AND BETA-CATENIN. THE INTERACTION BETWEEN AXIN AND BETA-CATE OCCURS VIA THE ARMADILLO REPEATS CONTAINED IN BETA-CATENIN. TERNARY COMPLEX (BY SIMILARITY). SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY). PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED
                                             MGI:1270862; Axin2.
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Q9Y271; Q9UH84;

01-CCT-2000 (Rel. 40, Created)

01-CCT-2000 (Rel. 40, Last sequence)

01-CCT-2000 (Rel. 40, Last annotate)

AXIN 2 (AXIS INHIBITION PROTEIN 2)
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                                           - -
                                                                                                                                                                                          Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.

-: FUNCTION: INHIBITOR OF THE WIT SIGNALING PATHWAY. DOWN REGULATES
-: BETA-CATENIN, PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-CATENIN AND APC BY GSK-3B (BY SIMILARITY).

-: SUBUNIT: INTERACTS WITH GLYCOGEN SYNTHASE-3 BETA (GSK-3B)
-: AND BETA-CATENIN. THE INTERACTION BETWEEN AXIN AND BETA-CATENIN.

OCCURS VIA THE ARMADILLO REPEATS CONTAINED IN BETA-CATENIN.
                                                                                                                                                                                                                                                                                                                                                       TISSUE-Brain, and Lymphoblast;
Zhang T., Fagotto F., Hsu W., Zeng L., Gilbert D., Copeland N.G.,
Jenkins N.A., Warburton D., Costantini F.;
"Properties of mouse Axin2 and human AXIN2: chromosomal location,
expression pattern, interaction with Axin and effects on embryoni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chromosome 17q23-q24.";
Genomics 55:341-344(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=99168905; PubMed=10049
Mai M., Qian C., Yokomizo A.,
"Cloning of the human homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HUMAN
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SIMILARITY: CONTAINS 1 RGS DOMAIN.
SIMILARITY: CONTAINS 1 DIX DOMAIN.
                                                                                                      SUBCELLULAR LOCATION: CYTOPLASMIC. TISSUE SPECIFICITY: EXPRESSED IN B PTM: PROBABLY PHOSPHORYLATED BY GS
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--aroa; Chordata;
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ON PROTEIN 2) (CONDUCTIN) (AXIN-LIKE PROTEIN)
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H -> Y (IN REF. 2).
S -> P (IN REF. 2).
F -> S (IN REF. 2).
G -> A (IN REF. 2).
A07D5EFB25DE7277 C
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BY GSK-3B
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                     SEQUENCE FROM N.A.

MEDLINE-20171051; PubMed-10704853;

MEDLINE-20171051; PubMed-10704853;

A Shimizu T., Yamanaka Y., Ryu S.-L., Hashimoto H., Yabe T., Hi
A Bae Y.-K., Hibi M., Hirano T.;

"Cooperative roles of Bozozok/Dharma and Nodal-related protei
formation of the dorsal organizer in zebrafish.";

L Mech. Dev. 91:293-303(2000).

C -!- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN RE
BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF
C CATENIN AND APC BY GSK-3B (BY SIMILARITY).

C -!- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).

C -!- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).

C -!- SIMILARITY: CONTAINS 1 RGS DOMAIN.

C -!- SIMILARITY: CONTAINS 1 DIX DOMAIN.
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Eukaryota; Metazoa; Chordata;
Actinopterygil; Neopterygil; T
                                                                                                                                                                                                                                                                                                      01-OCT-2000 (Rel. 40, Created)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
AXIN 2 (AXIS INHIBITION PROTEIN 2)
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PROSITE; PS50132; RGS; 1.

Developmental protein; Phosphorylation.

DowAIN 81 200 RGS.

DOMAIN 327 413 GSK-3B BIN

DOMAIN 413 476 BETA-CATEN
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; Neopterygli; Telosstei; Euteleostei; Ostariophysi
Cyprinidae: Rasborinae; Danio.
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Q -> R (IN REF. 2).

MISSING (IN REF. 2).

P -> S (IN REF. 2).

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Pred. No. 1.1e-26;
1; Mismatches (
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BETA-CATENIN BINDING SITE (BY
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the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by an
                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97373830; PubMed=9230313;
Zeng L., Fagotto F., Zhang T., Hsu W., Vasicek T.J.,
Lee J.J., Tilghman S.M., Gumbiner B.M., Costantini F.
"The mouse Fused locus encodes Axin, an inhibitor of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gallus.
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Developmental protein; Phosphorylation.
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- SIMILARITY:
- SIMILARITY:
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SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
DEVELOPMENTAL STAGE: EXPRESSED AT STAGE 12 TO 15.
PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPH
PP2A (BY SIMILARITY).
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(AXIS INHIBITION PROTEIN).
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CONTAINS 1 DIX DOMAIN.
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BETA-CATENIN BINDING SITE (BY
SIMILARITY).
POLY-SER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 246; DB 1
Pred. No. 2e-23;
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Best Local Similarity
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SEQUENCE
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InterPro; IPR00
Pfam; PF00615;
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01-OCT-2000 (Rel. 40,
01-OCT-2000 (Rel. 40,
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Pfam; PF00778; DIX; 1.
PROSITE; PS50132; RGS;
                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                    Hedgepeth C.M., Deardorff M.A., Klein "Xenopus axin interacts with glycogen expressed in the anterior midbrain."; Mech. Dev. 80:147-151(1999).
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01-0CT-2000
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DOMAIN 88 211
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InterPro; IPR001158;
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HSSP; P49799;
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xenopus laevis (African clawed frog).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AXIN (AXIS INHIBITION
                                                                     EMBL; AF097313; AAC71036.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE=99173782; PubMed=10072781;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=8355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xenopodinae;
                                                         HSSP; P49799;
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                                                                                                                                                                                                                                                        BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-CATENIN AND APC BY GSK-3B (BY SIMILARITY).
SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
DEVELOPMENTAL STAGE: WEAKLY AND UBIQUITOUSLY EXPRESSED THROUGHOUT EARLY DEVELOPMENT, AND HIGHLY EXPRESSED IN THE ANTERIOR MESENCEPHALON ADJACENT TO THE FOREBRAIN-MIDBRAIN BOUNDARY.
PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              σ
                                                                                                                                                                                                               PP2A (BY SIMILARITY).
SIMILARITY: CONTAINS 1 RGS DOMAIN.
SIMILARITY: CONTAINS 1 DIX DOMAIN.
                                                                                                                                                                                                                                                                                                                                              FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VTLGQFKELLTKKGNYRYYFKKVSDEFDCGVVFEEVREDDTILPIFEEKII 834
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Last annotation updat
PROTEIN) (XAXIN).
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RGS.
GSK-3B BINDING SITE (BY SIMILARITY).
BETA-CATENIN BINDING SITE (BY SIMILARITY).

DIX.
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Pred. No. 3.
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Mismatches 7;
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Best Local
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Developmental prote
DOMAIN 88
DOMAIN 348
    Interpro; IPR000342; -.
Interpro; IPR001158; -.
Pfam; PF00615; RGS; 1.
Pfam; PF00778; DIX; 1.
PROSITE; PS50132; RGS; 1
Developmental protein; P
NON_TER
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AXIN 1 (AXIS INHIBITATION AXIN 1)
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015169;
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SEQUENCE
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                                                                                                                                                                                                                                                               entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EW the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content use by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pathway that regulates embryonic axis Cell 90:181-192(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2000
01-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: CYTOPLASMIC.
TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED
PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATENIN AND APC BY GSK-3B.
SUBUNIT: INTERACTS WITH GLYCOGEN SYNTHASE KINASE-3 BETA (GSK-3B)
AND BETA-CATENIN. THE INTERACTION BETWEEN AXIN AND BETA-CATENIN.
OCCURS VIA THE ARMADILLO REPEATS CONTAINED IN BETA-CATENIN.
TERNARY COMPLEX. MAY ALSO BINDS TO PLAKOGLOBIN (GAMMA-CATENIN),
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: CONTAINS 1 RGS DOMAIN. SIMILARITY: CONTAINS 1 DIX DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF
                                                                                                                                                                      603816;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J.J., Tilghman S.M., Gumbiner B.M., Costantini F.; mouse Fused locus encodes Axin, an inhibitor of the Wnt signaling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 66.3
34; Conservative
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protein; P.
88 2J.
348
434
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(Rel. 40, Last annotation update)
INHIBITION PROTEIN 1) (HAXIN) (FRAGMENT).
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Phosphorylation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9;
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BETA-CATENIN BINDING SITE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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.7e-17
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OF BETA-
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Developmental

1. Phosphorylation

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                                                                                                                                                                                                                                                                                                                                                              Ikeda S., Kishida S., Yamamoto H., Murai H., Koyama S., Kikuchi A.;

Axin, a negative regulator of the Wnt signaling pathway, forms a
complex with 65K-3beta and beta-catenin and promotes GSK-3beta-
RT dependent phosphorylation of beta-catenin.*;

REMBO J. 17:1371-1384 (1998).

C. -1- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
CATENIN AND APC BY GSK-3B AND BETA-CATENIN. THE INTERACTION
C. -1- SUBGUNIT: INTERACTS WITH GSK-3B AND BETA-CATENIN. THE INTERACTION
C. ENWEEN AXIN AND BETA-CATENIN OCCURS VIA THE ARMADILLO REPEATS
C. CONTAINED IN BETA-CATENIN. TERNARY COMPLEX. ALSO BINDS TO
PLAKOGLOBIN (GAMMA-CATENIN). APC, DVI AND PP2A (BY SIMILARITY).
C. -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
C. -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN TESTIS, THYMUS AND LUNG
FOLLOWED BY CEREBRUM, CEREBELLUM, HEART, KIDNEY, SKELETAL MUSCLE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local 9
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070239;
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SEQUENCE
                                                         InterPro; IPR000342; -.
InterPro; IPR001158; -.
Pfam; PF00615; RGS; 1.
Pfam; PF00778; DIX; 1.
                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AXIN 1 PROTEIN AXIN1 OR AXIN.
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01-OCT-2000 (Rel.
01-OCT-2000 (Rel.
PROSITE; PS50132; RGS; 1.
Developmental protein; Phosphorylation.
NON_TER 1 1 1
DOMAIN 154 277 RGS.
                                                                                                                        EMBL; AF017756; AAC40066.1; ALT_INIT. HSSP; P49799; 1AGR.
                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-98151361;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
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                                                                                                                                                                                                                                                                                          SIMILARITY: CONTAINS 1 RGS DOMAIN. SIMILARITY: CONTAINS 1 DIX DOMAIN.
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                                                                                                                                                                                                                                                                                                        SIMILARITY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                      PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED
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385
471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          el. 40, Created)
el. 40, Last sequence update)
el. 40, Last annotation update)
el. 40, Last annotation (FRAGMENT).
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                                                                                                                                                                                                                                                                                                          CONTAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed-9482734;
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99803
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66.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 2e-:
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GSK-3B BINDING SITE (BY SIMILARITY).
BETA-CATENIN BINDING SITE (BY
SIMILARITY).
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                                                                                                                                                                                                                                                           collaboration
                                                                                                                                                                                                                                              outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                   commercia;
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RESULT
AXN1_MC
        THERE REPORTED TO THE PROPERTY OF THE PROPERTY
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Best Local S
Matches 33
Pfam; PF00615; RGS; 1.
Pfam; PF00778; DIX; 1.
PROSITE; PS50132; RGS; 1.
PROVELOPMENTAL PROTEIN; P
NON_TER 1 1 1
DOMAIN 10 18
DOMAIN 217 340
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DOMAIN
DOMAIN
SEQUENCE
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01-0CT-2000 (Rel. 40, Created)
01-0CT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
01-0CT-2000 (Rel. 40, Last annotation update)
AXIN 1 (AXIS INHIBITION PROTEIN 1) (FUSED PROTEIN) (FRAGMENT)
AXIN1 OR AXIN OR FU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOUSE
                                                                                                                                                                                                                                                                                                                                                                 between the Swiss Institute of Bioinformatics and the E the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zeng L., Fagotto F., Zhang T., Hsu W., Vasicek T.J. Lee J.J., Tilghman S.M., Gumbiner B.M., Costration "The mouse Fused locus encodes Axin, an inhibitor opathway that regulates embryonic axis formation.";
                                                                                                                                                                                MGD; MGI:1096327; Axin.
InterPro; IPR000342; -.
InterPro; IPR001158; -.
                                                                                                                                                                                                                                                             EMBL; AF009011;
HSSP; P49799; 1/
                                                                                                                                                                                                                                                                                                                                         or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pathway that regulates embryonic axis Cell 90:181-192(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORMS 1 AND MEDLINE-97373830; Pubmed-9230313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AXN1_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 LTLGHFKEQLSKKGNYRYYFKKASDEFACGAVFEEIWDDETVLPMYEGRIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: CONTAINS 1 RGS DOMAIN. SIMILARITY: CONTAINS 1 DIX DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATENIN AND APC BY GSK-3B (BY SIMILARITY).

SUBUNIT: INTERACTS WITH GSK-3B AND BETA-CATENIN. THE INTERACTION
BETWEEN AXIN AND BETA-CATENIN OCCURS VIA THE ARMADILLO REPEATS
CONTAINED IN BETA-CATENIN. TERNARY COMPLEX. ALSO BINDS TO
PLAKOGLOBIN (GAMMA-CATENIN), APC, DYL AND PP2A (BY SIMILARITY).

SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY)
ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE
PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE SPECIFICITY: EXPRESSED IN EMBRYONIC STEM CELLS.
DEVELOPMENTAL STAGE: WIDELY EXPRESSED AT E10.5 TO E16.5 DAY
PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
                                                                                                                                                                                                                                                                                                                                            an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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Rodentia;
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64.7%;
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    Phosphorylation;

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                                                                                                                                                                                                                                                                                                                                                                    agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 190; DB 1;
Pred. No. 2.6e-16;
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BETA-CATENIN BINDING SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                 Alternative
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'∩1 F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
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                                                                                 splicing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Perry W.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                              restrictions
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Best Local S
Matches 34
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01-0CT-2000
01-0CT-2000
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                                DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                    "Cooperative roles of Bozozok/Dharma and Nodal-related proformation of the dorsal organizer in zebrafish.";

Mech. Dev. 91:293-303(200).

-i- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN
BETA-CATEMIN. PROBABLY FACILITATE THE PHOSPHORYLATION
CATEMIN AND APC BY GSK-3B (BY SIMILARITY).

-i- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).

-i- PUN: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Cypriniformes; Cyprinidae; Rasborinae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BRARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARSPLIC
                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content
                                                                                                                                                                                                         entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                               Shimizu T., Yamanaka Y., Ryu
Bae Y.-K., Hibi M., Hirano T
                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-20171051; PubMed-10704853;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                    DOMAIN
                                                                                            DOMAIN
                                                                                                                  PROSITE;
                                                                                                                               Pfam;
                                                                                 DOMAIN
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                                                                                                                                                    InterPro; IPR000342; InterPro; IPR001158;
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m; PF00778; DIX; 1.
SITE; PS50132; RGS; 1.
elopmental protein; Phosphorylation.
elopmental protein; Phosphorylation.
AIN 92 214
AGS 3B BINDI
AIN 351 436
BETA-CATENIN
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                                                                                                                                                                                                                                                                                                                PP2A (BY SIMILARITY).
SIMILARITY: CONTAINS
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P49799; L
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992 AA;
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835
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562
                                                                                                                                                                                                                                                                                                                                                                                                                                             Yamanaka Y., Ryu S.-L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 40, Created)
(Rel. 40, Last sequence up
(Rel. 40, Last annotation
INHIBITION PROTEIN 1).
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                                  A,
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                                    835
94351
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Pred.
                                                         GSK-3B BINDING
BETA-CATENIN BI
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GSK-3B BINDING SITE (BY SIMILARITY).
BETA-CATENIN BINDING SITE (BY
SIMILARITY).
DIX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MISSING (IN ISOFORM); 70EEB53D387BD26F
                         DIX.
; 1C62FCF1F5937C87 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       190;
No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Hashimoto H.,
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2.9e-16;
les 8;
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                                                                       BINDING
                                                                                 SITE (BY SIMILARITY).
                                                                                                                                                                                                                                   Usage
                                                                                                                                                                                                                                                                                                                                          DEPHOSPHORYLATED
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Length 835
                                                                                                                                                                                                                                                                                                                                                                                                                                               Yabe
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                                                                       SITE
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                                                                                                                                                                                                                                                           restrictions
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H.,
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                                                                                                                                                                                                                                                                       EMBL
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                                                                                                                                                                                                                                                                         a collaboration -
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                                                                                                                                                                                                                                      for
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Query Match

.48;

Score

DB

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RESULT 11

RESULT 11

DSH_DDNDE

ID DSH_DD

AC P5114-DT

CO P520

DT 01-OC

DT 01-OC

DT 01-OC

DT 01-OC

DT 01-OC

CO EDHYD

OX NCB1-RA K1110-RA K1110-RA K1110-RA K1110-RA K1110-RA K110-RA 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DSH_DROME
P51140;
01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Arthropoda; Tracine
Pterygota; Neoptera; Endopterygota; Dit
Ephydroidea; Drosophilidae; Drosophila
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The Drosophila segment polarity protein required for response to Genes Dev. 8:118-130(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1996
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yanagawa S.-I., van Leeuwen F., Wodar
"The dishevelled protein is modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Theisen H., Purcell J., Bennett M., Kansa "Dishevelled is required during wingless cell polarity and cell identity."; Development 120:347-360(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEGMENT
                     EMBL; 126974; AAA16535.1;
EMBL; U02491; AAA20216.1;
FlyBase; FBgn0000499; dsh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=95262901; PubMed=7744250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=94200163; PubMed=8149913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Klingensmith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=94116855;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                      entities requires a
                                                                                                                                                                              modified and this statement
                                                                                                                                                                                                                                                           between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PHOSPHORYLATION.
                                                                                                                                                                                                                                                                                                                                   WHEN HYPERPHORPLATED.

TISSUE SPECIFICITY: FOUND IN EGG CHAMBERS OF THE OVARY AND TISSUE SPECIFICITY: FOUND IN EGG CHAMBERS OF THE OVARY AND UBIQUITOUSLY THROUGHOUT EMBRYOGENESIS AND IN DISCS. EXPRESSION 1 NOT SEEN IN SALIVARY GLANDS, MUSCLES OR VENTRAL GANGLIA BUT IS OBSERVED IN BRAIN LOBES.

OBSERVED IN BRAIN LOBES.

PTM: PHOSPHORYLATED. WG SIGNALING GENERATES HYPERPHOSPHORYLATED FORMS OF DSH WHICH ARE THE ACTIVE FORMS.

SIMILARITY: BELONGS TO THE DSH FAMILY.

SIMILARITY: CONTAINS 1 DEP DOMAIN.

SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: REQUIRED TO ESTABLISH COHERENT ARRAYS OF POLARIZED CELL AND SECMENTS IN EMBRYOS. PLAYS A ROLE IN WINGLESS (WG) SIGNALING POSSIBLY THROUGH THE RECEPTION OF THE WG SIGNAL BY TARGET CELLS AND SUBSEQUENT REDISTRIBUTION OF ARM PROTEIN IN RESPONSE TO THAT SIGNAL IN EMBRYOS. THIS SIGNAL SEEMS TO BE REQUIRED TO ESTABLISH PLANAR CELL POLARITY AND IDENTITY.

SUBCELLULAR LOCATION: CYTOPLASMIC. ASSOCIATED WITH THE MEMBRANE
                                                                                                                                                                                                                              s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POLARITY PROTEIN DISHEVELLED.
                                                                                                                               s requires a license agreement (S an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9:1087-1097(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J., Nusse R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34, Created)
34, Last sequence update)
40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=8288125;
                                                                                                                                                                                                           rmatics Institute. There are no restrictions institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58.8%;
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                                                                                                                                                                                    is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene dishevelled
the wingless sign
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gless signaling
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ches 9;
                                                                                                                                                            (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A
A
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                                                                                                                                                                                      Usage by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lled encodes signal.";
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establish both
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                                                                                                                                                                                         and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNALING,
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RESULT 12
DVL2_HUMAN
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Best Local S
Matches 24
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Pfam; PF00778; DIX; 1.
Pfam; PF00795; PDZ; 1.
PROSITE; PS50186; DEP; 1
PROSITE; PS50106; PDZ; 1
          InterPro;
InterPro;
                                                                                                                                                                                                                                             Genomics 42:302-310(1997).

-I- FUNCTION: MAY PLAY A ROLE IN THE SIGNAL MEDIATED BY MULTIPLE WNT GENES.

-I- SUBCELLULAR LOCATION: CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
01-CCT-2000 (Rel. 40, Last annotation update)
SEGMENT POLARITY PROTEIN DISHEVELLED HOMOLOG
                                              EMBL; AF006012; AAB65243.1; HSSP; P31016; 1BFE. MIM; 602151; -
                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammaila; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., SUBCELLULAR LOCATION, MEDLINE=97336056; PubMed=9192851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   014641;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DVL2_HUMAN
                                                                                                                                                                                                                                                                                                                          Semenov M.V., Snyder M.;
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                                  interPro;
                                                                                                                                                                                                                                                                                                   family.
                                                                                                                                                                                                                                                                                                                                                                                                                                      (DSH HOMOLOG
                                                                                                                                                                                                                                                                                                             Human dishevelled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35 VTLRDFKLVLNKQNNNYKYFFKSMDADF--GVVKEEIADDSTILPCFNGRVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 LTLGHFKEQLSKK-GNYRYYFKKASDEFACGAVFEEIWDDETVLPMYEGRIL
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                                                                                                                                                                                               PTM: PHOSPHORYLATED.
SIMILARITY: BELONGS TO THE DSH FAMILY.
SIMILARITY: CONTAINS 1 DEP DOMAIN.
SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         h 39.7%;
Similarity 46.2%;
24; Conservative 1
IPRO00591; -.
IPRO01158; -.
IPRO01478; -.
00610; DEP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                      2).
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                                                                                                                                                                                                                                                                                                             genes constitute a
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1.
Phosphorylation;
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POLY-GLN.
POLY-SER.
POLY-SER.
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D -> N (IN REF. 2).
T -> I (IN REF. 2).
S -> F (IN REF. 2).
M; OBA253CE4COB71F5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 109.5; DB 1
Pred. No. 2.6e-06;
0; Mismatches 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                736
                                                                                                                                                                                                                                                                                                             DHR-containing
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                                                                                                                                                                                                                                                                                                                                                 AND PHOSPHORYLATION
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                                                                                                                                                                                                                                                                          TRANSDUCTION PATHWAY
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DVL2_MOUSE

DVL2_MOUSE

AC Q60838;

DT 30-MAY-2000

DT 01-CCT-2000

DD 01-CCT-2000

DE SEGMENT POLL

CO Wammalia; EN

OC Mammalia; EN

OX NCBI_TaxID=1

RR SEQUENCE FR

RC STRAIN=BALB,

RX MINTERSTOLAI

RA Kilngensmitia

RA Kilngensmitia

RA Kilngensmitia

CC -!- FUNCTIOI

CC -!- SIMILAR

CC -!- SIMILA
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Best Local
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30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
SEGMENT POLARITY PROTEIN DISHEVELLED HOMOLOG
(DSH HOMOLOG 2).
                 HSSP; P31016; 1BFE.
MGD; MGI:106613; Dv12.
InterPro; IPR000591; -.
InterPro; IPR001158; -.
InterPro; IPR001478; -.
Pfam; PF00778; DIX; 1.
Pfam; PF00778; DIX; 1.
Pfam; PF00778; DIX; 1.
Pfam; PF00595; PDX; 1.
PROSITE; PS50186; DEP; 1.
PROSITE; PS50186; DED; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            *Conservation of dishevelled structure and function mice: isolation and characterization of Dvl2.*; Mech. Dev. 58:15-26(1996).
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DOMAIN
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DOMAIN
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                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- FUNCTION: MAY PLAY A ROLE IN THE SIGNAL TRANSDUCTI
MEDIATED BY MULTIPLE WAT GENES.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
-!- TISSUE SPECIFICITY: UBIQUITOUS.
-!- SIMILARITY: BELONGS TO THE DSH FAMILY.
-!- SIMILARITY: CONTAINS 1 DEP DOMAIN.
-!- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-BALB/C; TISSUE-Brain; MEDLINE-97042042; PubMed-8887313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sussman D.J.;
                                                                                                                                                                                                                                                EMBL; U24160; HSSP; P31016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38 ITLGDFKSVLQRPAGAKYFFKSMDQDF--GVVKEEISDDNARLPCFNGRVV
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339 P
507 D
694 P
78947 MW;
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Pred. No. 2.8e-05;
8; Mismatches 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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        C TISSUE-Bone marrow;

X MEDLINE-97191544; PLDMed-9039502;

A Nagase T., Seki N., Ishikawa K.-I., Ohira M., Kawarabayasi Y.,

A Ohara O., Tanaka A., Kotani H., Miyajima N., Nomura N.;

Prediction of the coding sequences of unidentified human genes. VI.

The coding sequences of 80 new genes (KIRA0201-KIRA0280) deduced by

Tanalysis of cDNA clones from cell line KG-1 and brain.";

LONA Res. 3:321-339(1966).

LONA Res. 3:321-339(1966).

C --- FUNCTION: MAY PLAY A ROLE IN THE SIGNAL TRANSDUCTION PATHWAY

C --- SUBCELULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).

C --- SIMILARITY: BELONGS TO THE DSH FAMILY.

CC --- SIMILARITY: CONTAINS 1 DEP DOMAIN.
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SEQUENCE
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                                                                                                                                                                                                                "cDNA characterization and chromosomal mapping of the Drosophila dishevelled polarity gene."; Hum. Mol. Genet. 5:953-958(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=98008870; PubMed=9344861;
Bui T.D., Beier D.R., Jonssen M., Smith K., Dorrington S.M.,
Kaklamanis L., Kearney L., Regan R., Sussman D.J., Harris A.L.;
Robla cloning of a human dishevelled DVL-3 gene, mapping to 3q27,
expression in human breast and colon carcinomas.";
Biochem. Biophys. Res. Commun. 239:510-516(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HUMAN
                                                                                                                                                                                                                                                          Pizzuti A., Amati F., Calabrese G., Mar
Giardino L., Ratti A., Penso D., Calza
Novelli G., Dallapiccola B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                         Genomics 42:302-310(1997).
                                                                                                                                                                                                                                                                                                                                                                            "Human dishevelled genes constitute a DHR-containing multigene
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE=97336056; PubMed=9192851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DYL3 OR KIAA0208.
                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                    MEDLINE-96414301;
Pizzuti A., Amati
                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                       family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 LTLGHFKEQLSKKGNYRYYFKKASDEFACGAVFEEIWDDETVLPMYEGRIL 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ITLGDFKSVLQRPAGAKYFFKSMDQDF--GVVKEEISDDNARLPCFNGRVV 86
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Pred. No. 2.8e-05;
8; Mismatches 20;
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ilza L., Pa
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Matches 21
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DOMAIN 424 9321
DOMAIN 422 496
CONFLICT 2 76
CONFLICT 76 76
CONFLICT 151 151
CONFLICT 152 182
CONFLICT 218 218
CONFLICT 222 222
CONFLICT 230 230
CONFLICT 236 236
CONFLICT 242 242
CONFLICT 445 445
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CONFLICT 553 554
CONFLICT 553 554
CONFLICT 562 629
CONFLICT 662 671
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EMBL; AF006013; AAB65244.1; -.
EMBL; U49262; AAB47447.1; -.
EMBL; D86963; BAA13199.1; -.
HSSP; P31016; 1BFE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00778; DIX; Pfam; PF00595; PDZ;
                                                DVL3_MOUSE STANDARD; PRT; 716 AA. 061062; 30-MAY-2000 (Rel. 39, Created) 30-MAY-2000 (Rel. 40, Last sequence update) 01-OCT-2000 (Rel. 40, Last annotation update) SEGMENT PROTEIN DISHEVELLED HOMOLOG (DSH HOMOLOG 3).
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       musculus
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21; Conserv
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); IPRO01158; -.
); IPRO011478; -.
'00610; DEP; 1.
'00778; DIX; 1.
'00595; PDZ; 1.
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       (Mouse)
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Pred. No. 0.00018;
11; Mismatches 16
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S -> I (IN REF. 3).
PPGRDLASVPPELTASRQSFRMAMGNPSEFFVDVM ->
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Bla55EBF9507D06E CRC64;
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R (IN REF. 3).

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                                                                                 DVL-3 (DISHEVELLED-3)
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Best Local Similarity 41.2
Matches 21; Conservative
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HSSP; P31016; 1BFE.
MGD; MGI:108100; Dv13.
InterPro; IPR000591; -
InterPro; IPR001158; -
InterPro; IPR001478; -
Pfam; PF00510; DEP; 1.
Pfam; PF00778; DIX; 1.
Pfam; PF00595; PDZ; 1.
                                                                                                                                                                                                               DOMAIN
SEQUENCE
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"Isolation and characterization of mouse dishevelled-3.";

Dev. Dyn. 207:253-262(1996).

-I- FUNCTION: MAY PLAY A ROLE IN THE SIGNAL TRANSDUCTION PATHWAY MEDIATED BY MULTIPLE WNT GENES.

-I- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).

-I- TISSUE SPECIFICITY: UBIQUITOUS.

-I- SIMILARITY: BELONGS TO THE DSH FAMILY.

-I- SIMILARITY: CONTAINS 1 DEP DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUE-Brain;
MEDLINE-97081279; PubMed-8922524;
                                                                                                                                                                                                                                               Developmental protein.
DOMAIN 249 321
                                                                                                                                                                                                                                                                          PROSITE; PS50186; DEP; PROSITE; PS50106; PDZ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tsang M., Lijam N., Yang Y., Beier D.R., Wynshaw-Boris A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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716 AA;
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78122 MW;
              7, 2001, 02:10:34
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DEP.
; 55412C03202301F0 CRC64;
                                                                                                                                     Score 95.5; DB 1; Length 716; Pred. No. 0.00018; 1; Mismatches 16; Indels
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Result
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Listing first 45 summaries
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 seq length: 0
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Match
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1: sp_archea:*
2: sp_bacteria:
3: sp_fung1:*
 June 7, 2001, 02:09:43; Search time 81.06 Seconds (without alignments) 73.743 Million cell updates/sec
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1 LTLGHFKEQLSKKGNYRYYF......VFEEIWDDETVLPMYEGRIL
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Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                       sp_plant:*
sp_rodent:*
sp_unclassified:*
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088566 mus musculu
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094x36 mus musculu
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042400 gallus gall
024900 gallus gall
024900 xenopus lae
015169 homo sapien
070239 rattus norv
035625 mus musculu
029ttp2 xenopus lae
094072 drosophila
09407 drosophila
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P72599 synechocyst
O62090 caenorhabdi
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## ALIGNMENTS

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Q9QXJ6;
01-MAY-2000
01-MAY-2000
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Science 2
EMBL; AFC
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"Functional interaction of an axin homolog, conductin, catenin, APC, and GSK3beta.";
Science 280:596-500/1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P49799; 1AGR.
MGD; MGI:1270862; Axin2.
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MEDLINE=98221239; PubMed=9554852;
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Mammalia; Eutheria;
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INTERPRO; IPR001158; -.
PFAM; PF00615; RGS; 1.
PFAM; PF00778; DIX; 1.
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                                                                                                                                                                                                      Submitted (NOV-1999) to the EMBL; AF205889; AAF22800.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2000
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                           PRINTS;
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                                                                                                           HSSP; P49799; 1AGR.
INTERPRO; IPR000342; -.
INTERPRO; IPR001158; -.
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SEQUENCE
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                     PF00615; RGS; 1.
PF00778; DIX; 1.
S; PR01301; RGSPR
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AF073788; AAC26047.1; -.
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etazoa; Chordata;
theria; Rodentia;
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RGSPROTEIN.
A; 92896 MW;
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Pred. No. 4.7e-26;
Mismatches 0;
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Sciurognathi; Muridae;
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F.;
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Q9UH84;
01-MAY-2000
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Q9Y2T1;
01-NOV-1999
01-NOV-1999
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                  Zhang T., Fagotto F., Hsu W., Zeng L., Gilbert D., Copel Jenkins N.A., Warburton D., Costantini F.;
"Properties of mouse Axin2 and human AXIN2: chromosomal expression pattern, interaction with Axin and effects or axis formation.";
submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases EMBL; AF205888; AAF22799.1; -.
HSSP; P49799; 1AGR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                             "Cloning of the human homolog chromosome 17q23-q24."; Genomics 55:341-344(1999). EMBL; AF078165; AADZ0976.1; -HSSP; P49799; 1AGR.
                                                                                                                                  Homo sapiens (Human).

Homo sapiens (Human).

Metazoa; Chordata;
                                                                            MEDLINE=99168905; PubMed=10049590; Mai M., Qian C., Yokomizo A., Smit
                                                                                                                            Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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PFAM; PF00615; RGS; 1.
PFAM; PF00778; DIX; 1.
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  INTERPRO; IPR000342; -.
INTERPRO; IPR001158; -.
PFAM; PF00615; RGS; 1.
                                                                                                SEQUENCE FROM N.A.
                                                                                                                   NCBI_TaxID=9606;
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etazoa; Chordata;
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A; 86857 MW;
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Pred. No. 1.4e-25;
1; Mismatches 0
                                                                                                                              Craniata; Vertebrata; Catarrhini; Hominidae;
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(AXIN2),
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[1]
SEQUENCE FROM N.A.
MEDLINE-99173782; PubMed-10072781;
MEDLINE-99173782; PubMed-10072781;
Hedgepeth C.M., Deardorff M.A., Klein P.S.;
Hedgepeth C.M., Deardorff M.A., Klein P.S.;
                                                                                                                                              01-MAY-1999
01-MAY-1999
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                       III Lee J.J., Tilghman S.M., Gumbiner B.M., Costantini F.;
"The mouse Fused locus encodes Axin, an inhibitor of the Wnt sign pathway that regulates embryonic axis formation.";
Cell 90:181-192(1997).
EMBL: AFORDARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JAN-1998
01-JAN-1998
01-OCT-2000
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                                                                                                 Xenopus laevis (African clawed frog).
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF009012; AAC60245
HSSP; P49799; 1AGR.
INTERPRO; IPR000342; .
INTERPRO; IPR001158; .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                      AXIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE-97373830; PubMed-9230313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                               PFAM; PF00615; RGS; 1. PFAM; PF00778; DIX; 1.
                                                                                                                                                                                                                                                                                                                                             PRODOM; PD001580; -; 1.
PRODOM; PD003639; -; 1.
SEQUENCE 841 AA; 94931 MW;
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3 (TrEMBLrel. 05,
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                                                                                                                                                                                                                                                                                          Conservative
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93557 MW;
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Pred. No. 1.5e-25;
1; Mismatches 0;
                                                                                                                                             Last sequence update)
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Pred. No. 3.1e-16;
0; Mismatches 7
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Best Local Similarity 66.7
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Best Local Similarity
Matches 34; Conser
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MeCh. Dev. 80:147-131(1999).

EMBL; AR097313; AAC71036.1; -.

HSSP; P49799; 1AGR.

INTEREPRO; IPRO00342; -.

INTERPRO; IPRO01158; -.

PFAM; PF00615; RGS; 1.

PFAM; PF00778; DIX; 1.
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070239;
01-AUG-1998
01-AUG-1998
01-OCT-2000
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015169;
01-JAN-1998
01-JAN-1998
01-OCT-2000
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRODOM; PD001580; -; 1.
PRODOM; PD003639; -; 1.
SEQUENCE 842 AA; 94459 MW;
  Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INTERPRO; IPRO01158; -. PFAM; PF00615; RGS; 1. PFAM; PF00778; DIX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pathway that regulates embryonic Cell 90:181-192(1997).
EMBL, AF0096674, AAC51624.1; -.
HSSP; P49799; LAGR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR01301; RGSPROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zeng L., Fagotto F., Zhang T., Hsu W., Vasicek T.J., Pe
III Lee J.J., Tilghman S.M., Gumbiner B.M., Costantini
"The mouse Fused locus encodes Axin, an inhibitor of the
pathway that regulates embryonic axis formation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE-97373830; PubMed-9230313;
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Pred.
      Craniata; Vertebrata; Euteleostomi;
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No. 5.6e-16;
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O35625;
O1-JAN-1998 (TrEMBLrel. 0
O1-JAN-1998 (TrEMBLrel. 0
O1-OCT-2000 (TrEMBLrel. 1
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INTERPRO; IPR000342; -.
INTERPRO; IPR001158; -.
PFAM; PF00615; RGS; 1
PFAM; PF00778; DIX; 1.
PRINTS; PR01301; RGSPROTEIN.
                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                 "The
    935
                                                                                                   SEQUENCE
                                                                                                                                                                                                 EMBL; AF009011;
                                                                                                                                                                                                                                                   MEDLINE=97373830; PubMed=9; Zeng L., Fagotto F., Zhang
                                                                                                                                                                                                                                          III Lee J.J., Tilghman S.M.,
                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090
                                                                                                                                                                                                                                                                                                                                             AXIN.
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PRODOM; PD003639; -; 1.
SEQUENCE 832 AA; 92856 MW;
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INTERPRO; IPRO01158; -.
PFAM; PF00615; RGS; 1.
PFAM; PF00778; DIX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ikeda S., Yamamoto H., Murai H., Kishida S., Kikuchi A.;
"Axin, a negative regulator of the Wnt signaling pathway, forms complex with GSK-3beta and beta-catenin and promotes GSK-3beta-dependent phosphorylation of beta-catenin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE-98151361; PubMed-9482734;
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EMBL; AF017756; AAC40066.1; -.
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                                                        Local Similarity
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10
                                                                                                                                                                                                                                 mouse Fused locus
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33; Conser
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                                             Conservative
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                                                                                                   109917 MW;
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                                                                                                                                                                                                                             hang T., Hsu W., Vasicek T.J., Perry W.L., S.M., Gumbiner B.M., Costantini F.; encodes Axin, an inhibitor of the Wnt signaling
                                                                                                                                                                                                                      embryonic
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                                                     Score 190;
Pred. No. 2.
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Pred. No. 2.3e-15;
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                                            Mismatches
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                                                     DB 11;
.8e-15;
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RESULT

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Q9PTP2
ID Q9PTP2
AC Q9PTP2;
AC Q9PTP2;
DT Q1-MAY-2000 (
DT Q1-JUN-2000 (
DT Q1-JUN-2000 (
DE AXIN-RELATED (
OC Eukaryota, Mace occ eukaryota, Mace
          Qy
                     Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Hank, Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos, G.L.G.,
RA Haris N.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos, G.L.G.,
RA Haris N.H., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davengort L.B., Davies P.,
RA Gebablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Durbin K.J., Evangelista C.C., Ferriac C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Harris N.L., Harvey D., Helman T., Wei M.-, Thomas G. J.,
RA Hostin D., Houston K. A. Howland T., Wei M.-, Thomas G. J.,
RA Hostin D., Houston K. A. Howland T., Wei M. Thomas G. J.,
RA Hostin D., Houston K. A. Howland T., Wei M. Thomas G. J.,
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RA Hostin D., Houston K. Houston K. Houston K. Houston K. Howland T. Houston K. J.,
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Best Local
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
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01-MAY-2000
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01-OCT-2000
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Battachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TIEMBLIE1. 13, 01-JUN-2000 (TIEMBLIE1. 14, AXIN-RELATED PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF140243; AAF22574.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=OVARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29; Conservative
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E 706 AA; 79196 MW;
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Harvey D., Heiman T.J., Hernandez buston K.A., Howland T.J., Wei M.-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to the EMBL/GenBank/DDBJ databases
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Last annotation update)
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displacing GSK3 from axin-GSK3
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RESULT
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                                                                      Query Match
Best Local S
Matches 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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Best Local Similarity
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INTERPRO; IPR000591; -.
INTERPRO; IPR001158; -.
INTERPRO; IPR001478; -.
PFAM; PF00595; PDZ; 1.
PFAM; PF00610; DEP; 1.
PFAM; PF00778; DIX; 1.
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Q9NL46;
01-OCT-2000
01-OCT-2000
01-OCT-2000
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01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-SHEVELLED HOMOLOG.
                                                                                                                                                              Imai K., Takada N., Satoh N., Satou Y.;
*An essential role of beta-catenin in the endoderm specification ascidian embryo.*;
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AB031541; BAA92183.1;
SEQUENCE 685 AA; 75759 MW; B7E211C6D448EC95 CRC64;
                                                                                                                                                                                                                                                                                                                                   Ciona intestinalis.
Eukaryota; Metazoa; Chordata; Urochordata;
Cionidae; Ciona.
                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                NCBI_TaxID-7719;
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                 LTLGHFKEQLSKK-GNYRYYFKKASDEFACGAVFEEIWDDETVLPMYEGRIL
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ITLGDFKAAI-KKINYKFFFKSTDADF--GVVKEEVTNDKSILPLCDNRIV
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                                                                    h 37.1%;
Similarity 41.2%;
21; Conservative
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illarity 46.2%;
Conservative 10
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68917 MW;
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Last sequence update)
Last annotation updat
                                                                    Score 102.5;
Pred. No. 0.00
L4; Mismatches
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Pred. No. 1.7e-05;
0; Mismatches 15
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                                                                    DB 5;
00014;
les 13;
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RESULT

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RESULT
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Matches 21
Query Match 30.8
Best Local Similarity 33.3
Matches 15; Conservative
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INTERPRO; IPRO01158; -.
INTERPRO; IPRO01478; -.
PFAM; PF00595; PDZ; 1.
PFAM; PF00610; DEP; 1.
PFAM; PF00778; DIX; 1.
PFAM; PF00778; DIX; 1.
SEQUENCE 695 AA; 75446 MW;
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01-NOV-1999
01-NOV-1999
01-JUN-2000
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Q9QUG5;
Q1-MAY-2000 (TrEMBLrel. 13,
Q1-MAY-2000 (TrEMBLrel. 13,
Q1-OCT-2000 (TrEMBLrel. 15,
                                                                                                                                                              homolog of axin.";
Science 283:1739-1742(1999).
EMBL; AF086811; AAD24886.1;
INTERPRO; IPRO00342; .
INTERPRO; IPRO01158; .
                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

MEDLINE-99174088; PubMed=10073940;

Hamada F., Tomoyasu Y., Takatsu Y., Nakamura M., Nagai S.,

Fujita F., Shibuya H., Toyoshima K., Ueno N., Akiyama T.;

"Negative regulation of Wingless signaling by D-axin, a Dro
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscc Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Does Dishevelled-1 determine sensitivity to cerebral ischaemic in a rat model of stroke?"; Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AF143546; AAD33897.2; -. EMBL; AF143545; AAD33896.2; -. HSSP; P31016, 1BE9.
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                                                                                                                        PFAM; PF00778; SEQUENCE 743
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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NCBI_TaxID=7227;
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## SUMMARIES

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Mus musculus
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Behrens,J., Jerchow,B.-A.
Direct Submission
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                                                               r Medicine, Robert-Roessle 10, Berlin
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Sciurognathi; Muridae;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 3016)
Zhang, T., Fagotto, F., Hsu, W., Zeng, L., Gilbert, D., Copeland, N.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (16-NOV-1999) Genetics & Development, University, 701 W168th St. HHSC 1416, New York,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zhang, T. and Cost.
Direct Submission
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PEDDKEFFKKLASVHALQASELVYTYFFCGEEIPYRRMLKAQSITLGHFKEQLSKKGNY
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1487 1327	aggggtctgagcaggccctgagctcacgggatggagcaccggtccagcacccctggccc	1428 1268
1427 1267	tggaaagccgccatagtctggaggagcggctgcagcagatccgggaggatgaagaaaagg	1368 1208
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1307 1147	gocaagtgtctctacctcattttccgagaacccaccgcctgcccaaggagatgacgcctg	1248 1088
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887 727	BABACACAGCTTACATGAGTAACGGGGGGACTGGGGGAGCCTAAAGGTCTTATGTGGCTACC	828 668
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767 607	agatcggctcggtcatgtttgaccaggcacagaccgagatccaggcagtgatggaggaaa 	708 548
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2347	GCAAGTGTCCACGCGCTCCAGGCCAGTGAGCTGGTTGTCACCT	2288	Db
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N	CTGCTGGTCAGGCAGGAGCCTCACCCTTCGCCAAGCCTGGCTCCAGAAGATCACA	22	₽ 5
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Rattus no
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Submitted (08-AUG-1997) Blochemistry, Hiroshima University, School
of Medicine, 1-2-3 Kasumi, Minami-ku, Hiroshima, Hiroshima 734,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Axil, a member of the Axin family, interacts with both glycogen synthase kinase 3beta and beta-catenin and inhibits axis formation of Xenopus embryos
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Yamamoto,H., Kishida,S., Uochi,T., Ikeda,S.,
and Kikuchi,A.
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Yamamoto, H., Ikeda, S., Murai, H., Kishida, S. and Kikuchi, A.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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1. Cell. Biol. 18 (5), 2867-2875 (1998)
    960
                            TEAMS AT LON-"MSSAVLVTLLPDPSSSFREDAPPPVPGEEGETPPCOPSVGKVQ
STKPMPVSSAARRNEDGLGEFEGRASEDSPLTRMTKSLISLLGDQDGAYLFRTFLERE
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   YFKKASDEFACGAVFEEIWDDETVLPMYEGRILGKVERID® 914 c 872 g 570 t
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ਰਿਧ	251 cccagcagcagcttccgcgaggatgctccgcgggcccccggttccgggagaagaaggaggag 310	
ਲੋਵੇ	311 accccaccgtgtcagcctagtgtgggcaaggtccagtccaaccaa	
ਲੇ ਲੋ	371 tctaatgctaggcggaatgaagatggactggggggagcccgagggggggg	
ਲੇ ਤੋ	431 tcccctttgaccaggtggaccaagtctttacactccttgttgggtgaccaggatggtgca 490	
ਲੋਂ ਵੱ	491 tacctcttccggactttcctggagaaggagaaatgtgtggatacgctggacttctggttt 550 	
ਲੇ ਵੱ	551 gcttgtaatgggttcaggcagatgaacctgaaggataccaaaactttgcgagtggccaaa 610	
ਲੋਂ ਤੋਂ	611 gcaatctataagaggtacattgagaacaacagcgttgtctccaagcagctgaagccggcc 670	
ğΫ	671 accaagacctacatacgagatggcatcaaggaagcaacagatcggctcggtcatgtttgac 730	
ਲੇ ਕੋ	731 caggcacagaccgagatccaggcagtgatggaggaanatgcctaccaggtgttcttgact 790	
ğ 3	791 totgacatttacotggaatatgtgaggagtgggggggaaaacacaggottacatgagtaac 850	
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	971 aaaactcttcgggccaccgcgagtgtgagatccacgggaaacagctgaaaacggattcagg 1030 	
ਲ ਤੋਂ. <b>⊥</b>	1031 tccttcaagagaagcgacccagtcaatccttatcacgtaggttccggctatgtctttgca 1090	
_	1091 ccagccaccagcgccaacgacagcgagttatccagcgacgcactgaccgacgattccatg 1150	

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CDS	JOURNAL FEATURES Sour	JOURNAL MEDLINE REFERENCE AUTHORS	AUTHORS	SOURCE ORGANISM	VERSION KEYWORDS	AF078165 LOCUS DEFINITION ACCESSION	3	263	Qy 2771	257	Qy 2711	Db 2515	o e	Qy 2591 Db 2455	Db 2395	Qy 2531	Db 2335			Db 2215	Оу 2351	Db 2155	Оу 2291	Db 2095	Оу 2231
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DEFINITION
ACCESSION
VERSION
                           REFERENCE
AUTHORS
                                                               KEYWORDS
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1 (bases 1 to 2538)
Zhang, T., Fagotto, F., Hsu, W., Zeng, L., Gilbert, D., Cope
Jenkins, N. A., Warburton, D. and Costantini, F.
Properties of mouse Axin2 and human AXIV2: chromosomal
expression pattern, interaction with Axin and effects
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Query Match 55.6%;
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Matches 2068; Conservative
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KASDEFACGAVEEIWEDETVLDMYEGRILGKVERID*
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	1433 1325	gccgccatagtctggaggagcggctgcagcagatccgggaggatgaagaaaaggaggggt 	1374 1266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (29-AUG-2000) to the DDBJ/EMBL/GenBank databases. S Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure Analysis, Human Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:cdnai@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fay.81-3-4,40-6415.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Okamoto,S., Okitani,R., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S. NEDO human cDNA sequencing project Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; CDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'-& 3'-end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 2104)
Sugano,S., Suzuki,Y., Ota,T., Obayashi,M.,
Shibahara,T., Tanaka,T. and Nakamura,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                oligo capping; fis (full insert sequence). Homo sapiens hepatoma cell_line:HepG2 cDNA
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Mammalia; Eutheria; Primates;
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/note="cloning vector pME18SFL3"
                                                                                                                                                                                                                                                                                                                                                                                              /cell_line="HepG2"
/cell_type="hepatoma"
/clone="HEP10566"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
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AUTHORS
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ORGANISM
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                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
2E 1 (bases 1 to 191041)

Metzker, M.L., Lewis, L.R., Hume, J., Edwards, C., Harris, C.,
Dederich, D., Thomas, S., Okwuonu, G., Carlock, C., Garner, T.,
Addison, S., Pace, A., Williams, G., Bonnin, D., Brooks, A., Brown, J.,
Buhay, C., Bunac, C., Burkett, C., Chacko, J., Chen, G., Chen, Z.,
Cox, C., Davis, C., Delgado, O., Ding, Y., Dugan-Rocha, S.,
Fernandez, C., Ferraguto, D., Forcum-Tansey, J., Gill, R.,
GOTrell, J.H., Gunaratne, P., Haller, G., Hernandez, J., Hogues, M.,
HOSak, H., HOU, X., Huber, J., Jackson, L., Jia, Y., Kelly, S.,
Kovar, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Martin, R.,
Massey, E., McLeod, M. P., Mei, G., Moore, S., Morgan, M., Morris, S.,
Neal, D., Nelson, A., Nguyen, R., Nguyen, N., Oguh, M., Parish, B.,
Perez, L., Reiter, D., Say, J., Shen, H., Vasquez, L., Watlington, S.,
Williamson, A., Wrensford, G., Zhou, X., Bouck, J., Hodgson, A.,
Milliamson, R., Ryes, M., Scherer, S., Sodergren, E., Weinstock, G.,
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                                    Muzny, D.M., Rives, M., Worley, K. and Gibbs, R. Direct Submission
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Direct Submission
Direct Submission
Submitted (24-FEB-2000) Human Genome Sequencing Center, Department
Of Molecular and Human Genetics, Baylor College of Medicine, One
Raylor Plaza, Houston, TX 77030, USA
Raylor Plaza, Houston, TX 77030, USA
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On Nov 4, 2000 this sequence version replaced gl:9929587
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Center clone name: RP23-278J12
Center clone name: RP23-278J12
Center clone name: RP23-278J12
Sequencing vector: M13; L08821
Chemistry: Dye-primer Bodipy: 95% of reads
Chemistry: Dye-terminator Big Dye: 5% of reads
Chemistry: Dye-terminator Big Dye: 5% of reads
Chemistry: Dye-terminator Big Dye: 990329
Consensus quality: 158769 bases at least Q40
Consensus quality: 179280 bases at least Q30
Consensus quality: 179280 bases at least Q30
Consensus quality: 179280 bases at least Q30
Consensus quality: 179390 bases at least Q30
Estimated insert size: 180377; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; sqarose-fp estimation
Quality coverage: 3.2x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 30 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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59711: gap of unknown length
67897: contig of 8186 bp in length
67997: gap of unknown length
77929: contig of 9932 bp in length
86605: contig of 8576 bp in len
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86705: gap of

93904: contig

94004: gap of

104236: contig

104336: gap of

113241: gap of

120271: gap of

120271: gap of

120599: contig

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131969: gap of

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/db_xref="taxon:10090"
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Hirano, T., Hibi, M. and Shimizu, T.
Direct Submission
Submitted (09-SBP-1999) to the DDBJ/EMBL/GenBank databases. Toshio
                                                                                                                                                                                                                                                                                                                                                           Hirano, Biomedical research center, Osaka Univ. Med. scool, Department of Molecular Oncology; 2-2, Yamadaoka, Suita, Os 565-0871, Japan (E-mail:hirano@molonc.med.osaka-u.ac.jp, URL:http://www.med.osaka-u.ac.jp/pub/molonc/www/index.html, Tel:81-6-879-3880, Fax:81-6-879-3889)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shimizu,T., Yamanaka,Y., Ryu,S.L., Hashimoto,H., Yabe, Hirata,T., Bae,Y.K., Hibi,M. and Hiratno,T. Cooperative roles of Bozozok/Dharma and Nodal-related the formation of the dorsal organizer in zebrafish Mech. Dev. 91 (1-2), 293-303 (2000)
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Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi
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BASE COUNT ORIGIN Query Match Best Local Similarity Matches 1561; Conserv 1015 CAGTAGCTTCAGAGAAGATGACCCACGTCCACCGGTCCCAGGGGAAGAGGGTGAGACGAC 385 gcgggcctcccccgattcccctttgaccaggtggaccaagtctttacactccttgttggg ggttggcttgtccagcaaaactcttcgggccaccgcgagtgtgagatccacggaaacagc 1014 agcttacatgagtaacggggggactggggagcctaaaggtcttatgtggctacctccccac TCAGATGTTTTTGACCTCGGACATATACCTCGAGTATGTCAGAACTGGGTGCGAGAACCC GGACCAGGATGGTGCTCAACTTTTCCGGGCATACCTTGAACGCGAGAAATGTGTGGACAC tgaccaggatggtgcatacctcttccggactttccttggagagggagaaatgtgtggatac CAGCGCATCCCCGGACTCCCCTCTTGCCCGGTGGACCAAATCTTTGCATTTTCTTCTCGG GGCTGATCTTCGTTGTTCCACGGCCAGGAGGGATGAGGATGGACTTGGGGAACCTGAGGG ATGCCACCATCCCAGCAAACTGGCCATGATGAGACCGAAGGATCCTGTCAAGACCATTAT 445 CAGTCATGTGAATCCCAATGGTCTAGGAGGTCTAAAGCTGGTGTGCGGATACTTGCCGAC AGTGGGTCTGTCTGCCAAAACACTACGGTCACCACC---TCTTCGTGCTGTGGAAGCACT TTTAAATGAAGAAGAAGAGTGGAGTTGTAATGACTTTAAAGCCAAAGCTTTGGCCACTGT 1045 Conservative ø RRSDPGNPNRFTSGYSFAPATSANDSEVSSDALTDDSMSMTDSSVDAIPPYKLGSKKQ
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2095 gagcaagtccaagccccatagtgcccaaagcataagaaaga	ОУ
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                              Worley, K.C.
Direct Submission
Submitted (06-JUN-1998) Molecular and Human Genetics, Baylor
College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 184263)
                                                                                                                                                                                                                                          Muzny, D., Arenson, A.D., Adams, C., Brundage, E., Bunac, C., Carvelli, K., Chacko, J., Chen, J., Di, W., Ding, Y., Dugan, S., Durbin, J., Forcum, J., Gancha, R., Garcia, C., Goodman, M., Gorrell, J.H., Haywood, M., Hernandez, J., Jackson, L., Jin, S., Gorrell, J.H., Haywood, M., Hernandez, J., Jackson, L., Lichtarge, O., Liu, W., Logan, O., Lu, J., Ly, T., Martinez, C., Oswal, G., Perez, L., Liu, W., Logan, O., Lu, J., Ly, T., Martinez, C., Oswal, G., Perez, L., Scherer, S.E., Shen, H., Simon, M., Stovall, K., Timms, K.M., Todd, J., Vo, O., Williamson, A., Worley, K.C., Yu, W., Chinault, C., Nelson, D. and Gibbs, R.A.
Worley, K.C.
Direct Submission
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Homo sapiens Xp22 bins 16-17 BAC GSHB-531117
BAC Library) complete sequence.
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Muzny,D., Arenson,A.D., Adams,C.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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On Oct 1, 1998 this sequence version replaced gi:3482897.
Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality does not meet this standard, it will be indicated in the annotation.
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Baylor Plaza, Houston,
4 (bases 1 to 184263)
Worley, K.C.
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                                                                                                                                                                                              complement(13861. .14169)
/rpt_family="AluSx"
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complement(12591. .
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complement(11332. .
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15682. .15827
                                                                        /rpt_family="(TAAA)n"
15211. .15513
                                                                                                                                                                                                                                             /rpt_family="MLT1F"
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REFERENCE AUTHORS TITLE

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ACCESSION VERSION

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                                 agaccccaccgtgtcagcctagtgtgggcaaggtccagtccaccaacccaacctatgcccgttt
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AGACCCCACCGTGTCAGCCAGGGGTGGGCCAAGGGCCAGGTCACCAAACCCATGCCTGTCT
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/rpt_family="L2"
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complement(40374. .40
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/rpt_family="AluSp"
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22424. .22475

family="AluSx" family-"Alu"

22407

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repeat\_region

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.21702)

21626

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repeat\_region

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repeat\_region

repeat\_region

repeat\_region

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repeat\_region

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.20330)

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repeat\_region repeat\_region repeat\_region

complement (19079

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3. .19966)

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/rpt\_family="MIR" complement(18578.

.18879)

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.17678

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.18006

repeat\_region

repeat\_region

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.15996

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5, 3401"

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repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region

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\_family-"AluJb"

. 27250

repeat\_region

complement(30127...30432)
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complement(30433...30589)
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complement/25200"

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complement(25147..25299)

/rpt\_family="AluJo"
complement/2/6/ /rpt\_family="Alusx"
complement(24676...

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ACCESSION
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Metzker, M.L., Lewis, L.R., Hume, J., Edwards, C., Harris, C., Dederich, D., Thomas, S., Okwuonu, G., Carlock, C., Garner, T., Addison, S., Pace, A., Williams, G., Bonnin, D., Brooks, A., Brown, J., Buhay, C., Bunac, C., Burkett, C., Chacko, J., Chen, G., Chen, Z., Cox, C., Davis, C., Delgado, O., Ding, Y., Dugan-Rocha, S., Fernandez, C., Ferraguto, D., Forcum-Tansey, J., Gill, R., Gorrell, J.H., Gunaratne, P., Haller, G., Hernandez, J., Hogues, M., Hosak, H., Hou, X., Huber, J., Jackson, L., Jia, Y., Kelly, J., Kelly, S., Kovar, C., Liu, J., Liu, W., Loulseged, H., Lozado, R. J., Marrith, R., Massey, E., McLeod, M.P., Meil, G., Moore, S., Morgan, M., Morris, S., Neal, D., Nelson, A., Nguyen, R., Nguyen, N., Oguh, M., Parish, B., Perez, L., Reiter, D., Say, J., Shen, H., Vasquez, L., Watlington, S., Muzny, D. M., Rives, M., Scherer, S., Sodergren, E., Weinstock, G., Morrley, K., and Gibbs, R.
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                                                                                                                                                                                                  Worley, K.C.
Direct Submission

Direct Submission

Submitted (24-FEB-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Maylor Plaza, Houston, TX 77030, USA

Ravlor Plaza, Houston, TX 77030 replaced g1:9929587.
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Mus musculus chromosome 11 clone
SEQUENCE, 30 unordered pieces.
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AC024114.8 GI:11094615
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                  Center project name: MACA center clone name: RP23-278J12 Sequencing vector: M13; L08821
                                                                                                     Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
------ Project Information
Chemistry:
                                                                                                                                                             Center code: BCM
                                                                                                                                                                               Center: Baylor College
                                                                                                                                                                                                                                                                                                                                         1 to 191041)
  Dye-primer Bodipy: 95% of reads
                                                                                                   Project Information
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.) NOTE: This is a 'working draft' sequence. It currently consists of 30 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             as soon as it is
be preserved.
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Consensus quality: 158769 bases at least Q40
Consensus quality: 172780 bases at least Q30
Consensus quality: 179030 bases at least Q20
Estimated insert size: 180377; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 3.2x in Q20 bases; sum-of-contigs estimation
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                                  Eukaryota; Metazoa; Chordata; Crani Mammalla; Eutheria; Primates; Catax 1 (bases 1 to 3411)
Vasicek, T.J., Zeng, L., Guan, X.-J., Tilghman, S.M.
Two dominant mutations in the mouse transposon insertions Genetics (1997) In press
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/db_xref="taxon:10090"
/chromosome="11"
/clone="RP23-278J12"
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TLNEDEEMKCDODMDEDDGRDAPPGRLPQKILLETTAPRVSSSRYYSEGREFRYSG
REPVNPYYVNAGYALAPATSANDSEQOSLSSDADTLSLTDSSVDGIPPYRIRKOHRRE
MQESAQVNGRVULDHITRTYKVVKEVRVEQDKRAEELLHRLEAVQRTTREAEEKLEERI
KRYRKEEEGEDCDPSSGPGPCHKLPDAPAMHHFPPRLCWTWACAGLRDAHEENPESI
LDEHVQRYLRTTGRQSPGFGHRSPDSGHVAKMPVALGGAASGHGKHVVKSGAKLDAAG
LHHHRIYHHIYHHSTARRKEQVEAEATRAQSSFAMGLEPHSHGARSRGYSESVGAAP
NASDGLAHSGRKYGYACKRANKKAESGKSASTEVPGASEDAEKNQKIMONITEGEKEIE
RHRRTGHGSSGTRKPQPHENSRPLSLEHPMAGPQLKTSVQFSHLFIQDPTMFPHPAPN
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LSETETRSQRKYGGGSAQPCDSIVVAYYFCGEPLPYRTILVRGRAVTLGQFKELLTKKG
SYRYYEKKVSDEFDCGVVFEEVREDEAVLPVFEEKIIGKVEKVD*
1 1010 c 1066 g 582 t 1 others
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/db_xref="G1:2252820"
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FPLDLGASFTEDAPRPPVPGEEGELVSTDPRPASYSFCSGKGVGIKGETSTATPRRSD
LDLGYEPEGSASPTPPYLKWAESLHSLLDDQDGISLFRTFLKQEGCADLLDFWFACTG
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may inhibit embryonic axis
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/db_xref="taxon:9606"
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Pred. No. 4.9e-85;
0; Mismatches 1052; Indels 114; Gaps
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gagaggatcgactgagccttggcctcctcggcgtgcaacctgggcaagcacctcggcgtg 2	Ν	gagatctgggacgacgagacagtgctccccatgtacgaaggcaggatcctgggcaaagtg 27	N	aattacaggtattatttcaagaaggcgagtgacgaatttgcctgcggagcagtttttgag 2	TI II II I I I I I I I I I I I I I I I	N	CCGTGTGACAGCATCGTTGTGGCGTACTACTTCTGCGGGGAACCCATCCCCTACCGCACC 2		ATGGAGCTCTCCGAGACAGAGAAGATCGCAGAGGAAGGTGGGCGGGGGGGG		CGCCTGCGTCAGGCCAGCGTGCCGGCCGGGTGCTGCTGCTGCTGCTGCTGCTGCTG		AUGUSTA GENERALITA GEN	N	CCAGCTCCCAACCCCTAACCCAGCTGGAGGAGGCGCCCGACGTCTGGAGGAAGAA 2		THE CONTROL OF THE CO		tetgeeegtgegeeecaaggagaaaegagteageeggeaceatetgttggggeeagegga / 		cggcagagtccaagccccatagtgcccaaagcataagaagagctacccattggag 2		cttcctggggaagaaggagaccggtcacaggatgtctggcagtggatgttggagagtgag 2	GCGTGCAAAAGAATGCCAAGAAGGCTGAGTCGGGGAAGAGCGCCAGCACCGAGGTGCCA 1			gaggtggtaccttgccaaaacggaatgcaaagggcaccgaa			AAGGAGCAGGTGGAGGCCGAGGCCCACCCGCAGGGCCCAGAGCA 1		GCCGGCCTGCACCACCGACACGTCCACCACCACCACAGCAGCAGCAGCCCGGCCC 175	acagacgacgaagcacgttcaccaccactacatccaccaccaccaccgccgtccccaagacc 178	GGGGGTGCCGCCTCGGGGCACGGGAAGCACGTACCCAAGTCAGGGGCGAAGCTGGACGCG 169	
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                            tccacgcgctccaggccagtgagctggttgtcacctactttttctgtggagaagaaattc
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catacaggaggatgctgaaggctcaaagcttgaccctgggccacttcaaggagcagctca
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Identification of 3' UTR of Axin2

Published Only in DataBase (2000) In press

2 (bases 1 to 1863)

Nakamura,Y., Furukawa,Y. and Takahashi,M.

Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (16-DEC-2000) to the DDBJ/EMBL/GenBank databases. Yoichi Furukawa, Institute of Medical Science, Human Genome Center; 4-6-1 Shirokanedai, Minato-Ku, Tokyo 108-1639, Japan (E-mail:furukawa@ims.u-tokyo.ac.jp, Tel:81-35449-5373,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (E-mail:furukawa@ims.u-tokyo.ac.jp,
Fax:81-35449-5406)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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SLAPEDHKEPKKLAGVHALQASELVVTYFFCGEEIPYRRMLRAQSLTLGHFKEQLSKK
GNYRVYFKKASDEFACGAVFEEIWEDETVLPMYEGRILGKVERID"
447. 1863
/gene="Axin2"
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/product="conductin"
/protein_id="BAB19762.1"
/db_xref="GI:11967904"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TUMOR ILLNESSES
Patent: WO 9911780-A 7 11-MAR-1999;
BIRCHMEIER WALTER (DE); BEHRENS JUE
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 369)
Birchmeier,W. and Behrens,J.
CONDUCTINE PROTEIN AND A RELATED AGENT FOR DIAGNOSING AND TREATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unidentified
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/db_xref="taxon:32644"
82 c 99 g 8
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Pred. No. 3.9e-77;
0; Mismatches 0;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 3761)
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/protein_id="AAC53285:1"
/db_xref="GI:2252816"
/translation="LGSGSRLRBALAAAAGACWGRAGAWFQRGLYRVSSRFWRRSAA
/translation="LGSGSRLRBALAAAAGACWGRAGAWFQRGLYRVSSRFWRRSAA
CLAPPPGHGSPSRRRRBDGGPPGPRPRRFPPLDLGAWSFTEDAPRPPVPGEEGE
ERLIPLGAVSTTVLGCSAHCSLMQSPKNNVQEQGFPLDLGASFTEDAPRPPVPGEEGE
LVSTDSRPVNHSFCSGKGTSIKSETSTATPRRSDLDLGYEPESSAFTPYLAGAESL
LVSTDSRPVNHSFCSGKGTSIKSETSTATPRRSDLDLGYEPESSAFTPYLAGAESL
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KQRYVQAVMQRGRTCVRPACAPVLSVVPAVSDLELSETETKSQRKAGGGSAPPCDSIV
VGYYFCGEPIPYRTLVRGRAVTLGQFKELLTKKGSYRYYFKKVSDEFDCGVVFEEVRE
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GHVAKTAVLGGTASGHCKHVPKLGLKLDTAGLHHHRHVHHHVHHNSARPKEQMEAEVA
RRVQSSFSWGPETHGHAKPRSYSENAGTTLSAGDLPFGGKTSAPSKRNTKKAESGKNA
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YILDSNGIVSROTKPATKSFIKDCVMKOQIDPAMFDQAQTEIQSTMEENTYPSFLKSD
IYLEYTRTGSESPKVCSDQSSGSGTGKGMSGYLPTLNEDEEWKCDQDADEDDGRDPLP
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/product="Axin"
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                                        CCTTCTGGCCCCATGGCAAGTCACAAGCTGCCTTCTGTCCCAGCTTGGCACCATTTCCCA
                  ccggcagctatgaagaggacccacaaaccattttggacgaccacctctccagggtcctca
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ggtattatttcaagaaggcgagtgacgaatttgcctgcggagcagtttttgaggagatct 2669
                                                            GGGGCCGTGCTCACCCTGGGCCAGTTCAAGGAGCTGCTAACCAAGAAGGGGAGCTACA
                                                                                          aggetemangettgaeeeetgggeeaettennggagengetenagennanggganattaen 2609
                                                                                                                                                                                                                                                                                                                                                                                                               GTGTCAGGCCAGCTTGTGCACCGGTGCTGAGTGTGGTACCCAGCCGTGTCGGACTTGGAAC
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## x23369 standard; cDNA; 2825 BP. x23369; 17-JUN-1999 (first entry) Human conductin DNA. Conductin; tumour; diagnosis; treatment; beta-catenin; anti-tumour; therapy; cytoplasmic degradation; blockade; Wnt signalling pathway; Wingless signalling pathway; Adenomatous Polyposis Coli; APC; tumour suppressor; ss.

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CDS
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                                                                                                         protein_bind
                                                                                                                                                            misc_signal
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/note= "as described in Claim
2561..2713
                                           /*tag= c
/bound_molety= GSK-3beta
/note= "as described in Claim
1403..163
                                                                                                            /*tag= b
/note= "regulator of G-protein signalling region
/note described in Claim 19"
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215..2737
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes a novel human conductin protein which has anti-tumour activity. Detecting the presence or amount of conductin, at protein or nucleic acid levels, is used to disgnose tumours, while agents that (re)activate conductin are used for tumour therapy. Conductin binds to beta-catenin and induces its cytoplasmic degradation, resulting in blockade of the Wntt-Wingless signalling pathway in vertebrates. Conductin also binds to Adenomatous Polyposis Coli (APC) fragments and, in conjunction with APC, acts as a tumour suppressor.
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tive 0; Mismatches
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Query Match 89.3%;
Best Local Similarity 100.0%;
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                                                                              This invention describes a novel human conductin protein which has anti-tumour activity. Detecting the presence or amount of conductin, at protein or nucleic acid levels, is used to diagnose tumours, while agents that (re)activate conductin are used for tumour therapy. Conductin binds to beta-catenin and induces its cytoplasmic degradation resulting in blockade of the Winty Wingless signalling pathway in vertebrates. Conductin also binds to Adenomatous Polyposis Coli (APC) fragments and, in conjunction with APC, acts as a tumour suppressor.
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Nucleic acids encoding mutant and wild type Axin and oligonuclectides derived from them are useful for detecting mutations in the Axin gene and for determining whether a subject is likely to develop cancer (including breast, colorectal, gastrointestinal, esophageal, carcinomas or melanomas). The wild type Axin and homologues of Axin are useful for traeting subjects who are likely to develop cancer (thyroid carcinomas). The nucleic mutations in cancerous cells. Wild type Axin, its antisense molecule and identified compounds form pharmaceutical compositions
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Query Match 12.0%;
Best Local Similarity 51.1%;
Matches 1238; Conservative
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pred. No. 2.7e-80;
0; Mismatches 1084;
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Query Match Best Local

Score 322.2; DB 21; Pred. No. 2.1e-76;

Length 1205

0;

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sequences A77722-A78199 represent 478 cDNAs encoding proteins or CC portions of proteins which are associated with human colon tumours. CC The invention also specifically discloses 8 human colon tumour proteins CC (B11897-B11904). The nucleic acids, the polypeptides they encode, and CC antigen presenting cells (APCs, preferably dendritic cells) expressing CC such polypeptides may be used in vaccines that target tumour cells, color tumour cells, thereby inhibiting the development of CC cancer. T-cells specific for the polypeptide expressed by the APC are CC used to remove tumour cells, thereby inhibiting the development of CC cancer. T-cells specific for the polypeptide expressed by the APC are CC polypeptide can then be used to inhibit cancer development. CD4+ and/or CD8+ T-cells from a patient may be incubated with a polypeptide or the nucleic acid of the invention, or an APC expressing such a polypeptide, to cause the proliferation of specific T-cells. The T-cells can be CC cloned and then administered back to the patient to inhibit cancer development. Nucleic acids encoding the polypeptides and antibodies of a tumour protein of the invention, and therefore to determine whether concerce cells are present. Such diagnostic methods may also be used to cancer cells are progression of a cancer by repeating the processes at time intervals, and comparing the current result to previous results. The concerned concerned sequence represents a cDNA encoding a human colon tumour
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CC The invention also specifically discloses 8 human colon tumours.

CC (B11897-B11904). The nucleic acids, the polypeptides they encode, and colon tumour proteins.

CC antigen presenting cells (APC5, preferably dendritic cells) expressing.

CC such polypeptides may be used in vaccines that target tumour cells, cespecially colon tumour cells, thereby inhibiting the development of color to the polypeptide expressed by the APC are colored. The sample or the isolated Tells specific for the colored are colored to remove tumour cells from biological samples, especially blood or conserve tumour cells from biological samples, especially blood or colored to remove tumour cells from biological samples, especially blood or colored there invention, or an APC expressing such a polypeptide cor colored and then administered back to the patient to inhibit cancer colored and then administered back to the patient to inhibit cancer colored and then administered back to the patient to inhibit cancer colored and then administered back to the patient to inhibit cancer colored and then administered back to the patient to inhibit cancer colored and then administered back to the patient to inhibit cancer colored and then administered back to the patient to inhibit cancer colored and then administered back to the patient to inhibit cancer colored and then administered back to the patient to inhibit cancer colored and then administered back to the patient to inhibit cancer colored and then administered back to the patient to inhibit cancer colored and then administered back to the patient to inhibit cancer colored and then administered back to the patient to inhibit cancer colored and then administered back to the patient to inhibit cancer colored and then administered back to the patient to inhibit cancer colored and then administered back to the patient to inhibit cancer colored and then administered back to the patient to inhibit cancer colored and then administe
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                  Recombinant production of PIGI-1 allows the study of the structure, function and role in oncogenesis of the protein. PIGI-1 and nucleic acid encoding it can also be used to develop products for use in treating tumours and cancer and in the diagnosis of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                T11418;
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                                                                         Claim 3;
                                                                                                      New isolated nucleic acid encoding p53 response protein PIGI-1 used to develop prods. for the study, diagnosis and treatment of
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P-PSDB; W08133.
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               ccgacctcaagtgcaaactctcacccaccgtggtttggcttgtccagcaaaac 975
                                                       agatccaggcagtgatggaggaaaatgcctaccaggtgttcttgacttctgacatttacc
                                                                                                                                                                                                                       agctgacgaggatgaacctgcagactgccacagccacatgctttgatgcggctcagggga
                                                                                                                                                                                                                                          tacgagatggcatcaagaagcaacagatcggctcaggtcatgtttgaccaggcacagaccg
                                                                                                                                                                                                                                                                             agttcatttg-----cagtgaggcccctaaagaggtcaacattgaccatgagacccgcg
                                                                                                                                                                                                                                                                                              tcaggcagatgaacctgaaggataccaaaactttgcgagtggccaaagcaatctataaga
                                                                                                                                                                                                                                                                                                                                                                                           ggtggagagtcgttcgacctgctgctgagcagtaaaaatggagtggctgccttccacg
tcacccatccccgaggtggctgcccctgtgtgggaggcaggttctgcaaagc
                                                                                                                            tggaatatgtgaggagtgggggaaaacacagcttacatgagtaacgggggactgggga
                                                                                                                                                                  agacacgtaccctgatggagaaggactcctacccacgcttcctgaagtcgcctgcttacc
                                                                                                                                                                                                                                                                                                                                     tca---agaagatccgatcagctaccaagctggcctccagggcacaccagatctttgagg
                                                                                                           gggacctggctgcccaagcctcagccgcctctgccactctgtccagctgcagcctggacc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       e response proteins and genes - used in the detection and of diseases caused by a mutation in the CR coding region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'n
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 58.8; DB 18;
Pred. No. 1.1e-05;
0; Mismatches 272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               656
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Best Local Similarity
Matches 251; Conserv
                                                                                                                                                                                                                      This invention describes a novel isolated antibody or antibody fragment (I) which selectively binds to a polypeptide encoded by cytokine response gene 2 (CR2) and modulates CR2 activity. The products of the invention have cytostatic, anti-allergic, immunosuppressive and antimicrobial activity. The antibodies are useful as therapeutic agents for regulating cellular proliferation and differentiation and for treating all kinds of cancers, immune diseases such as allergic, autoimmune, and rheumatologic diseases, transplant rejection, and as anti-infectives for fighting viral, bacterial, parasitic and fungal infections. This sequence encodes the human CR1 protein described in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-NOV-1991;
10-AUG-1993;
27-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CR2; human; antibody; immunosuppressive; an cell differentiation;
                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                 Example IV; Column
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                                                                                                                                                                                                                                                                                                                                                                                                           Beadling
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            ggtacattgagaacaacagcgttgtctccaagcagctgaagcccgccaccacgacctaca
                                                                                      ctttcctggagagggagaaatgtgtggatacgctggacttctggtttgcttgtaatgggt 563
                                                                                                                            ggtggaccaagtctttacactccttgttgggtgaccaggatggtgcatacctcttccgga
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agttcatttg-----cagtgaggcccctaaagaggtcaacattgaccatgagacccgcg
                                                tcaggcagatgaacctgaaggataccaaaactttgcgagtggccaaagcaatctataaga
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93US-0104736.
94US-0330108.
96WO-US08992.
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/product- "CR1"
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                                                                                                                                                                                                      565 A; 621 C;
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antimicrobial; therapy; cell proliferation; treatment
on; cancer; lumune disease; rheumatologic disease;
on; anti-infective; CR1; ss.
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                                                                                                                                                       0;
                                                                                                                                                       Score 58.8; DB 21;
Pred. No. 1.1e-05;
0; Mismatches 272;
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10-AUG-1993;
27-OCT-1994;
05-JUN-1996;
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 Sequence
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                                                                                                                                                                                                                                                                                                                                          Unidentified
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 606 BP;
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This invention describes a novel isolated antibody or antibody fragment (I) which selectively binds to a polypeptide encoded by cytokine response gene 2 (CR2) and modulates CR2 activity. The products of the invention have cytostatic, anti-allergic, immunosuppressive and antimicrobial activity. The antibodies are useful as therapeutic agents for regulating cellular proliferation and differentiation and for treating all kinds of cancers, immune diseases such as allergic, autoimmune, and rheumatologic diseases, transplant rejection, and as anti-infectives for fighting viral, bacterial, parasitic and fungal infections. This sequence is presented in the Seq ID list but is not described in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CR2; human; antibody; cytokine response gene; cytostatic; anti-allergic; immunosuppressive; antimicrobial; therapy; cell proliferation; treatment cell differentiation; cancer; immune disease; rheumatologic disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cytokine response gene-related cDNA sequence (Seq
                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Column 113-116; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel antibody or antibody fragment which selectively binds polypeptide encoded by cytokine response gene 2\,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (DART-) DARTMOUTH COLLEGE
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human RATH1.1 DNA.
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04-OCT-1996;
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                                                     CDS
                                                                                                                   RATH1.1; RGS gene family: regulator of G-protein signalling; murine; regulation; activation; modulation; signal transduction; T Cell; T helper cell; treatment; autoimmune disorders; arthritis; infection; graft rejection; asthma; allergy; neoplasm; ss.
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Pred. No. 0.0015;
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roles in immune responses, cell death, cell proliferation and stimulation of cell differentiation. M68 lacks a transmembrane domain and is a secreted factor suggesting that it functions as a natural inhibitor for its ligand. The altered expression pattern of M68 in a multitude of tissues suggests that M68 may play a role in cancer by binding to its ligand and blocking apoptotic cell death induced by such a ligand. This anti-apoptopic role of M68 suggests that modulators of M68 will be useful in treatment of apoptosis related diseases such as various forms of cancer and various bone disorders. M68 nucleic acids and proteins are therefore useful for treating conditions involving atypical apoptosis and for identifying modulators of M68. Modulators of M68 are useful for treatment of cancer and other diseases associated with abnormal levels of cancer and other diseases associated with abnormal levels of

The

protein is a member of a family of proteins which n immune responses, cell death, cell proliferation

Claim 19; Page 76-78; 80pp; English osteoporosis, Alzheimer's disease

Isolated human M68 nucleic acids and proteins which are part of the tumor necrosis factor receptor (TNFR) family, useful for identifyin modulators that may be used to treat various diseases e.g. cancer,  $\frac{1}{2}$ 

identifying

apoptosis including systemic lupus erythematosus, Hashimoto's thyrolditls, Grave's disease, idiopathic myzodmia, autoimmune diabetes, thrombotic thrombotycopenic purpura, multiple scelerc liver diseases, autoimmune gastritis, ulcerative colitis,

multiple sclerosis

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05-FEB-1999;
20-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                               exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         atherosclerosis; aplastic anaemia; myelodisplastic syndromes; osteoporosis; Alzheimers disease; Parkinsons disease; stroke; myocardial infarction; human; ds.
                                                                                                                                                                                                                       P-PSDB;
                                                                                                                                                                                                                        WPI; 2000-506066/45
P-PSDB; Y97246.
                                                                                                                                                                                                                                                 Bai C;
                                                                                                                                                                                                                                                                                                            04-FEB-2000;
                                                                                                                                                                                                                                                                                                                            10-AUG-2000.
                                                                                                                                                                                                                                                                                                                                            WO200046247-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  glomerulonephritis; pulmonary fibrosis; heart failure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Grave's disease; idiopathic myxodema; autoimmune diabete thrombotic thrombocytopenic purpura; multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genomic DNA encoding M68 TNF receptor related protein.
                                                                                                                                                                                                                                                                                                                                                                                                       intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                         intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bone disease; systemic lupus erythematosus; Hashimoto's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              receptor;
                                                                                                                                                                                                                                                                 (MERI )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            iver diseases; autoimmune gastritis; ulcerative colitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tumour necrosis factor; TNF; programmed cell death;
ptor; immune response; cell differentiation; ligand;
                                                                                                                                                                                                                                                                  MERCK &
                                                                                                                                                                                                                                                                                                            2000WO-US03037
                                                                                                                                                                                                                                                                                  99US-0118902.
99US-0172754.
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/label- Exon
6004..6139
                                                                                                                                                                                                                                                                  CO INC
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/label= Intron
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                                                                                                                                                                                                                                                                                                                                                             Exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            autoimmune diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    thyroiditis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      apoptosis;
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RESULT 1
Q55750/c
ID Q55750/c
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      glomerulonephritis, pulmonary fibrosis, heart failure, atherosclerosis, aplastic anaemia, myelodisplastic syndromes, osteoporosis, Albeimers disease, Parkinsons disease, stroke, myocardial infarction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1472 cagcacccctggccctcctaccctccggcagctatgaagaggacccacaaaccattttg 1531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q55750;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q55750 standard;
                                                                                                                                                                                                           03-FEB-1994
                                                                                                                                                                                                                                                                                                                     TATA_signal
                                                                                                                                                                                                                                                                                                                                                                  CAAT_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brassica napus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plants; transformation; food crops; toxins; insects;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-JUL-1994 (first entry)
                          Baszczynski CJ,
                                                                                                                   16-JUL-1992;
                                                                                                                                                                12-JUL-1993;
                                                                                                                                                                                                                                                        WO9402619-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      infection;
                                                                      (PION-) PIONEER HI-BRED INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
nes 153; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14
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                                                                                                                      92US-0915246
                                                                                                                                                                93WO-US06541.
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485..488
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/note= "translation
438..440
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                              Bellemare G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.7%;
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Pred. No. 0.0075;
0; Mismatches 173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2589
                              Boivin R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2340 G;
                                                                                                                                                                                                                                                                                                                                                                                               start site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1417
                                   Fallis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Η,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence shows the GlIF genomic clone isolated from DNA from the roots of Brassica napus and containing a promoter sequence upstream from the translation start site. The promoter enhances gene expression in roots and can be used to confer disease resistance or immunity upon a susceptible plant root by transforming the plant with a composite gene capable of abundant expression in the gene, comprising the promoter and the gene of interest. This method can be used to transform plants, partic food crops that have roots susceptible to fungal or insect diseases. The roots of the transformed susceptible to fungal or insect diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      plants express a toxin or substance that provides immunity or resistance to the fungal or insect diseases. See also Q55749 and Q56913-5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 4; 54pp; English
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                                                                                                                                                                                                                                                                                                                                                                                          TapCS1; wheat; phytochelatin synthase; heavy metal;
transgenic plant; bioremediation; phytoremedation;
soil; groundwater; decontamination; detoxification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wheat phytochelatin synthase TaPCS1 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A89195 standard;
                                                                                                                                                                                                                                                                                   Triticum aestivum.
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                                                         /*tag=
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Pred. No. 0.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid is provided in antisense orientation, the transgenic plant is used to prevent removal of a heavy metal from soil. When the nucleic acid is provided in sense orientation, the transgenic the nucleic acid is provided in sense orientation, the transgenic plant is capable of removing a heavy metal from soil or groundwater, the heavy metal being e.g. cadmium, arsenate, arsenite, mercury, lead, zinc, nickel, bismuth, selenium, silver, gold or copper. PCS nucleic acids can also be used to decrease the level of heavy metal in the harvestable portion of a plant by expressing PCS in a non-harvestable portion and involves inhibiting expression of PCS in the harvestable portion of the plant. PCS polypeptides are used for the harvestable portion of the plant. PCS polypeptides are used for in vitro or in vivo biosynthesis of phytochelatins, and in a method of transferring a gamma-glutamylcysteine unit from 1 thiol peptide to another. The methods allow cost-effective and efficient bioremediation of contaminated soils and groundwaters, as well as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 186; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expressed in yeast. The cDNA was obtained from a screening assay designed to identify genes that conferred tolerance to cadmium. Phytochelatins play major roles in metal detoxification in plants. Phytochelatins provides PCS nucleic acids (see A89183-97) and enzymes (see B1934-38) from Arabidopsis, wheat, yeast and nematode. The nucleic acids are used to generate transgenic plants. When the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is that of cDNA encoding TaPCS1 (see B19936), a novel wheat phytochelatin synthase (PCS) that is capable of high rates of Cd2+-activated phytochelatin biosynthesis from glutathione, and which confers strong cadmium tolerance when
                                                                                                                                                                                                                                                                                                             1422 aaaaggaggggtctgagcactgagctcacgggatggagcaccggtccagcaccccc 1481
                                                                                                                                                                                                                                                                                                                                                                                                                                               1362 tggagctggaaagccgccatagtctggaggagcggctgcagcagatccgggaggatgaag 1421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-032031/04.
P-PSDB; B19936.
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                                          1542 totocagggtoctcaagacccccggctgtcaatcccctggtgtgggtcgctacagcccac 160:
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15-JUL-1999;
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          392
                                                                                                                                                                                                                                                                                                                                                                                                     272 cggcggaggggaagcggctgttcgcggaggcgctgcagggcgggaccatggagggcttct 331
tercegregreereacegeceregecaregaceceggecgregregaaggggecergge 451
                                                                                                                                     tcaacctcatctcctacttccagacgcagtcggagccggccttctgcggcctcgcctccc
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Pred. No. 0.23;
0; Mismatches 239;
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                                                                                                                                                                                                                                                           452 gctggttcgacgagtccatgctcgactgctgcgagcccctccacaaggtcaaggccgagg 511
632 cccag 636
                                                                                                                                                                        512 gcatcaccttcggcaaggtcgtctgcctcgcgcactgcgccggcgcccgtgtccagtcct 571
                                                                                                                                                                                                 tttcgactggggcaagctgcccccgtggcttgccccctccttggaggcaagagct 1721
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Search completed: June Job time: 8618 sec 7, 2001, 00:31:40

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Minimum DB
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Maximum Match 100%
Listing first 45 summaries
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Match 2. Local Similarity 47. es 251; Conservative	HET 1  Quence 1, Application US/08274318  Lent No. 5667987  ENERAL INFORMATION: APPLICANT: Buckbinder, Leonard APPLICANT: Seizinger, Bernd R. APPLICANT: Kley, Nikolai TITLE OF INVENTION: No. 5667987  CONRESSEE: Bristol-Myers Squistion CONRESSEE: Bristol-Myers Squistion CONTRY: 3005 First Avenue CITY: Seattle STATE: Washington COUNTRY: USA COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-I COMPUTER: IBM PC compatible OPERATION NUMBER: US/08/27/ FILING DATE: 11-UUL-194 CLASSIFICATION: 530 ATTORNEY/AGENT INFORMATION: NAME: BOGDEN, James M. REGISTRATION UMBER: 32,962 REFERENCE/DOCKET NUMBER: 00.001 TELECOMMUNICATION INFORMATION: TELEPHONE: 206-727-3661 TELEPHONE: 206-727-3661 STRANDEDNESS: Single TOPOLOGY: linear MOLECULE TYPE: CDNA 8-274-318-1		
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TELEFAX: 20 INFORMATION FOR
                NAME: Bogden, James M.
REGISTRATION NUMBER: 32,962
REFERENCE/DOCKET NUMBER: ON01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-727-3688
TELEFAX: 206-727-3601
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                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Kley, Nikolai TITLE OF INVENTION: NO. 5886149el NUMBER OF SEQUENCES: 3
                                                                                                                    APPLICATION NUMBER: 08/274,318
FILING DATE: 11-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: BOOGGO TEMOS M
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                                                                                                                                                                                                                    FILING DATE:
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Best Local Similarity 47.2%;
                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Smith, Kendall A. & Beadling, Carol
TITLE OF INVENTION: Nucleic Acids Encoding CR5
TITLE OF INVENTION: Vector and Transformed Cel
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LENGTH: 2383 base pair
          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                       NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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CITY: Los Angeles
STATE: California
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                                                                                                                                                           E: PRETTY, SCHROEDER & POPLAWSKI 444 South Flower St. - Suite 1900
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Version #1.25
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Pred. No. 2.5e-06;
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CURRENT APPLICATION DATA:

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US-08-461-379A-1; Sequence 1, Ap
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                                 RESULT
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Best Local Similarity
Matches 251; Conserv
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 07/796
FILING DATE: 20-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                 TCACCCATCCCGAGGTGGCTGCCCCTGTGTGGGAGGCAGGTTCTGCAAAGC
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Application US/08461379A
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ilarity 47.2%;
Conservative
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Pred. No. 2.5e-06;
D; Mismatches 272;
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US-08-461-379A-1
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Best Local Similarity 47.2%;
Matches 251; Conservative
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GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
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ATTORNEY/AGENT INFORMATION:
NAME: VIVIana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: DAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 2406 base pair
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744 agatccaggcagtgatggaggaaaatgcctaccaggtgttcttgacttctgacatttacc
                                                     528 AGCTGACGAGGATGAACCTGCAGACTGCCACAGCCACATGCTTTGATGCGGCTCAGGGGA 587
                                                                                                                             474 AGTTCATTTG-----CAGTGAGGCCCCTAAAGAGGTCAACATTGACCATGAGACCCGCG
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APPLICATION NUMBER: & 07/796,066
FILING DATE: 27-0CT-1994; 10-AUG-1993 & 20-NOV-91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
SOFTWARE: Version #1.25
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STATE: Pennsylvania
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ADDRESSEE: Ratner & Prestia
(B) STREET:One Westlakes-Berwyn
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(70 TD NO: 1:
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IBM PC compatible
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5-JUNE-1995
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Nucleic Acids Encoding CR5 Polypeptide,
Vector and Transformed Cell Thereof, an
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Pred. No. 2.5e-06;
0; Mismatches 272;
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                                                                    Query Match
Best Local Similarity
Matches 251; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: Nucleic Acids Encoding CR8 Polypeptide, Vector and
TITLE OF INVENTION: Transformed Cell Thereof, and Expression Thereof
NUMBER OF SEQUENCES: 35
                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 2406 base pair
                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: (610)407-0700
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PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: USSN 08/330,108 FILING DATE: 27-OCT-1994
APPLICATION NUMBER: USSN 08/104,736 FILING DATE: 10-AUG-1993
APPLICATION NUMBER: USSN 07/796,066 FILING DATE: 20-NOV-91.
                                                                                                                                                                                      NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/462,390B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Viviana Amzel, Ph. D. REGISTRATION NUMBER: 30,930
                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
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                                                                          Conservative
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                                                                                            Score 58.8; DB 2;
Pred. No. 2.5e-06;
                                                                          Mismatches
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                                                                            272;
                                                                                                              Length 2406;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                              TELECOMMUNICATION INFORMATION: TELEPHONE: (213) 622-7700
                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
FILING DATE: 20-NOV-91
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                        FILING DATE: 5-JUN-1 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                       SOFTWARE: Version #1.2
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Smith, Kendall A. & Beadling, Carol TITLE OF INVENTION: Nucleic Acids Encoding CRl
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                                                                                            NAME: Viviana Amzel, Ph. D. REGISTRATION NUMBER: 30,930
                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 10-AU
                                                                                                                                                                                                                                           APPLICATION NUMBER: US/
FILING DATE: 5-JUN-1995
                                                                                                                                                                                                                                                                                                     SOFTWARE:
                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Los Angeles
STATE: California
                                  TELEFAX:
                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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Version #1.25
                                                                                                                                                                                                                                                                                                                       IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRETTY,
                                                                                                                                                                                          10-AUG-1993
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                                                                                                                                                          Sequence 1, Application US/08465585C

Patent NO. 6027914

GENERAL INFORMATION:
APPLICANT: Smith, K. A., & Beadling, C.
TITLE OF INVENTION: Nucleic Acids Encoding CR6 Polypeptide, Vecto
TITLE OF INVENTION: Transformed Cell Thereof, and Expression Thereof
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
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                                                                            COUNTRY: US
ZIP: 900071
                                                                                                        CITY: Los Angeles
STATE: California
                                                                                                                                     ADDRESSEE:
                                                                                                                                                    ADDRESSEE:
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                                                                                                                                     (B)
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                                                                                                                                     STREET:
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Pred. No. 2.5e-06;
0; Mismatches 272;
    Version
      #1.25
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   RESULT 8
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; NAME/KEY:
; LOCATION:
US-08-465-585C-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
TELEPAX: (213) 4894210
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/
FILING DATE: 5-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 0
FILING DATE: 27-CCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 20-NOV-1991 ATTORNEY/AGENT INFORMATION:
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768 TCACCCATCCCCGAGGTGGCCTGCCCCTGTGTGGGAGGCAGGTTCTGCAAAGC
                                   924 ccgacctcaagtgcaaactctcacccaccgtggttggcttgtccagcaaaac 975
                                                                                                                                                                                               804 tggaatatgtgaggagtggggggaaaacacagcttacatgagtaacgggggactgggga
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                                                                                                                                                                                                                                                                                                                                                                                                    474 AGTTCATTTG-----CAGTGAGGCCCCTAAAGAGGTCAACATTGACCATGAGACCCGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Viviana Amzel, Ph. D. REGISTRATION NUMBER: 30,930 REFERENCE/DOCKET NUMBER: P66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: USSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 27-OCT-1994
APPLICATION NUMBER: USSN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
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                                                                            GGGACCTGGCCCAAGCCTCAGCCGCCTCTGCCACTCTGTCCAGCTGCAGCCTGGACC
                                                                                                                                                                                                                                        AGACACGTACCCTGATGGAGAAGGACTCCTACCCACGCTTCCTGAAGTCGCCTGCTTACC
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Pred. No. 2.5e-06;
0; Mismatches 272;
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US-08-652-446-1
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                                                                                                                                                            NFORMATION FOR SEQ ID NO:
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                                                             FEATURE:
                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 2406 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRILING DATE: 5-JUN-1995
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
08/462,390
                                                                           MOLECULE TYPE:
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CURRENT APPLICATION DATA:
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TITLE OF INVENTION:
                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: 08/461,379
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                                              NAME/KEY:
                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                NAME: Viviana Amzel, Ph. REGISTRATION NUMBER: 30,
                                                                                         TOPOLOGY:
                                                                                                                                                                                       TELEPHONE:
                                                                                                                                                                                                                    REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: FP66 40035
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/330,108 FILING DATE: 27-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: EP APP. # 96921319.8 FILING DATE: 5-JUN-1998 APPLICATION NUMBER: PCT/US/96/09194 FILING DATE: 5-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                       FILING DATE:
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                                COCATION:
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                                                                                                                  nucleic acid
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                            CDS
116..722
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VENTION: Nucleic Acids Encoding CR5
VENTION: Polypeptide, Vector and Transformed Cell Thereof, and
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Version #1.25
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29-OCT-1996
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Best Local Sim:
Matches 251;
                                                     APPLICATION NUMBER: US/OFFILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                                                                 SOFTWARE:
                             APPLICATION NUMBER: US 08/104,736 FILING DATE: 10-AUG-1993
                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                           STREET:
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Sequence 27, Application US/08463081B Patent No. 5871960 Patent No. 5871960 5837487
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                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
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                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGGACCTGGCCGAGCCTCAGCCGCCTCTGCCACTCTGTCCAGCTGCAGCCTGGACC
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                                                                                                                                                                                                                                 Los Angeles
California
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                                                                                                                                                                                                                                                                                 444 South Flower
                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                 Smith, Kendall A. & Beadling, Carol VENTION: Nucleic Acids Encoding CR5 Polypeptide, VENTION: Vector and Transformed Cell Thereof, and
                                              PatentIn Release #1.0,
Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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47.2%;
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                                                                                                                                                                                                                                                                               SCHROEDER & POPLAWSKI Flower St. - Suite 1900
US/08/463,081B
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RESULT 10
US-08-461-379A-27
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TELEFAX: (213) 489-4210
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 606 base pairs
TYPE: nucleic acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                       Sequence 27, Application US/08461379A Patent No. 5871961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 2.0%;
Best Local Similarity 51.4%;
Matches 187; Conservative
                                                                                                                                                                                                                                                           ARERL INC. CONTROL REPORTS AND REPORT OF INVENTION: Nucleic Acids Encoding CR5 Polypeptide, TITLE OF INVENTION: Vector and Transformed Cell Thereof, and
                                                                                                                                                                                                                               TITLE OF INVENTION: Nuc
TITLE OF INVENTION: Vec
TITLE OF INVENTION: Exp
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
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                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: P6
TELECOMMUNICATION INFORMATION:
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                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                   COUNTRY: UZIP: 19482
                                                                                                                                                      CITY: Valley Forge
STATE: Pennsylvania
                                                                                                                                                                                          ADDRESSEE: Ratner & Prestia
ADDRESSEE: (B) STREET:One Westlakes-Berwyn
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                                                                                                                                     USA
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OR SEQ ID NO: 27:
PatentIn Release #1.0,
Version #1.25
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Pred. No. 3.4e-06;
0; Mismatches 168;
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US-08-462-3908-27; Sequence 27, Application US/08462390B; Patent No. 5882894
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Best Local Similarity 51.4%;
                                                                                                                                                                                                        GENERAL INFORMATION:
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APPLICATION NUMBER: & 07/796,066
FILING DATE: 27-OCT-1994; 10-AUG-1993 & 20-NOV-91
ATTORNEY/AGENT INFORMATION:
                                                                                                            NUMBER OF SEQUENCES: 3
                                                                                                                              APPLICANT: Smith, K. A., & Beadling, C.
TITLE OF INVENTION: Nucleic Acids Encoding CR8 Polypeptide, Vector
TITLE OF INVENTION: Transformed Cell Thereof, and Expression Therec
NUMBER OF SEQUENCES: 35
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LENGTH: 606 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: (610)470-0700
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APPLICATION NUMBER: US/08/461,379A
FILING DATE: 5-JUNE-1995
PRIOR APPLICATION DATA:
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TELEFAX: (
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COUNTRY: UZIP: 19482
                                 CITY: Valley Forge
STATE: Pennsylvania
                                                                         ADDRESSEE: Ratner & Prestia ADDRESSEE: . (B) ST
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TOPOLOGY: lin
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                                                                       (B)
                                                                         STREET:One
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                                                                         Westlakes-Berwyn
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<u>ب</u>

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com

MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:

PatentIn Release #1.0, Version

#1

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                                                                                                              RESULT 12
US-08-463-074B-27
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Sequence 27, Application US/08463074B
Patent No. 6020155
GENERAL INFORMATION:
APPLICANT: Smith, Kendall A. & Beadling, Carol
TITLE OF INVENTION: Nucleic Acids Encoding CRI Fusion Protein,
NUMBER OF SEQUENCES: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 2.0%;
Best Local Similarity 51.4%;
Matches 187; Conservative
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APPLICATION NUMBER: USSN 08/330,108

FILING DATE: 27-OCT-1994

APPLICATION NUMBER: USSN 08/104,736

FILING DATE: 10-AUG-1993

APPLICATION NUMBER: USSN 07/796,066
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NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 606 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                           tacgagatggcatcaagaagcaacagatcggctcggtcatgtttgaccaggcacagaccg
                                                                                                                                                                                                                      tgga 807
                                                                                                                                                                                                                                                          AGACACGTACCCTGATGGAGAAGGACTCCTACCCACGCTTCCTGAAGTCGCCTGCTTACC
                                                                                                                                                                                                                                                                               agatccaggcagtgatggaggaaaatgcctaccaggtgttcttgacttctgacatttacc 803
                                                                                                                                                                                                                                                                                                                                                                                                          AGTTCATTTG-----CAGTGAGGCCCCTAAAGAGGTCAACATTGACCATGAGACCCGCG 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      606 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5-JUNE-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US/08/462,390B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 57.2; DB 2; Length 606; Pred. No. 3.4e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (213) 489-4210 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 20-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: VIVIANA AMZEI, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66 38
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/463,074:
FILING DATE: 5-JUN-1995
PRIOR APPLICATION NUMBER: US 08/104,736
FILING DATE: 10-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
ADDRESSEE: (B) STREET:
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Releasoftware: Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: CDNA
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  182 GGTGGAGAGAGTCGTTCGACCTGCTGCTGAGCAGTAAAAATGGAGTGGCTGCCTTCCACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        444 ggtggaccaagtctttacactccttgttgggtgaccaggatggtgcatacctcttccgga 503
                                                                             473
                                                                                                                                                                                 684 tacgagatggcatcaagaagcaacagatcggctcggtcatgtttgaccaggcacagaccg
                                                                                                                                                                                                                                                                 624 ggtacattgagaacaacagcgttgtctccaagcagctgaagcccgccaccaagacctaca
                                                                                                                                                                                                                                                                                                                       302
                                                                                                                                                                                                                                                                                                                                            564 tcaggcagatgaacctgaaggataccaaaactttgcgagtggccaaagcaatctataaga
                                                                                                                                                                                                                                                                                                                                                                                                    504 ctttcctggagagggagaaatgtgtgggatacgcttggacttctggtttgcttgtaatgggt 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
533
                                     804 tgga 807
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
                                                                                                  agatocaggcagtgatggaggaaaatgcctaccaggtgttcttgacttctgacatttacc 803
                                                                                                                                                        AGCTGACGAGGATGAACCTGCAGACTGCCACAGCCACATGCTTTGATGCGGCTCAGGGGA
                                                                                                                                                                                                                                       AGTTCATTTG-----CAGTGAGGCCCCTAAAGAGGTCAACATTGACCATGAGACCCGCG 412
                                                                                                                                                                                                                                                                                                                       TCA---AGAAGATCCGATCAGCTACCAAGCTGGCCTCCAGGGCACACCAGATCTTTGAGG
                                                                           AGACACGTACCCTGATGGAGAAGGACTCCTACCCACGCTTCCTGAAGTCGCCTGCTTACC
536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   606 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-NOV-91
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Best Local Similarity
Matches 187; Conserv
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ATTORNEY/AGENT INFORMATION:
NAME: VIYIAND AMZEL; Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66
TELECOMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (213) 489421 (NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/0
FILING DATE: 5-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Nucleic Acids Encoding CR
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                                                                                                                                                                                                                                                        624
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                   744
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                                                                                                                                                                                                                                                                                                                              182 GGTGGAGAGTCGTTCGACCTGCTGAGCAGTAAAATGGAGTGGCTGCCTTCCACG
                                                                                684 tacgagatggcatcaagaagcaacagatcggctcggtcatgtttgaccaggcacagaccg 743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 27-OCT-1994
APPLICATION NUMBER: USSN 08/104,736
FILING DATE: 10-AUG-193
APPLICATION NUMBER: USSN 07/796,066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
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agatccaggcagtgatggaggaaaatgcctaccaggtgttcttgacttctgacatttacc 803
                                                                                                                                            ggtacattgagaacaacagcgttgtctccaagcagctgaagcccgccaccaagacctaca 683
                                                    AGCTGACGAGGATGAACCTGCAGACTGCCACAGCCACATGCTTTGATGCGGCTCAGGGGA 472
                                                                                                                      AGTTCATTTG-----CAGTGAGGCCCCTAAAGAGGTCAACATTGACCATGAGACCCGCG
                                                                                                                                                                                         TCA---AGAAGATCCGATCAGCTACCAAGCTGGCCTCCAGGGCACACCAGATCTTTGAGG
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5. 6027914
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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Nucleic Acids Encoding CR6 Polypeptide, Vecto
Nucleic Acids Encoding CR6 Polypeptide, Vecto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USSN 08/330,108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P66 38149 (DART-050)
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                                                                                                                                                                                                                                                                                                                                                                                                Score 57.2; DB 3;
Pred. No. 3.4e-06;
0; Mismatches 168;
                                                                                                                                                                                                                                                                                                                                                                                                    168;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 606;
                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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US-08-652-446-27
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                      TELEFAX: (213) 489-47
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                          REFERENCE/DOCKET NUMBER: FP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/330,108
PRIVING DATE: 27-0CT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP App. # 96921319.8
FILING DATE: 5-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Releasing #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
TITLE OF INVENTION:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 08/465, VUL

ETLING DATE: 5-JUN-1995

PRIOR APPLICATION DATA:

PRIOR APPLICATION UNBER: 08/461,379
                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 08/462,390
FILING DATE: 5-JUN-1005
FILING DATE: 5-JUN-1005
PRIOR NUMBER: 08/462,390
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                                                                                                                                                  FILING DATE: 29-OCT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                            APPLICATION NUMBER: 08/
FILING DATE: 5-JUN-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/465,585 FILING DATE: 5-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: 5-JUN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Los Angeles
STATE: California
                                                                                                                  NAME: Viviana Amzel, REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                          TELEPHONE:
                                                                                                                                                                                          APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/08652446
                                        (213)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                            (213) 622-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRETTY, SCHROEDER & POPLAWSKI
(B) STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kendall A. & Beadling, Carol
: Nucleic Acids Encoding CR5
: Polypeptide, Vector and Transformed Cell Thereof, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Expression Thereof
                                                                                                                                                                                              08/739,523
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                                                                                                          Ph. D.
30,930
                                                                                                FP66 40035
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; STRANDEDNESS: sin; TOPOLOGY: linear; MOLECULE TYPE: cDNA US-08-652-446-27

single

Length 606;

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RESULT 15
US-08-870-815-3
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Best Local Similarity
Matches 187; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                            ATTORNEY/AGENT INFORMATION:
NAME: LAURA A. COTUZZÍ
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-074
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                          COMPUTER REALABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Levinson, Douglas A.

APPLICANT: Gimeno, Carlos J.

TITLE OF INVENTION: FOR THE TREATMENT AND DIAGNOSIS OF IMMUNE DISORDERS
                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
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                                                                                                                                        APPLICATION NUMBER: US/08/870,815
FILING DATE: 06-JUN-1997
CLASSIFICATION: 435
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CITY: New York
STATE: New Yor
             TELEPHONE: (212) 790-9090
TELEFAX: (212) 896-8864/9741
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ZIP: 10036-2711
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1155 Avenue of the Americas
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Best Local
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Search completed: June Job time: 19729 sec 7, 2001, 00:26:26

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Minimum DB
Maximum DB
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gb\_est44:\*
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em\_estro16:\*
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em\_estro18:\*

em\_estro15:\*

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gb\_est62:\*
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gb\_est57: gb\_est58: gb\_est59: gb\_est60: gb\_est61:

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gb\_est56

gb\_est48:\* gb\_est49:\*

gb\_est50:

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Result
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 140 BE872155
102 AIR 18109
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122 AW962356
17 AIZ20032
7 AA446378
149 BF521997
169 BF512711
168 BF757617
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231 CNSO1YMO
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BE872155 601446262
AIB18109 wk27c05.x
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AW962356 EST374429
AI220032 9g78h02.x
AA446378 zw58b07.r
BF521997 UI-R-Y0-a
BF521997 UI-R-Y0-a
BF521711 RC3-C1019
BF757617 MR2-C7059
AI912345 tz24c04.x
AL266841 Tetraodon
AL172875 Tetraodon
AL172875 Tetraodon
AA489718 aa43402.r
AI307112 9189f01.x
AI272864 q143h03.x
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BE872155
                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 798)

NIH-MGC http://mgc.ncl.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
                                                                                                                             http://lmage.llnl.gov
Plate: LLAM9569 row: k column:
                                                                                                                                                                                             Email: Robert_Strausberg@nih.gov Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                        Homo sapiens
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                                                                                                                                              found through the I.M.A.G.E. Consortium/LLNL at:
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
218
                                                                                                           quality sequence stop: 544.
Location/Qualifiers
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          /clone="IMAGE:3850502"
/clone_lib="NIH_MGC_65"
/clone_lib="NIH_MGC_65"
/tissue_type="adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
/site_2: Sali; Cloned unidirectionally. Primer: Oligo d
Average insert size 1.8 kb. Library constructed by Li
Technologies. "
Technologies.
                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                      AI818109
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similar to
AI818109
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 591)
                                               Homo sapiens
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                                                                                         GI:5437188
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81.7%;
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Pred. No. 1.5e-112;
0; Mismatches 130;
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Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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Location/Qualifiers
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DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 700. Std Error: 0.00
Seq primer: -40UP from Gibco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological
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/clone="IMAGE:2413544"
/clone_lib="NCI_CGAP_Brn25"
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/lab_host="DH10B"
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Pred. No. 1.6e-101;
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National Institutes of Health, Mammalian
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/clone="IMAGE:3910867"
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Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT
Average insert size 2.1 kb.
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                                                                                                                                                Assessment of gene expression patterns in a model of colon metastasis using a 19,200 element CDNA microarray Unpublished (2000)
Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
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Hegde, P., Q1, R., Abernathy, K.,
, I.E., Saeed, A.I., Sharov, V., I
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                                                                                                                         Email: johng@tigr.org
Plate: 174
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGCAGGCTAGCTGAGGTGTCGAAGCCCCCAAAGCAGCGGTGCTGTGTGGCCAGTCAGCAG
        Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 752 Std Error: 0.00
                                                                                                                                                                                                                                                          A1220032 543 bp mRNA 220032 50A clone qg78h02 x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1841331 3′ similar to TR:042400 042400 AXIN. ;, i
                                                                                                             Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 543)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Pro
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Gibco
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DEFINITION
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AA446378 548 bp mRNA
zw58b07.rl Soares_total_fetus_Nb2HF8_9w
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a 149 c 176 g 130 t 1 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
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82.7%;
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Pred. No. 5.4e-90;
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Homo sapiens cDNA clone
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AUTHORS
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SOURCE
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AA446378.1
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Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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312

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 548)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.

WashU_Merck_EST_project 1997.
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28m13 rev2 ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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/clone_tib="Soares_total_fetus_Nb2HF8_9w"
/dev_stage="8-9 weeks"
                                                   Score 375.2; DB 7; Pred. No. 1.3e-85;
48;
                                                                                                                      Length 548;
Indels
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Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: msoares@blue.weeg.uiowa.edu cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) This clone is also available through the I.M.A.G.E. Consortium at LLNL (info@image.linl.gov). IMAGE ID= 1791410 Seg primer: M13 Forward.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  451 Eckstein Medical Research Building Iowa
Tel: 319 335 8250
Fax: 319 335 9565
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University of Iowa
451 Eckstein Medical Research Building Iow
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                                   ilbrary (UI-R-Y0) was constructed as follows: PCR amplified cDNA inserts from previous library clones from which 3 ESTs had been derived were used as a driver in a hybridization with the normalized whole-eye library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DHIOB bacteria (Life Technologies) to generate the UI-R-Y0 library. This procedure has been previously described
                                                                                                                                                                                                                                              /lab_host="DHIOB (Life Technologies)"
//note="Vector: pT/T3D-Pac (Pharmacia) with a modified note="Vector: pT/T3D-Pac (Pharmacia) with a modified polylinker; Site_I: Not I; Site_2: Eco RI; The UI-R-Y0 library is a subtracted library derived from an individually tagged normalized whole-eye (minus the lens) library. The driver for the subtraction consisted of a pool of all previous libraries (UI-R-AO, UI-R-AI, UI-R-EO, UI-R-EI, UI-R-CO, and UI-R-CO). The tag is a string of UI-R-EI, UI-R-CO, and UI-R-CO). The tag is a string of oligo-of track which allows identification of the library of origin of a clone within the mixture. The subtracted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Rattus norvegicus"
/strain="Sprague-Dawley"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /dev_stage="adult"
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                     (Bonaldo,
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                 Email: asimpsoneludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl7tl=RC3&t2=RC3-CI0195-
221100-021-a10&t3=2000-11-22&t4*1)
Seq.primer: puc 18 forward
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RC3-CI0195-221100-021-a10 CI0195
BF812711
                                                                                                                                                                                                           Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
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Fax: +55-11-2707001
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                                                                                                                                                                     CACGCACTCCAAGCCAGCGAGCTGATTGTTACCTACTTTTTCTGTGGAGAAGAATTCCA
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394;
                                                                                                                                      BF757617 521 bp mRNA EST 12-JAN-2001
MR2-CT0596-091100-001-f12 CT0596 Homo sapiens cDNA, mRNA sequ
BF757617
BF757617.1 GI:12105621
                                                                                           Eukaryota;
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Location/Qualifiers
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/db_xref="taxon:9606"
/clone_lib="CI0195"
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                                                                                           Metazoa;
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                                                                            Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 1.1e-83;
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Query Match
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                 tgtccatgacggacggtagatggagtccctccttaccgcatggggagtaagaaac
                                                                                                       caccagccaccagcgccaacgacagcgagttatccagcgacgcactgaccgacgattcca
                                                                                                                                                                                          gtccttcaagagaagcgacccagtcaatcc-ttatcacgtaggttccggctatgtctttg
                                                                                                                                                                                                                                                                                 caaaactcttcgggccaccgcgagtgtgagatccacggaaaacagctgaaaacggattcag
                                                                                   CACCAGCCACCAGCGCCAACGAAAGTGAGATATCCAGTGATGCGCTGAGGGATGATTCCA
                                                                                                                                                                      GTCCTTCAAGAGGAGCGATCCTGTTAATCCTTTATCACATAGGTTCTGGCTATGTCTTTG
                                                                                                                                                                                                                                                         CAAAACTCTGAGGGCCACGGCGAGTGTGAGGTCCATGGAAAGTGTTGACAGTGGATACAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR2&t2=MR2-CT0596-
091100-001-f12&t3=2000-11-09&t4=1)
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Simpson A.J.G
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/clone_lib="CT0596"
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/db_xref="taxon:9606"
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Pred. No. 1.7e-82;
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                                     cagagagtccgctgcctctgtcctgggggaacagattattattgctactccaaatgcaaa 1876
accttgccaaaacggaatgcaaagggcaccgaaccgggtcttgcactgtcggccagggat 1996
                                                                                                                 CAGCGGGTGCACTGCTTCTGCCCTGGGGGCAGCGAGTATTACTGCTACTCGAAATGCAAA
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similar to
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CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 2487 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 414.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-*Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT Average insert size 1.85 kb. Life Technologies catalog # 11539-012"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   adenocarcinoma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2289510"
/clone_lib="NCI_CGAP_Ut2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="DH10B"
/note="no---
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83.7%;
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Pred. No. 5.4e-77;
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Roest-Crollius, Fizames, C., Wincker, P., Brottier, P., Quetle Saurin, W. and Weissenbach, J.
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                                 GSS; genome survey sequence.
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Tetraodon nigroviridis
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Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Eurypterygii; Ctenosquamata; Acanthomorpha; Euacanthomorpha;
Holacanthopterygii; Acanthopterygii; Percomorpha;
Tetraodontiformes; Tetraodontoidei; Tetraodontidae; Tetraodon.
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Unpublished (1997)
Contact: Wilson RK
Washington Train
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This clone is available royalty free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 380.
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aa43d02.rl Soares_NhHMPu_S1 Homo saplens cDNA clone IMAGE:823683
5', mRNA sequence.
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Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                               /note-*Organ: mixed (see below); Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHPU, and fetal heart NbHHJ9W) were mixed, and so circles NbHPU, and so circles
                                                                                                                                                                                                                                                                                                                                                                                                                         pregnant uterus"
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                                                                                                                                                                                                                                                                                                                                                                                                     Tel: (301) 496-1550

Email: Robert_Strausberg@nih.gov

Email: Robert_Strausberg@nih.gov

This clone is available royalty-free through LLNL;

IMAGE Consortium (info@image.lhnl.gov) for further i

Insert Length: 534 Std Error: 0.00

Seg primer: -40UP from Gibco

High quality sequence stop: 471.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1997)
Contact: Robert Strausberg,
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1 (bases 1 to 487)
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National Cancer Institute, Cancer Genome Anat
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/note="Organ: mixed (see below); Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanncyte 2NbHM, pregnant uterus NbHPU, and fetal heart NbHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."
                                                                                                                                                                                                                                                                /tissue_type="Pooled human melanocyte, pregnant uterus"
                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
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/clone="IMAGE:1879513"
                                                                                                                                                                                                                                           /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                       /clone_lib="Soares_NhHMPu_S1"
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ORIGIN

Query Match Best Local Sim Matches 403;

Similarity

11.5%;

Score 325.6; Pred. No. 7.2 Mismatches

5; DB 1 7.2e-73; 18;

Length

487;

7;

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Conservative

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                                                         This clone is available royalty-free through LLNL; IMAGE Consortium (info@image.llnl.gov) for further i Insert Length: 740 Std Error: 0.00 Seq primer: -40UP from Gibco
                                                                                                                    Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                       Mammalia; Eutheria; Primates; Catarrhini; Hon 1 (bases 1 to 460) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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AI419942.1
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tg40dll.xl Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
IMAGE:2111253 3' similar to TR:042400 042400 AXIN. ;, r
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                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                        National Cancer Institute, Cancer Genome
                          quality sequence stop: 421.
Location/Qualifiers
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Primates;
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Catarrhini;
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Search completed: June Job time: 15523 sec

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:9606"
/clone="IMAGE:2111253"
/clone_lib="Soares_NFL_T_GBC_S1"
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PATENT: WO 9911780-A 7 11-MAR-1999;
BIRCHMEIER WALTER (DE); BEHRENS JUERGEN (DE)
Location/Qualifiers
1. 369
1. 369
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                                                                                                                                                                                                                                                                                                                                                       unclassified.

1 (bases 1 to 369)

Birchmeier, W. and Behrens, J.

CONDUCTINE PROTEIN AND A RELATED AGENT FOR DIAGNOSING AND TREATING
                                                                                                                                                                                                                                                                                                                                                                                                                                    unidentified. unidentified
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atccaggcagtgatggaggaaatgcctaccaggtgttcttgacttctgacatttacctg 360	cyagatygcatcaayaagcaacayatcygctcygtcatytttyaccayycacayaccyag 300 	tacattgagaacaacagcgttgtctccaagcagctgaagcccgccaccaagacctacata 240 	aggcagatgaacctgaaggataccaaaactttgcgagtggccaaagcaatctataagagg 180 	ttcctggagagggagaaatgtgtggatacgctggacttctggtttgcttgtaatgggttc 120 	tggaccaagtctttacactccttgttgggtgaccaggatggtgcatacctcttccggact 60 	Match 100.0%; Score 369; DB 9; Length 2825; ocal Similarity 100.0%; Pred. No. 4.4e-94; s 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	/organism="unidentified" /db_xref="taxon:32644" 703 a 815 c 813 g 494 t	Patent: WO 9911780-A 6 11-MAR-1999; BIRCHMEIER WALTER (DE); BEHRENS JUERGEN (DE) Location/Qualifiers 1. 2825	I (bases 1 to 2825)  1 (bases 1 to 2825)  Birchmeler, W. and Behrens, J.  CONDUCTINE PROTEIN AND A RELATED AGENT FOR DIAGNOSING AND TREATING TIMOR TILLNESSES	unidentified unidentified	A98521 2825 bp DNA PAT 26-JAN-2000 Sequence 6 from Patent WO9911780. A98521 A98521 GI:6781607	GAATATGTG 369	gaatatgtg 369	ATCCAGGCAGTGATGGAGGAAAATGCCTACCAGGTGTTCTTGACTTCTGACATTTACCTG 360	atccaggcagtgatggaggaaaatgcctaccaggtgttcttgacttctgacatttacctg 360	cgagariggcatcaagaagcaacagatcggctcggtcatgtttgaccaggcacaggaccgag 300	TACATTGAGAACAACAGCGTTGTCTCCAAGCAGCTGAAGCCCGCCAACAAGACCTACATA 240	tacattgagaacaacagcgttgtctccaagcagctgaagcccgccaccaagacctacata 240	AGGCAGATGAACCTGAAGGATACCAAAACTTTGCGAGTGGCCAAAGCAATCTATAAGAGG 180	aggcagatgaacctgaaggataccaaaactttgcgagtggccaaagcaatctataagagg 180	TTCCTGGAGAGGAGAAATGTGTGGATACGCTGGACTTCTGGTTTGCTTGTAATGGGTTC 120

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Behrens, J., Jerchow, B.-A., Wurtele, M., Grimm, J., Asbrand, C., Wirtz, R., Kuhl, M., Wedlich, D. and Birchmeier, W. Functional interaction of an axin homolog, conductin, with beta-catenin, APC, and GSK3beta Science 280 (5363), 596-599 (1998)
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PPLTPPNTLAQLEEACRRLAEVSKPQKQRCCVASQQRDRNHSAAGQAGASPFANPSLA
PEDHKEPKKLASVHALQASELVVTYFFCGEEIPYRRMLKAQSLTLGHFKEQLSKKGNY
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TKHVHHHYIHHHAVPKTKEEIEAEATQRVRCLCPGGTDYYCYSKCKSHPKAPEPLPGE
QFCGSRGGTLPKRNAKGTEPGLALSARDGGMSSAAGGPQLPGEEGDRSQDVWQMMLES
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SDPVRPYHVGSGYVFAPATSARDSELSSDALTDDSRMYDSSVOGVPFVRMGSKKOLQ
REMHRSVKANGQVSLPHFPRTHILPKENTFVEPAAFAREIISRLEKIKLELESRHSLE
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KCVDTLDFWFACNGFRQMNLKDTKTLRVAKAIYKRYIENNSVVSKQLKPATKTYIRDG
IKKQQIGSVMFDQAQTEIQAVMEENAYQVFLTSDIYLEYVRSGGENTAYMSNGGLGSL
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/translation="MSSAVL/TLLPDPSSSFREDAPRPPVPGEEGETPPCQPSVGKVQ
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/db_xref="taxon:10090"
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Submitted (24-FEB-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA ON NOV 4, 2000 this sequence version replaced gi:9929587.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fernandez,C., Ferraguto,D., Forcum-Tansey,J., Gill,R.,
Gorrell,J.H., Gunaratne,P., Haller,G., Hernandez,J., Hogues,M.,
Hosak,H., Hou,X., Huber,J., Jackson,L., Jia,Y., Kelly,J., Kelly,S.,
Kovar,C., Liu,J., Liu,W., Loulseged,H., Lozado,R.J., Martin,R.,
Kovar,C., Liu,J., Liu,W., Loulseged,H., Lozado,R.J., Martin,R.,
Massey,E., McLeod,M.P., Mei,G., Moore,S., Morgan,M., Morris,S.,
Meal,D., Nelson,A., Nguyen,R., Nguyen,N., Oguh,M., Parish,B.,
Nel,D., Nelson,A., Nguyen,R., Nguyen,N., Oguh,M., Parish,B.,
Perez,L., Reiter,D., Say,J., Shen,H., Vasquez,L., Watlington,S.,
Williamson,A., Wrensford,G., Zhou,X., Bouck,J., Hodgson,A.,
Muzny,D.M., Rives,M., Scherer,S., Sodergren,E., Weinstock,G.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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AC024114.8 GI:11094615
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                                Center project name: MACA
Center clone name: RP23-78012
Center clone name: RP23-78012
Center clone name: Statistics
Sequencing vector: M13; L08821
Chemistry: Dye-primer Bodiby: 95% of reads
Chemistry: Dye-terminator B1g Dye: 5% of reads
Chemistry: Dye-terminator B1g Dye: 5% of reads
Assembly program: Phrap: version 0.990329
Consensus quality: 1780 bases at least Q40
Consensus quality: 179030 bases at least Q30
Consensus quality: 179030 bases at least Q30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center: Baylor College of Medicine Center code: BCM
Web site: http://www.hgsc.bcm.tmc.
                                                                                                                                                                                                                                                                                                                                                                                                                                  ------ Project Information
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180377; sum-of-contigs estimation
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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NOTE: This is a 'working draft' sequence. It currently consists of 30 contigs. The true order of the pieces is not known and their order in this sequence record is
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                                                                                                                                                                                   Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertek
Eukaryota; Metazoa; Chordata; Craniata; Vertek
Mammalia; Eutheria; Rodentia; Sciurognathi; M.
1 (bases 1 to 3016)
Zhang, T., Fagotto, F., Hsu, W., Zeng, L., Gilbert
Jenkins, N.A., Warburton, D. and Costantini, F.
Properties of mouse Axin2 and human AXIN2: chn
expression pattern, interaction with Axin and
                                                                                                                                                                                                                                                                                                               AF205889
AF205889.1
                                                                                                                                                                                                                                                                                                                                         Mus musculus Axin2 (Axin2) mRNA, complete cds
                                                                                                  University,
                                                                                                   Submitted (16-NOV-1999) Genetics & Development, University, 701 W168th St. HHSC 1416, New York,
                                                                                                                         Zhang, T. and Costantini, F. Direct Submission
                                                                                                                                                             Unpublished
                                                                                                                                                                                                                                                                                                                                                    AF205889
                                                                                                                                                                            axis formation
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/organism="Mus musculus"
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a 43523 c 42989 g 51816
                                                                                                                                                                                                                                                                                                                                                                                                               111053
               /map="between
1. .3016
/gene="Axin2"
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/chromosome="11"
                                                                                    Location/Qualifiers
                                                              organism="Mus musculus"
                                                                                                  701 W168th St. HHSC
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Pred. No. 6.7e-94;
                          Wnt3 and Pkca"
                                                                                                                                                                                                                                                                                                                                                       mRNA
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Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus

03-JAN-2000

111062

Gilbert, D.,

Copeland, N.G.,

chromosomal location, and effects on embryon

embryonic

Columbia NY 10032,

USA

FEATURES

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KEYWORDS
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Matches 367
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5 GAATATGTG 654
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367; Conser
                                                        Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; F
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                               AF017757 3216 bp mRNA Rattus norvegicus GSK-3beta interacting
1 (bases 1 to 3216)
Yamamoto, H., Kishida, S., Uochi, T.,
                                                                                                                                                                                                                               AF017757.1
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REMHRSYKANGGVSLPHFPRTURLPKEMTPVERAFAAELISRLEKLKLELEESRHSLE
ERLQQIREDEEKEGSEQALSSROBAFWQHFLALLPSGSYEEDPQTILDDHLSRYLKTP
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RYYFKKASDEFFACGAVFEEINDDETVLPMYEGRILGKVERID*

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/translation="mSSAVLVTL"
/transla
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/codon_start=1
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Pred. No. 3.6e-93;
0; Mismatches 2
  Ikeda,S.,
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  Koyama,S.,
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                                                                                      Euteleostomi;
Murinae;
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                                                                                                                                                                                                                                             aggcagatgaacctgaaggataccaaaactttgcgagtggccaaagcaatctataagagg
and Kikuchi,A.

Axil, a member of the Axin family, interacts with both glycogen synthase kinase 3beta and beta-catenin and inhibits axis formation of Xenopus embryos

Mol. Cell. Biol. 18 (5). 2867-2075 (1997)
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Yamamoto,H., Ikeda,S., Murai,H., Kishida,S. and
Direct Submission
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STKPMPVSSNARRNEDGLGEPEGRASPDSPLTRWTKSLHSLLGDQDGAVLFRTFLERE
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LTPPNTLAQLEEACRRLAEVSKPQKQRCVASQQRDRNHPATGGAGPTSFSNPSLASE
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YFKKASDEFACGAVFEEIWDDETVLPMYEGRILGKVERID"
1 914 c 872 g 570 t
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/db_xref="taxon:10116"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
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Pred. No. 5.3e-85;
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                       121 aggcagatgaacctgaaggataccaaaactttgcgagtggccaaagcaatctataagagg 180
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                                                                                                                                                                                                    1 tggaccaagtctttacactccttgttgggtgaccaggatggtgcatacctcttccggact 60
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                                                                                                                                                                               TGGACCAAGTCCTTACACTCCTTATTGGGCGATCAAGACGGTGCTTACCTGTTCCGAACT 397
  AGGCAGATGAACCTGAAGGATACCAAAACTTTACGAGTAGCCAAAGCGATCTACAAAAGG
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AF205888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (16-NOV-1999) Genetics & Development, University, 701 W168th St. HHSC 1416, New York, Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zhang,T., Fagotto,F., Hsu,W., Zeng,L., Gilbert,D., Copeland,N.G., Jenkins,N.A., Warburton,D. and Costantini,F. Properties of mouse Axin2 and human AXIN2: chromosomal location, expression pattern, interaction with Axin and effects on embryonic
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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DPVNPYHIGSGYVFAFATSANDSEISSDALTDDSMSMTDSSVGI FPYRYGSKKQLQR
EMHRSYKANGRVSLPHFFATHLLPKEKMFPVEPBAFTFALELISRHSLEE
RLQQIREDEEREGSELTLNSREGAPTQHPLSLLPSGSYEEDPQTILDDHLSRVLKTPG
CQSPGVGRYSPRSRSPDHHHHHHSQYHSLLPPGGKLPPAASPGACPLLGGKGFVTKQ
TTKHYHHAY LHHHAVPKTKEILAEAATQRVHGCPGGGSSYCYSKCKSHSKAPETMPS
EQPGAQSTKKAYPLESARSSPGERASRHLMGGNSGHPRTTPRAHLFTQDPAMPSLTP
BYTLAHLEEACRRLAEVSKPFKQRCCVASQQRDRNHSATVQTGATPFSNPSLAPEDHK
EPKKLAGVHALQASELTVTYFFCGEEITPYRRMLKAQSLTLGHFKEQLSKKGNYRYYFK
KASDEFACGAVFEEIMEDETVLPMYEGRILGKVERID"
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CVDTLDFWFACNGFROMNLKDTKTLRVAKAIYERYIENNSIVSKQLKPATKTYIRDGI
KKQQIDSIMFDQAQTEIQSVMEENAYQMFLTSDIYLEYVRSGGENTAYMSNGGLGSLK
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/db_xref="taxon:9606"
/chromosome="17"
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/note="similar to ESTs 823683 and 446378"
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AF078165.1 GI:4454790
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Genomics 55 (3), 341-344 (1999)
99168905
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Direct Submission
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mmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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ERLOQJ REDEBREGSELTLNSREGAPTOH PLSLLPSGS YEEDPOI I LDDHLSRVLKTP
GCQSPGVGRYSPRSRSPDHHHHHSQYHSLLFPPGGKLPPAAASPGACELLGGKGFVK
QTKHYHHHYLHHHAVKTKEEL EALBATQRVHCFCPGGSEYYCYSKCKSHSKAPETMP
SEQFGGSRGSTLPKRNGKGTEPGLALPAREGGAPGAALQLFREEGDRSQDWQWML
                     GNYRYYFKKASDEFACGAVFĒEIWEDETVLPMYEGRILGKVERID"
1 838 c 883 g 582 t
                                                          ESEROSKPKPHSAOSTKKAYPLESARSSPGERASRHHLWGGNSGHPRTTPRAHLFTOD
PAMPPLTPPNTLAOLEEACRRLAEVSKPPKORCCVASQORDRNHSATVOTGATPPSNP
SLAPEDHKEPKKLAGVHALQASELVVTYFFCGEEIPYRRNLKAOSLTLGHFKEOLSKK
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                                                                                                                                                                                                                                                                                                                                                     /product="conductin"
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/chromosome="17"
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Query Match Best Local Similarity

83.5%; 89.7%;

Score 308.2; DB 88; Pred. No. 7.7e-77;

Length 3072;

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Worley,K.C.

Direct Submission

Submitted (07-OCT-1998) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Oct 1, 1998 this sequence version replaced gi:3482897.
                                                                                               Submitted (01-OCT-1998) Human Genome Sequencing of Molecular and Human Genetics, Baylor College Baylor Plaza, Houston, TX 77030, USA (bases 1 to 184263)
                                                                                                                                                                                               2 (bases 1 to 184263)
Worley,K.C.
Direct Submission
Submitted (06-JUN-1998) Molecular and Human Genetics, Baylor
College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 184263)
                                                                                                                                                                                                                                                                                                            Muzny,D., Arenson,A.D., Adams,C., Brundage,E., Bunac,C.,
Carvelli,K., Chacko,J., Chen,J., Di,W., Ding,Y., Dugan,S.,
Durbin,J., Forcum,J., Ganesh,R., Garcia,C., Goodman,M.,
Gorrell,J.H., Haywood,M., Hernandez,J., Jackson,L., Jin,S.,
Kampal,R., Karpathy,S., Kovar,C., Leal,B., Li,Y., Lichtarge,O.,
Llu,W., Logan,O., Lu,J., Ly,T., Martinez,C., Oswal,G., Perez,L.,
Rashid,N.D., Rowland,K., Saves,L., Scherer,S.E., Shen,H.,
Simon,M., Stovall,K., Timms,K.M., Todd,J., Vo,O., Williamson,A.,
Worley,K.C., Yu,W., Chinault,C., Nelson,D. and Gibbs,R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC004805 184263 bp DNA PRI Homo sapiens xp22 bins 16-17 BAC GSHB-531I17 BAC Library) complete sequence.
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1 (bases 1 to 184263)
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Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality does not meet this standard, it will be indicated in the annotation.

Adrian The repeat regions shown were identified using RepeatMasker by

Sequence similarities were identified using Powerblast by Jinghui

were canonical splice junctions that across the splice junctions. Exon/Intron boundaries of identified genes were chosen if there maintained sequence continuity

repeat\_region source repeat\_region /rpt\_famil 14538. .14 4032. /rpt\_family="MIR" 17679. .17977 /rpt\_family="AluS) /rpt\_family="MLT1F"
complement(13861..14169)
/rpt\_family="Alusx" /rpt\_famil 13339. .13 /rpt\_famil 8392. .869 complement(17311.
/rpt\_family="L2" /rpt\_t 15211. /rpt\_family="AluSx" 7129. .7410 /rpt\_family="GC\_rich"
5406. .5436 complement(12591. /rpt\_family="AluSx"
complement(11332. . /organism="Homo sapiens" /db\_xref="taxon:9606" /clone="GSHB-531117" /rpt\_family="AluJ" /rpt\_family-"AluSg" /rpt\_fam: rpt\_family="Alusx" /rpt\_family="(CCCCG)n" /rpt\_family="GC\_rich" /chromosome="xp22-16-17" rpt\_family="(GAAA)n" rpt\_famil rpt\_family="GC\_rich" \_family-"Alur" \_famil \_famil \_famil famil \_famil ly-"AluSg"
2219 Qualifiers y="L1PA9" y-"AluJ" y="AluSq" y="MIR" y="(CA)n" y-"(TAAA)n" y="AluSq" y="AluSp" /-"AluSq" .12905)

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complement(30433. .30589)
/rpt_family="MLT1AA"
complement(30640
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complement(19079. .19360.
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19493. .19800
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/rpt_family="LTR16C"
complement(33298..33423)
/rpt_family="MIR"
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21967. 22000
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complement(40374. .40687)
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41491. .41619
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39771
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complement(35781. .35902)
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complement(29910. .30126)
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complement(20034.
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2 (bases 1 to 3485)
2 (bases 1 to 3485)
Birect Submission
Submitted (09-SEP-1999) to the DDBJ/EMBL/GenBank databases. Toshio
Hirano, Biomedical research center, Osaka Univ. Med. scool,
Department of Molecular Oncology; 2-2, Yamadaoka, Suita, Osaka
                                                                                           Shimizu,T., Yamanaka,Y., Ryu,S.L., Hashimoto,H., Yabe,T.,
Hirata,T., Bae,Y.K., Hibi,M. and Hirano,T.
Cooperative roles of Bozozok,Dharma and Nodal-related proteins
the formation of the dorsal organizer in zebrafish
Mech. Dev. 91 (1-2), 293-303 (2000)
                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi (ypriniformes; Cyprinidae; Rasborinae; Danio.
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complement(43274..4
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AF009012 3156 bp n
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GEEIPKRMMKTHSLTLGHFKEQLRKKGNYRYFFKRASDEFECGAVFEEVWDDCTVLP
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GGLKLVGGYLFTLNEEEEWSCNDFKARALATVGLSAKTLRSPFDLRAYEALEKGRSY
RRSDDGNPNRFTSGYSFAPATSANDSEVSSDALTDDSMSMTDSSVDAIPPYKLGSKYQ
LQREMQRNMRNNGQVSLPPFPRTRRPPKEMTPVEPAAFAAQLIARLERLKREQETMSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation-"MNRTLTDPMVSSFREDDPRPPVPGEEGETTCHHPSKLAMMRPKD
PVKTIMADLRCSTARRDEDGLGEPEGSASPDSPLARWTKSLHFLLGDQDGAQLFRAYL
EREKCVDTLDFWFACNGFRQMDLKDTKTHRVAKAIYKRYIENNSIVAKQLKPATKTFI
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297. .2735
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/db_xref="GI:7229080"
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/db_xref="taxon:7955"
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                                                                 aggcagatgaacctg-----aaggataccaaaactttgcgagtggccaaagcaatc 171
                                                                                                                                                                                                                                  ttcctggagagggagaaatgtgtggatacgctggacttctggtttgcttgtaatgggttc 120
                                                                                                                                                                                                                                                                                             TGGGCCGAGTCGCTGCACTCCTTGCTGGACGATCAAGACGGTATCAATCTCTTCAGGACT 569
                                                                                                                                                                                                                                                                                                                 tggaccaagtctttacactccttgttgggtgaccaggatggtgcatacctcttccggact 60
                                           TACAAAAAGTACATTCTCGACAACAACGGCATTGTGTCCCGGCAGATCAAACCAGCCACA
                                                                                                                             AGGAAGCTGGAGCCGTGTGTCCCAATGAGGAAAAAAAGACTCAAACTGGCAAAAGCCATT
                                                                                                                                                                                                                TTCCTGAAACAGGAGGACTGTGCGGATCTGCTGGACTTCTGGTTTGCCTGCAGCGGCTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gallus gallus
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1 (bases 1 to 3156)
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TQRATSTRYSGSGTGKGLPGYLPTLNEDEEMKCDQDTEPEASRDSAPSSRLTQKLLLETA
TQRATSTRYSGSGASGASAPSWREDVNPY VNTGYAMAPATSANDSEQQSMSSDADTMS
LTDSSJDGIPPYRLTKKQHRREMGESAKANGRYVPLPHIPRTYRMYRDIHLEPEKKFALEL
INRLEEVQKEREAEEKLEERLKRVRAEEEGEDADISGPSVISHKMPSAQPFHHFAPR
YSEMGCAGMQMRDAHEENPESILDEHVQRVMKTPGCOGSGPGFHRSPKCPASPESGHLGK
LSGTLGTIPPGHGKHTTYKSGMKLDAANLYHHKHHYWHHHHHSMMKPREDIEARATQRV
QNSFAMNVDSHNYATKSRNVSENLGMAPVPMDSLGYSGKASLLSKRNIKKTDSGKSDG
ANYEMPGSPEDVERNQKILOWIIEGEKEISRHKKTNHGSSGVKKQLSHDMVRPLSIER
PVAVHPWVSAQLRNVVQPSHPFIQDPTMPPNPAPNPLTQLEEARRRLEEEERAGKLP
LKQRLKPQKRPGSGASQDCENITVAYYFCGEPIPYRTLVKGRVVTLGQFKELLTKKGN
YRYYFKKVSDEFDCGVYFEEVREDDTILPIFEEKIIGKVEKID*
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KPATKSFIKDCVMKLQIDPDMFDQAQTEIQCMIEDNTYPLFLKSDIYLEYTRTGGESP
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YSSKSDAVRNETSTATPRRSDLDLGYEPEGSASPTPPYLKWAESLHSLLDDQDGINLF
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/db_xref="GI:2252818"
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/db_xref="taxon:9031"
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Neognathae; Galliformes; Phasianidae;
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Vasicek, T.J., Zeng, L., Guan, X.-J., Zhang, T., Costantini, F. and
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                                REPVNPYYVNÄGYALAPATSANDSEQQSLSSDADTLSLTDSSVDGIPPYRIRKQHRRE
MQESAQVNGRVPLPHIPRTYRVPKEVRVEPQKFAEELIHRLEAVQRTREAEEKLEERL
                                                                         LDLGYEPEGSASPTPPYLKWAESLHSLLDDQDGISLFRTFLKQEGCADLLDFWFACTG
FRKLEPCDSNEEKRLKLARAIYRKYILDNNGIVSRGTRPATKSET KGCIMKQLLDPAM
FDQAQTEIQATMEENTYSPEFLKSDIVLEYTRFGSESPKVCSDQSSGSGTGKGLSGYLD
TLNEDEEWKCDQDMDEDDGRDAAPPGRLPQKLLLETAAPRVSSSRRYSECREFRYGSW
                                                                                                                                                  /protein_id="AAC51624.1"
/protein_id="AAC51624.1"
/db_xref="G1:2252820"
/translation="GPGSRHHRARDRLIHFGAVSTDVLGCSAHCSLTQSPKMNTQEQG
/translation="GPGSRHHRARDRLIHFGAVSTDVLGCSAHCSLTQSPKMNTQEQGFTaranslation="GPGSRHHRARDRLIHFGAVSTDVLGCSAHCSLTQSPKMNTQEQGFT"
FPLDLGASFTEDAPRPPVPGEEGELVSTDPRPASYSFCSGKGVVIKGETSTATTPRRSD
                                                                                                                                                                                                                                                                        /note="contains RGS domain
may inhibit embryonic axis
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adults"
                                                                                                                                                                                                                                                                                                                                                                                      /gene="AXIN"
/note="Fused
                  KRVRMEEEGEDGDPSSGPPGPCHKLPPAPAWHHFPPRLCWTWACAGLRDAHEENPESI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /chromosome="16"
/map="16p13.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
LDEHVQRVLRTTGRQSPGPGHRSPDSGHVAKMPVALGGAASGHGKHVPKSGAKLDAAG
                                                                                                                                                                                                                                /product="axin"
                                                                                                                                                                                                                                                        /codon_start=2
                                                                                                                                                                                                                                                                                             /function="may inhibit embryonic axis formation"
/note="contains RGS domain and Daughterless similarity;
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258; Conserv
                                             clonerequest@sanger.ac.uk

On Apr 8, 1998 this sequence version replaced gi:2578104.

IMPORTANT: This sequence is the entire insert of clone 415C1.

true left end of clone 415C1 is at 1 in this sequence. The true right end of clone C333B10 is at 8634.

The true left end of clone C367G8 is at 23683.

415C1 is from a 400kb clone contig on 16p.

415C1 is from a 400kb clone contig on 16p.
Higgs D.R., Flint J. unpublished. MRC Molecular Haematology Unit.
Institute of Molecular Medicine, Oxford.
415C1 came from the Los Alamos flow sorted human Chromosome 16
                                                                                                                                                                        submitted (23-OCT-1997) Chromosome 16 Project Group
(http://wwwsanger.ac.uk/HGP/Chr16/) Sanger Centre, Wel
Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK.
enquires: humquery@sanger.ac.uk Clone requests:
                                                                                                                                                                                                                                           Eutheria; Primates; Cata
1 (bases 1 to 23786)
Smye,R. and Lightning,J.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                Human DNA sequence from cosmid 415C1 from a contig
the short arm of chromosome 16, spanning 2Mb of 16p
EST and CpG islands.
                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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16p13.3; CpG.
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Eutheria; Primates; Catarrhini; Hominidae; Homo
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WASDGLAHSGKYGVACKRNAKKAESGKSASTEVFGASEDAEKNOKIMOWITEGEREIS
RHRTGHGSGTRKPOPHENSRPLSLEHFWAGPDLRTSVOPSHLETODDFWPHPPHP
PLTQLEEARRALEEEEKKASRAPSKORVVQEVWHRGRACVRPACAPVLHVVPAVSDME
LSETETRSQRKVGGGSAQPCDSIVVAYYFCGEPIPYRTLVRGRAVTLGQFKELLTKKG
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Query Match 43.7%;
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Matches 258; Conservative
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/note="AluSq repeat: matches 293. .
23258 . 23548
/note="AluY repeat: matches 298. .1
23549 . 23786
/note="AluY repeat: matches 298. .6
incomplete repeat"
) a 7039 c 6768 g 4599 t
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/note="match: mouse 5'
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13740. 14039
/note="AluSg repeat: matches 1.
14042. 14348
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incomplete repeat"
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/map="16p13.3"
/clone="LA16-415C1"
                                                                                                                                                                                                                                                                                                        /note="AluSp repeat: matches
16370. 16505
/note="AluSq repeat: matches
incomplete repeat"
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15009. .15277
/note="AluJb repeat: matches 1.
1ncomplete repeat"
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incomplete repeat"
9773. .11262
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/db_xref="taxon:9606"
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cotation/Qualifiers
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                                                                                                                                                                                                                                            note="putative CpG island"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="pTR5 repeat: matches
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te="AluSx repeat:
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   0;
   Score 161.2; DB 91;
Pred. No. 4.7e-35;
0; Mismatches 108;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HS333B10
Human DNA
                                                                                                                                                                                                                                                                                                          Submitted (04-NOY-1996) Sanger Centre, Hinxton, Cambridgeshire, CB10 1RQ, UK. E-mail enquires: humpub@sanger.ac.uk IMPORPANT: This sequence is the entire insert of clone 333B10. true left end of clone 333B10 is at 1 in this sequence. The true right end of clone 419C1 is at 10356.

The true right end of clone 333B10 is at 35054.

333B10 is from a 280kb clone contig extending from the telomere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              281450.1
16p13.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 35054)
                                                                                                                                                                                                                 Institute of Molecular Medicine, Oxford.
333B10 came from the Los Alamos, flow sorted human Chromosome
libraries constructed by Norman Doggett (unpublished).
                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                Daniels R, Flint J, Higgs D.R. unpublished.
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DNA sequence from cosmid 333B10 from a contig from the tip of nort arm of chromosome 16, spanning 2Mb of 16p13.3 contains
                                               /note="AluJb repeat:
incomplete repeat"
                                                                                            /clone="LA16-333B10"
/clone_lib="LA16"
                                                                                                                          /map="16p13.3"
                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                     Location/Qualifiers
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    /note="AluSx repeat:
incomplete repeat"
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                    matches
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3050. 3155
/note="2 copies of 53 mer 95 % conserved"
3151. 3242
/note="2 copies of 46 mer 90 % conserved"
3418. 3558
/note="AluJo repeat: matches 141. .293 of conserved incomplete repeat"
                                                                                                                                                                                            13665 .13834
/note="AluSx repeat: matches 302 .1.
incomplete repeat"
13835 .14153
/note="AluXb8 repeat: matches 308 ...
14154 .14286
/note="AluSg repeat: matches 133 .1
incomplete repeat"
                                  'note="AluJo repeat: matches 294. .4 of consensus"
5755. .>16037
'note="match: 3' EST AA007531 clone 429378; match: 9202. .>19484; Paired with EST AA007530 matching
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="MER44A repeat:
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 note="AluY repeat: matches 1.
7136. .17272
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hte="Alux repeat: matches 1.
complete repeat"
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Le="TAGCT consensus f
62. .13568
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ce="Alux repeat: matches 1.
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mplete repeat"
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9. .13232
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. .6036
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5. .13515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         e="AluY repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             = "AluSc repeat: matches 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ="AluJb repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -- AluSq repeat: matches 1. .302 of consensus
3. .10635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      = 14 copies of 2 mer 93 % conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . 889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ="20 copies of 2 mer 85 % conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "2 copies of 51 mer 100 % conserved"
.5917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .7360
                                                                        .16246
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                                                                                                                                                                                                                                                                                                                                                   from single read"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          matches
                                                                                                                                                                                                                                                                                                                                                                                       from single read"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          204.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .282 of consensus;
                   .301 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .300 of consensus*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .294 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             .301 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .300 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .294 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .1 of consensus"
                                                                                                                                                                                                                       .1 of consensus;
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                                                                                                                                                                                                                                                                                                                  .133 of
                                                                                                                                                                                                                                                           .1 of consensus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of consensus;
                                                                                                                                                                                                                                                                                                                  consensus
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                                                                        9740 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24246. .24261
/note="12 copies of 3
                                                                                           /note="AluJb repeat: matches 301.
incomplete repeat"
                                                                                                                                                                   /note="AluJo repeat: matches 2.
33038. .33342
                                                                                                                                                                                                                                              29654. .29955
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="pTR5 repeat: matches 743. .1641 of consensus"
25932. .26608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(<17999. .20054)
/note="match: 5 'EST AA007530 clone 429378; Paired
EST AA007531 matching this clone; contains L1 repeated</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="AluSx repeat: matches 132. .296 of consensus;
incomplete repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="FLAM_C repeat: matches 1. .133 of consensus"
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/note="A,C rich region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="A,C rich region"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="AluSp repeat: matches 1.
17566. .17634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="AluJo repeat: matches 13.
incomplete repeat"
                                                                                                                                                                                                        note="AluSp repeat: matches 1.32740. .33035
                                                                                                                                                                                                                                                             note="AluSp repeat: matches 303. .1 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33226. .23280
'note="AluSp/q repeat: matches 169. .121 of consensus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note="extra T in one clone"
                                                                                                                                                                                                                                                                                                                                                                                                                                            note="pTR5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="Alux repeat: matches 1. .301 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   omplete repeat"
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89. .21390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          te="AluSq repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                      te="AluSx repeat: matches 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  te="match: 3' EST AA007531 clone 429378; match:
55. .>16037; Paired with EST AA007530 matching this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ce="AluSq repeat: matches 1.
20. .23259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           e="AluY repeat: matches 41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    e="AluY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            =="AluY repeat: matches 1. .301 of consensus"
3. .21738
=="13 copies of 2 mer 92 % conserved"
                                                                                                                                                                                                                                                                                                                = "AluY repeat:
5. .28587
 43.78;
                                                                                                                                                                                                                                                                                                                                                                                                                           "pTR5 repeat: matches 1533. .2438 of consensus" .27943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .>19484
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                                                                                                                                                repeat:
                                                                          8620 g
 Score 161.2;
                                                                                                                                                                                                                                                                                                                                   matches 1. .297 of consensus"
                                                                                                                                                  matches 1. .301 of consensus"
                                                                            7104 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mer 86 % conserved"
   DΒ
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   91;
                                                                                                                                                                                                                           .303 of consensus
                                                                                                                                                                                                                                                                                                                                                                        .302 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .1 of consensus; incomplete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .298 of consensus"
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                                                                                                                                                                                      .293 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                            .302 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .144 of consensus;
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                                                                                                                .21 of consensus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of consensus'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of consensus"
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/db_xrefr"taxon:9606" /clone="RT290" /chromosome="16"	FEATURES Location/Qualiflers source 139170 /Organism="Homo sapiens"	TITLE Direct Submission  JOURNAL Submitted (30-JUN-1998) Center for Human Genome Studies, DOE Joint Genome Institute, Los Alamos National Laboratory, MS M888, Los Alamos, NM 87545, USA	t,J., Tesmer,J., Meincke,L., Longn , Tatum,O., Campbell,C., Fawcett, en,L.	Ricke, D.O., Bruce, D., I Robinson, D., Jones, M.,	Comparison Analysis (SCAN) System JOURNAL Unpublished REFERENCE 3 (bases 1 to 39170)			Misra,M. and Deaven,L.  TITLE Sequencing of Human Chromosome 16p13.3	GOOdwin,L., Bryant,J., Tesmer,J., Meincke,L., Longmire,J., White,S., Ueng,S., Tatum,O., Campbell,C., Fawcett,J., Maltbie,M.,	Ricke,D.O., Bruce,D., Mundt,M., Doggett,N., Mu Robinson,D., Jones,M., Buckingham,J., Chasteer	<pre>utheria; Primates; Catarrhini; Hominidae, to 39170)</pre>	hordata;	2	VERSION AC005202.1 GI:3273384  KEYWORDS HTG	sequence.	ACO05202 39170 bp DNA PRI 30-JU	RESULT 15		II IIIII IIIIIIII	349 gacatttacctggaatat 366	289 gcacagaccgagatccaggcagtgatggaggaaaatgccacgaggtgttcttgacttct 348	HANNOCT TO A TANNOGRAC TRACE CALIBRATICAL TRACE TO BE TO BE TO CALIBRATICAL TRACE AND A TOP A TO	asyaccacatacgagacgycaccaagaagcaacagaccggctcggtcatgtrtgaccag	TACCGAAAGTACATTCTTGATAACAATGGCATCGTGTCCCGGCAGACCAAGCCAGCC		++++++++++++++++++++++++++++++++++++++	121 aggcagatgaacctgaaggataccaaaactttgcgagtggccaaagcaatc 171	30934 TTCCTGAAGCAGGAGGCTGTGCCGACTTGCTGGACTTCTGGTTTGCCTGCACTGGCTTC 30875	61 ttcctggagaggagaaatgtgtggatacgctggacttctggtttgccttgtaatgggttc 120	1   1   1   1   1   1   1   1   1   1	vactive () mismacches 100; inders 12; Go	38; Pred. No. 4.9e-35;
	repeat_region repeat_region	misc_feature repeat_region	misc_feature	prim_transcript	misc_feature	repeat_region	repeat_region	repeat_region	repeat_region	LTR		repeat_region		repeat_region	repeat_region	repeat_region	misc_feature		repeat_region		repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	prim_transcript	repeat_region.		repeat_region	. 1	
/rpt_family="Alu" 2267922976 /rpt_family="Alu"	2045920980 /rpt_family="Alu" complement(2161821911)	0 = =	<pre>complement(1800118938) /note="87% identity mouse AF009011 GSK-3beta interacting protein rAxin"</pre>	complement(1800118938) /standard_name="axin"	<pre>/rpt_ramily="ALU" complement(1797318854) /note="GRAIL 2 excellent exon, frame 0"</pre>	/rpt_family="Alu" 17244. 17557	<pre>/rpt_family="Alu" complement(16264 . 16619)</pre>	/rpt_family="Alu" 1598016286	/standard_name="LTR12" 1523215863	/rpt_unit=A 1291314225	<pre>/note="(A)22" /rpt_type=tandem</pre>	/rpc_unit=A 1134011361	/rpt_type=tandem	/ PC_ram_+1	10892. 11524	) (A))) <sup>†</sup>	9976 10049  9976 10049  notes "GRAII 2 excellent exon. frame 0"	/rpt_type-tandem /rpt_unit=A	9327. 9346 /note="(A)20"	/rpt_type=tandem /rpt_unit=A	/rpc_taml1y="A1u" 89799006 /note="(A)28"	71PC_tamity	/rpc_ramily="A10" 8352. 8670	7043 8075	/ I D _ I d   I I I I I I I I I I I I I I I I I	.4444 	join( /stan	/*pt_duit==. complement(12562195) /rpt_family="Alu"	/note="(A)3" /rpt_type=tandem /rpt init=t	/rpt_family="Alu" /rpt_family="Alu" /rpt_family="Alu" /rut_rut_rut_rut_rut_rut_rut_rut_rut_rut_	1,0	/map="16p13.3"

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BASE COUNT
ORIGIN
Search completed: June 7, 2001, 00:35:26 Job time: 20940 sec
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Best Local Similarity 68.3
Matches 258; Conservative
                                                                             349 gacatttacctggaatat 366
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18242 GATATTTATTTGGAATAT 18225
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                                                                                                                                                                                                                                                                                                                                                        121 aggcagatg-----aacctgaaggataccaaaactttgcgagtggccaaagcaatc 171
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9832 a 11267 c 10484 g
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complement(36899..37594)
/rpt_family="Alu"
complement(37579..37894)
/rpt_family="Alu"
38736..39069
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27770. .28373
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/rpt_family="TAR1"
complement(27430: .27745)
/rpt_family="Alu"
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/rpt_family="Alu"
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30394. .30851
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Title:
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                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                         161.2
147.4
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369
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## ALIGNMENTS

ВP

Tumor-suppressing protein conductin diagnosis of tumors Conductin; tumour; diagnosis; treatment; beta-catenin; anti-tumour; therapy; cytoplasmic degradation; blockade; Wnt signalling pathway; Wingless signalling pathway; Adenomatous Polyposis Coli; APC; tumour suppressor; ss. WPI; 1999-214706/18 P-PSDB; W93570. Behrens J, Birchmeier WO9911780-A2. (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX. 97DE-1038205. 98WO-DE02621. • used for treatment and

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                                                            cgagatggcatcaagaagcaacagatcggctcggtcatgtttgaccaggcacagaccgag
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                                                                                                                                                                                                        ttcctggagagggagaaatgtgtggatacgctggacttctggtttgcttgtaatgggttc
atccaggcagtgatggaggaaaatgcctaccaggtgttcttgacttctgacatttacctg
                                                                                                          tacattgagaacaacagcgttgtctccaagcagctgaagcccgccaccaagacctacata
                                                                                                                                             aggcagatgaacctgaaggataccaaaactttgcgagtggccaaagcaatctataagagg
                                                cgagatggcatcaagaagcaacagatcggctcggtcatgtttgaccaggcacagaccgag
                                                                                              tacattgagaacaacagcgttgtctccaagcagctgaagcccgccaccaagacctacata
                                                                                                                                                                                              ttcctggagagggagaaatgtgtggatacgctggacttctggtttgcttgtaatgggttc
                                                                                                                                                                                                                                            tggaccaagtctttacactccttgttgggtgaccaggatggtgcatacctcttccggact
                                                                                                                                                                                                                                                                                             369;
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                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                             Conservative
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/note= "as desci
2561..2713
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/note= "as desc:
1403..1609
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Claim 22"
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                                                                                                                                                                                                                                                                                                                                                       703 A; 815 C; 813 G; 494 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                conjunction with APC, acts as a tumour
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described in Claim
                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                        Score 369; DB 20;
Pred. No. 1.1e-110;
                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    homology region as
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                                                                                                                                                                                                                                                                                                                    Length 2825;
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                                                                                                                                                                                                                                                                                                                                                                                suppressor
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                                    Query Match
Best Local
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                                                                                                                                                                                                                                               Constantini F,
                                                                                                                                                                                                                                                                                                                                                    Key
                                                                                                                                                                                                                                                                             10-JUL-1997;
                                                                                                                                                                                                                                                                                          09-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                            gastrointestinal cancer; esophageal cancer; carcinoma; melanoma;
diagnosis; treatment; therapy; thyroid carcinoma; tumorigenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X09012 standard;
                                                                Sequence 3411
                                                                                                                                                                                      Disclosure; Figure 10A-10B; 95pp; English.
                                                                                                                                                                                                                                                             (UYCO ) UNIV COLUMBIA NEW YORK
                                                                                                                                                                                                                                                                                                         21-JAN-1999
                                                                                                                                                                                                                                                                                                                       WO9902179-A1
                                                                                                                                                                                                                                                                                                                                                                                       beta-catenin;
                                                                                                                                                                                                                                                                                                                                                                                                                         Human axin gene
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       tggaccaagtctttacactccttgttgggtgaccaggatggtgcatacctcttccggact 60
                                                                                                                                                                                                                                 1999-120510/10.
tgggctgagtcactgcattccctgctggatgaccaagatgggataagcctgttcaggact 424
                                                                                                                                                                                                                                                                                                                                                                                                           cancer; breast cancer; colorectal cancer;
                           h 43.7%;
Similarity 68.3%;
58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                BP; 752 A; 1010 C; 1066 G;
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2..2704
/*tag= a
                                                                                                                                                                                                                                                                                                                                     /product= Axin
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                            0
                           Score 161.2; DB 2
Pred. No. 1.3e-42;
0; Mismatches 108
                                                                582 T; 1 other;
                                          DB 20;
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                           Indels
                                         Length
                            12;
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RESULT
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Nucleic acids encoding mutant and wild type Axin and oligonucleotides derived from them are useful for detecting mutations in the Axin gene and for determining whether a sullikely to develop cancer (including breast, colorectal, gastrointestinal, esophageal, carcinomas or melanomas). The type Axin and homologues of Axin are useful for treating sul
                                                                                                                                                                                                                                                                                                                              CDS
                                                                                                                                                                                                                                                                                                                                                              Mus
                                                                                                                                                                                                                                                                                                                                                                                            Axin; cancer; breast cancer; colorectal cancer; gastrointestinal cancer; esophageal cancer; carcinoma; diagnosis; treatment; therapy; thyroid carcinoma; tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                          Murine axin gene
                                                                               Claim
                                                                                                   Newly isolated nucleic acid encoding "axis inhibition" (Axin) - useful for detecting, diagnosing and treating
                                                                                                                                     P-PSDB;
                                                                                                                                                                     Constantini F,
                                                                                                                                                                                                                  10-JUL-1997;
                                                                                                                                                                                                                                       09-JUL-1998;
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                                                                                                                                                                                                                                                                                   W09902179-A1
                                                                                                                                                                                                                                                                                                                                                                                    beta-catenin;
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                                                                                                                                                1999-120510/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aggaagctggagccctgtgactcgaacgaggagaagaggctgaagctggagagagccatc
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                                                                              Figure 9A-9B;
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1..2981
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                                                                           95pp; English.
  melanomas). The wild for treating subjects
  treating subjects
                                                                                                    cancer
                                                                                                                                                                                                                                                                                                                                                                                                           melanoma;
                                   subject is
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Best Local :
             10-AUG-1993;
27-OCT-1994;
05-JUN-1996;
                                                                                                                                                                    CR2; human; antibody; cytokine response gene; cytostatic; anti-allergic; immunosuppressive; antimicrobial; therapy; cell proliferation; treatment; cell differentiation; cancer; immune disease; rheumatologic disease; transplant rejection; anti-infective; ss.
                                                  20-NOV-1991;
                                                                        05-JUN-1996;
                                                                                                02-MAY-2000
                                                                                                                       US6057427-A
                                                                                                                                               Unidentified
                                                                                                                                                                                                                              Cytokine response gene-related cDNA sequence (Seq
                                                                                                                                                                                                                                                                                                                                                                   1002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  who are likely to develop cancer (thyroid carcinomas). The nucleic acids are also useful for diagnosing cancer and for detecting mutations in cancerous cells. Wild type Axin, its antisense molecule and identified compounds form pharmaceutical compositions in the treatment of cancer. The compositions are also useful for treating cancer by inhibiting tumorigenesis (by inducing degradation of beta-catenin). The nucleic acid encoding Axin acts through negative regulation of the Wnt pathway in the Nieuwkoop Center.
                                                                                                                                                                                                                                                        18-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           tataagaggtaca---ttgagaacaacagcgttgtctccaagcagctgaagcccgccacc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ttcctgaagcaggagggctgtgctgacctgctggacttctggtttgcctgcagtggcttc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ttcctggagagggagaaatgtgtggatacgctggacttctggtttgcttgtaatgggttc
                                                                                                                                                                                                                                                                                                     standard;
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            91US-0796066.
93US-0104736.
94US-0330108.
96WO-US08992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B₽;
                                                                        96US-0652446
                                                                                                                                                                                                                                                                                                       cDNA; 606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39.9%;
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Pred. No. 4.6e
0; Mismatches
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ches 116;
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Best Local
             graft
             RATHI.1; RGS gene family; regulator of G-protein signalling; human; regulation; activation; modulation; signal transduction; T Cell; T helper cell; treatment; autoimmune disorders; arthritis; infection graft rejection; asthma; allergy; neoplasm; ss.
                                                                                   Human
                                                                                                               11-SEP-1998
                                                                                                                                                                    V34780 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention describes a novel isolated antibody or antibody fragment (I) which selectively binds to a polypeptide encoded by cytokine response gene 2 (CR2) and modulates CR2 activity. The products of the invention have cytostatic, anti-allergic, immunosuppressive and antimicrobial activity. The antibodies are useful as therapeutic agents for regulating cellular proliferation and differentiation and for treating all kinds of cancers, immune diseases such as allergic, autoimmune, and rheumatologic diseases, transplant rejection, and as anti-infectives for fighting viral, bacterial, parasitic and fungal infections. This sequence is
                                                                                                                                         V34780;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          presented
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                                                                                                                                                                                                                                           535
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                                                                                   RATH1.1
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           asthma; allergy;
                                                                                                                                                                    DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               147
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                                                                                                            entry)
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Pred. No. 2.9e
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2.9e-08;
hes 168;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence encodes a novel member of the human regulator of G-protein signalling (RGS) gene family, RATHI.1. The encoded protein participates in the regulation, control and/or modulation of G-protein mediated signal transduction, involved in T cell activation, including T-helper (TH) cell and TH cell subpopulation activation. The protein can be used to develop products for treating autoimmune disorders, arthritis, graft rejection, asthma, allergy, infections or neoplasms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-JUN-1997;
04-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Fig 2A-B; 127pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New activated T helper cell specific gene, RATH - used for developing products for treating e.g. autoimmune disorders, arthritis, graft rejection, asthma, allergy, infections or neoplasms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-240085/21.
P-PSDB; W59294.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 746 BP; 172 A; 217 C; 215 G; 142 T; 0 other;
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                                                                                                                          cgagatggcatcaagaccagatcggctcggtcatgtttgaccaggccacagaccgag
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96US-0726228.
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'Pred. No. 3.2e-08; 
0; Mismatches 168;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
                                                                                                                                                                                                                                                                                                                Sequence 2383 BP;
                                                                                                                                                                                                                                                                                                                                      use in treating tumours and cancer and in the diagnosis
                                                                                                                                                                                                                                                                                                                                                                                              Claim 3; Figure 6; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated nucleic acid encoding p53 response used to develop prods. for the study, diagnosis
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atccaggcagtgatggaggaaaatgcctaccaggtgttcttgacttctgacatttacctg
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                        ctgacgaggatgaacctgcagactgccacagccacatgctttgatgcggctcaggggaag
                                     cgagatggcatcaagaagcaacagatcggctcggtcatgtttgaccaggcacagaccgag
                                                                   ttcatttg-----cagtgaggcccctaaagaggtcaacattgaccatgagacccgcgag 506
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                                                                                                                                                                                                                                                                                                               561 A; 603 C; 657 G; 562 T; 0 other;
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Pred. No. 5.7e-08;
0; Mismatches 168;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tumour; p53;
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                                                                                                                                                                                                                                                                             Length 2383;
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05-JUN-1995;
05-JUN-1995;
05-JUN-1995;
05-JUN-1995;
05-JUN-1995;
                                                                                                                                                                                                                          8 Clones (T43376-83) contg. interleukin-2 (IL-2)-induced genes were isolated from a human IL2 receptor-positive T blast cell cDNA library following IL-2 stimulation. 6 Of these ligand-induced genes (CRI, 2, 3, 5, 6, 8) are novel. CRI expression is rapidly and transiently induced by IL-2, and mRNA expression is suppressed by elevated intracellular cAMP. It encodes an intracellular protein (W08133) that shows homology to GOS8 and BL-34. CR genes and polypeptides (W08133-40) can be used as diagnostic or therapeutic agents; CR gene sequences can be used to detect and treat allelic
                                                                                                                                                                           Sequence 2406 BP; 565 A; 621 C;
                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 11-12; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cytokine response proteins and genes - used in the detection and therapy of diseases caused by a mutation in the CR coding region
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             tggagagagtcgttcgacctgctgctgagcagtaaaaatggagtggctgccttccacgct 358
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                                                                                        Conservative
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95US-0461379.
95US-0462337.
95US-0462390.
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No. 5.
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5.7e-08;
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               RESULT
A39660
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           This invention describes a novel isolated antibody or antibody fragment (I) which selectively binds to a polypeptide encoded by cytokine response
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20-NOV-1991;
10-AUG-1993;
27-OCT-1994;
                                                                                                  WPI; 2000-338623/29.
P-PSDB; Y87952.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CR2; human; antibody; cytokine response gene; cytostatic; anti-allergic; immunosuppressive; antimicrobial; therapy; cell proliferation; treatment cell differentiation; cancer; immune disease; rheumatologic disease; transplant rejection; anti-infective; CR1; ss.
                                      Novel antibody or antibody fragment which selectively binds polypeptide encoded by cytokine response gene 2\, -
                                                                                                                                                           Beadling
                                                                                                                                                                                                                                          05-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                           02-MAY-2000
Example IV; Column 75-78; 66pp; English.
                                                                                                                                                                                                                                                                                                                                        05-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                  US6057427-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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93US-0104736.
94US-0330108.
96WO-US08992.
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Matches 185;
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Best Local
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                                                                                                                                                                                         regulation; activation; modulation; signal transduction; T Cell; T helper cell; treatment; autoimmune disorders; arthritis; infection; graft rejection; asthma; allergy; neoplasm; ss.
              06-OCT-1997;
                                         09-APR-1998.
                                                                                                                                                                   Mus sp.
                                                                                                                                                                                                                                     RATH1.1; RGS gene family; regulator of G-protein signalling; murine;
                                                                                                                                                                                                                                                                   Mouse RATH1.1 DNA.
                                                                                                                                                                                                                                                                                            11-SEP-1998 (first entry)
                                                                                                                                                                                                                                                                                                                          V34779;
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                                                                   W09814579-A1
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           97WO-US18259
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51.1%;
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Pred. No. 5.7e-08;
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RESULT 11
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Best Local Similarity 50.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TH) cell and TH cell subpopulation activation. The protein can be used to develop products for treating autoimmune disorders, arthritis, graft rejection, asthma, allergy, infections or neoplasms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence encodes a novel member of the mouse regulator of G-protein signalling (RGS) gene family, RATHI.1. The encoded protein participates in the regulation, control and/or modulation of G-protein mediated signal transduction, involved in T cell activation, including T-helper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New activated T helper cell specific gene, RATH - used for developing products for treating e.g. autoimmune disorders, arthritis, graft rejection, asthma, allergy, infections or neoplasms
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04-OCT-1996;
               Human; regulator; G-protein signalling; HRGS; cancer;
hypertension; cardiovascular shock; arrhythmias; asthm
                                                          Human regulator of G-protein signalling encoding cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2272 BP; 548 A; 584 C; 625 G; 515 T; 0 other;
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                                                                                           14-SEP-1998
                                                                                                                                                         V38084 standard; cDNA;
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                                                                                          (first entry)
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96US-0726228.
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Pred. No. 2.1e-06;
0; Mismatches 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 2272;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Regulator of G-protein signalling - treating e.g. cancer, inflammation, shock, arrhythmias or asthma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96US-0748483
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Pred. No. 0.014;
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                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               179 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                        DB 19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RGS; regulators of G-protein signaling; GTPase activating protein; GAP; G-alpha protein; cell adhesion; chemotaxis; vulnerary; immunosuppressor; anti-rheumatic; anti-arthritic; anti-diabetic; anti-inflamatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel regulator of G-protein signaling nucleic acids and polypeptides, useful as diagnostic and investigative tools and to treat G-protein signaling disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 102-104; 105pp; English
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P-PSDB; Y97154.
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0; Mismatches
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ches 180;
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protein, RGS5. The specification also describes an activator of G protein signalling (ARS) protein. The AGS cDNA sequence was isolated from a human liver cDNA library. The AGS protein exhibits homology to ras-related G proteins, and contains alterations in conserved amino acids consistent with a deficiency in GTP hydrolysis activity. AGS stimulates G protein activity, G protein-coupled signal transduction and the pheromone response pathway in a receptor-independent manner. The AGS protein also shows G-gamma selectivity, as measured by growth asseays in yeast expressing various mammalian G-gamma constructs, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Activator of G protein signalling; AGS; ras-related G protein; GTP hydrolysis; G protein activity; pheromone response pathway G protein coupled signal transduction; G-gamma selectivity; cellular signal transduction; regulator of G protein signalling.
                                                                                                                                                             Claim
                                                                                                                                                                                    A new activator of G protein signalling used to treat disorders characterized by an aberrant {\sf AGS} protein activity -
                                                                                                                                                                                                                                                                             Cismowski M,
                                                                                                                                                                                                                                                                                                                                    08-MAY-1998;
07-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                              07-MAY-1999;
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                                                                                                                                The present sequence encodes a regulator of G protein signalling (AGS)
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                                                                                                                                                            Page 139-140;
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05-SEP-1997;
05-SEP-1997;
05-SEP-1997;
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                                                                                                                                                                                                                                                                                                                                                                                      inflammatory disorder; skin disorder; tumour; atherosclerosis; restenosis; autoimmune disorder; Alzheimer's disease; peripheral neuropathy; trauma; spinal cord injury; allergy; hematopoietic disorder; skeletal disorder; neurological disord arthritic disorder; asthma; immunodeficiency disease; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human secreted protein; cancer; immune disorder; infection;
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                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                    transplant rejection;
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97US-0058974.
97US-0057626.
97US-0057663.
97US-0057669.
97US-0058666.
                                                                                                                                                         98WO-US18360
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RESULT 15
C41294
ID C41294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 their corresponding secreted proteins. The polynucleotides and their corresponding secreted polypeptides are useful for preventing, treating or ameliorating medical conditions, e.g. by protein or gene therapy. Pathological conditions can also be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each polynucleotide, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer; immune disorders, infection, inflammatory disorders, skin disorders, tunours, atherosclerosis, restenosis, autoimmune disorders, they are disorders, seeletal disorders, highlers, hematopoietic disorders, seeletal disorders, neuropathies, trauma, spinal cord injuries, allergy, hematopoietic disorders, asthma, immunodeficiency diseases, AIDS and transplant rejection. The polypeptides are also useful for identifying their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated human genes and the secreted polypeptides they encode - useful for diagnosis and treatment of e.g. neurological disorders, tumours, immune disorders, inflammation or haematological disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-204988/17
P-PSDB; Y12958.
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12-SEP-1997;
   C41294 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1923 BP; 604 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 175-176; 215pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rosen GA,
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                                                                                                                                                                                                                                                                                                                            121 aggcagatgaacctgaaggataccaaaaactttgcgagtggccaaagcaatctataagagg
                                                                                                                                                                                                                                                                                                                                                                                      61 ttcctggagagggagaaatgtgtggatacgctggacttctggtttgcttgtaatgggttc
                                                                                                                                                                                                                                                                                                                                                                                                                                               1 tggaccaagtctttacactccttgttgggtgaccaggatggtgcatacctcttccggact
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| gagt 799
                                                                                                                                                  atocaggcagtgatggaggaaaatgcctaccaggtgttcttgacttctgaccatttacctg
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Shi Y;
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21-APR-1999;
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05-MAR-1999;
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23-MAR-1999;
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01 - JUN - 1999

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Pred. No. 0.049;
0; Mismatches 60
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Job time: 8625 sec

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Result
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                           seq length: 0 seq length: 2000000000
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Match
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1: /cgn2_6/ptodata/2/1na/5A_COMB.seq:*

2: /cgn2_6/ptodata/2/1na/5B_COMB.seq:*

3: /cgn2_6/ptodata/2/1na/6A_COMB.seq:*

4: /cgn2_6/ptodata/2/1na/6B_COMB.seq:*

5: /cgn2_6/ptodata/2/1na/pcTUS_COMB.seq:*

6: /cgn2_6/ptodata/2/1na/backfiles1.seq:*
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US-08-461-379A-27
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US-08-949-004-3
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Query Match

15.0%; Score 55.2;

DB 2;

Length 606;

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; Sequence 27, Application US/08461379A

; Patent No. 5871961
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INFORMATION FOR SEQ ID NO:
                                                                                 APPLICATION NUMBER: USSN 08/330,108; 08/104,736
APPLICATION NUMBER: 6.07/796,066
FILING DATE: 27-OCT-1994; 10-AUG-1993 6.20-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: DART-070
TELEPHONE: (610,470-0700)
                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/461,379A FILING DATE: 5-JUNE-1995 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1,0,
SOFTWARE: Version #1.25
CURRENT APPLICATION DATA:
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STATE: Pennsylvania
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0; Mismatches 168;
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Best Local Similarity
                                                                                 APPLICATION NUMBER: US/08,
FILING DATE: 5-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN (
FILING DATE: 27-OCT-1994
APPLICATION NUMBER: USSN (
FILING DATE: 10-AUG-1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Smith, K. A.,
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph.
REGISTRATION NUMBER: 30,
                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ratner & Prestia
                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Smith, K. A., & Beadling, C.
TITLE OF INVENTION: Nucleic Acids Encoding CR8 Polypeptide, Vector and
TITLE OF INVENTION: Transformed Cell Thereof, and Expression Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
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                                                  FILING DATE: 10-AUG-19
APPLICATION NUMBER: US
FILING DATE: 20-NOV-91
                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                         COUNTRY: U
ZIP: 19482
                                                                                                                                                                                                                                                                                                                                                        CITY: Valley Forge
STATE: Pennsylvania
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TOPOLOGY: li
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Pred. No. 8.4e-09;
0; Mismatches 168;
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US-08-463-074B-27; Sequence 27, Application US/08463074B
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 606 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                           Patent No. 6020155
GENERAL INFORMATION:
GENERAL INFORMATION:
MITH, Kendall A. & Beadling, Carol
TITLE OF INVENTION: Nucleic Acids Encoding CR1
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 185; Conserv
              SOFTWARE: Patentin Release #1.0, SOFTWARE: Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/463,07 FILING DATE: 5-JUN-1995 PRIOR APPLICATION DATA:
                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION
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                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                  CITY: Los Angeles
STATE: California
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                                                                                                                                                                                                                                COUNTRY:
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                                                                                                                                                                                                                  ZIP: 90071
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51.1%;
                                                        US/08/463,074B
US 08/104,736
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Pred. No. 8.4e-09;
D; Mismatches 168;
                                                                                                                                                                                                                                                                                                                                                                     Fusion Protein, Vector an
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US-08-465-585C-27
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; Patent No. 6027914
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Best Local Similarity
Matches 185; Conserv
                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Smith, K. A., & Beadling, C.
TITLE OF INVENTION: Nucleic Acids Encoding CR6 Pol
TITLE OF INVENTION: Transformed Cell Thereof, and
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 606 base pairs
TYPE: nucleic acid
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ATTORNEY/AGENT INFORMATION:
NAME: Viviana Ampai
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 10-AUG-1993 PRIOR APPLICATION DATA:
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REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66 38143 (DART-020)
                                                             ZIP:
                                                                                                 CITY: Los Angeles
STATE: Californiaa
                                                                             COUNTRY:
                                                                                                                                       ADDRESSEE:
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                                                                                                                                                         PRETTY, SCHROEDER & POPLAWSKI
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51.1%;
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Pred. No. 8.4e-09;
0; Mismatches 168;
                                                                                                                                                                                                             Encoding CR6 Polypeptide, Vecto ell Thereof, and Expression Thereof
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                                    GENERAL INFORMATION:
APPLICANT: Smith, Ke
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                   Sequence 27, Application US/08652446 Patent No. 6057427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: 966 38149 (DART-050)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
TELEPHONE: (213) 4894210
INFORMATION FOR SEQ ID NO: 27:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 27-OCT-1994
APPLICATION NUMBER: USSN 08/104,736
FILING DATE: 10-AUG-1993
APPLICATION NUMBER: USSN 07/796,066
FILING DATE: 20-NOV-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-USOFTWARE: Patentin Rel
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LENGTH: 606 base pairs
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                      NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 606 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 ttcctggagagagagaaatgtgtggatacgctggacttctggtttgcttgtaatgggttc 120
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                                  Smith, Kendall A. & Beadling, Carol VENTION: Nucleic Acids Encoding CR5 VENTION: Polypeptide, Vector and Tr ENTION: Expression Thereof
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                                                             and Transformed Cell Thereof,
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Best Local
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INFORMATION FOR
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PRIOR APPLICATION DATA:
APPLICATION NITMERS
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: FP66 40035 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 29-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/461,379
FILING DATE: 5-JUN-1991
PRIOR APPLICATION DATA:
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FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 08/330,108
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FILING DATE: 5-JUN-1995
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STATE: California
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185; Conserv
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OR SEQ ID NO: 2
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Version #1.25
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(B) STREET:
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5-JUN-1995
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                                                                                                                         Score 55.2; DB 3;
Pred. No. 8.4e-09;
0; Mismatches 168
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; NAME/KEY: Coding Sequence; LOCATION: 39...644; OTHER INFORMATION: US-08-870-815-3
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             Query Match 15.0%;
Best Local Similarity 51.1%;
 Matches 185;
                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Laura A. COCTUZZI
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 896-8864/9741
TELEX: 66141 PENNIE
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APPLICANT: Levins
                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PT C PC - DOS/MS - DOS
OPERATING SYSTEM: PC - DOS/MS - DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/870,815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Gimeno, Carlos J.
TITLE OF INVENTION: RATH GENES AND POLYPEPTIDES AND METHODS
TITLE OF INVENTION: FOR THE TREATMENT AND DIAGNOSIS OF IMMUNE DISORDERS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 746 base pairs
TYPE: nucleic acid
                                                                                                                                  FEATURE:
                                                                                                                                               MOLECULE TYPE: DNA
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CLASSIFICATION: 435
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ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: New York
STATE: New York
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                                                                                                                                                                TOPOLOGY:
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1155 Avenue of the Americas
Conservative
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             Score 55.2; DB 3; Pred. No. 9.3e-09;
 Mismatches
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Gaps
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; NAME/KEY: CDS
; LOCATION: (39)..(644)
US-08-949-004-3
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Best Local Similarity 51.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Levinson, Douglas A.
APPLICANT: Gimeno, Carlos J.
TITLE OF INVENTION: RATH GENES AND POLYPEPTIDES AND METHODS FOR
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF IMMUNE DISORDERS
FILE REFERENCE: 7853-109
CURRENT APPLICATION NUMBER: US/08/949,004
CURRENT FILING DATE: 1997-10-10
EARLIER APPLICATION NUMBER: 08/870,815
EARLIER APPLICATION NUMBER: 08/870,815
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1996-10-04
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a---agaagatccgatcagctaccaagctggcctccagggcacaccagatctttgaggag
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                                                                                                              ttcctgaagacagagttcagtgaggagaacctggagttctggcttggcctgtgaggagttc
                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                       Score 55.2; DB 4;
Pred. No. 9.3e-09;
0; Mismatches 168;
                                                                                                                                                                                                                                                                                                                                                                                                Length 746;
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                                                                                                                                               Query Match 15.0%;
Best Local Similarity 51.1%;
Matches 185; Conservative
                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 206-727-3601
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/274,318
FILING DATE: 11-JUL-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Bodden, James M.
REGISTRATION NUMBER: 32,962
REFERENCE/DOCKET NUMBER: 000127-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: No. 5667987el p53 Response Genes NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 206-727-3688
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                                                                      276 TGGAGAGAGTCGTTCGACCTGCTGAGCAGTAAAAATGGAGTGGCTGCCTTCCACGCT 335
 336
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ZIP: 98121
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STATE: Washington
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                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: sing
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                   ttcctggagagggagaaatgtgtggatacgctggacttctggtttgcttgtaatgggttc 120
                                                                                           tggaccaagtctttacactccttgttgggtgaccaggatggtgcatacctcttccggact 60
   INFORMATION:
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                                                                                                                                                                                                                                                                                                                                2383 base pairs
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                                                                                                                                             Score 55.2; DB 1;
Pred. No. 1.6e-08;
0; Mismatches 168;
                                                                                                                                                                                    Length 2383;
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                                                                           ; TOPOLOGY: 11; MOLECULE TYPE: US-08-754-108-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application Patent No. 5886149
GENERAL INFORMATION:
Matches
               Query Match
Best Local
                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 98121
COMPUTER READABLE FORN:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING PAtentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/274,318
FILING DATE: 11-JUL-1994
ATTORNBY/AGENT INFORMATION:
                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 2383 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                      NAME: Bogden, James M. REGISTRATION NUMBER: 32, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 3005 |
CITY: Seattle
                                                                                                                         STRANDEDNESS: single
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                                                                                                                                                                                                                       TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
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                Similarity
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Kley, Nikolai
                                                                                                                                                                                                         206-727-3688
206-727-3601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Buckbinder, Leonard
                                                                                                              linear
                                                                                               CDNA
                15.0%;
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   0;
                Score 55.2; DB 2;
Pred. No. 1.6e-08;
                                                                                                                                                                                                                                                           ON0127-
   Mismatches
     168;
                                   Length 2383;
     Indels
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US-08-463-081B-1
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Patent No. 5871960
Patent No. 5871960 5837487
                                                                                        COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
SOFTWARE: Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,081B
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/104,736
FILING DATE: 10-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/796,066
FILING DATE: 20-NOV-91
APPLICATION NUMBER: Dh. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66 38150 (TELECHMUNICATION: TELECHMUE: (213) 622-7700
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELECHMUNICATION: (213) 622-7700
TELECHMUNICATION: (213) 622-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             atent No. 307-7-2
GENERAL INFORMATION:
GENERAL INFORMATION: Smith, Kendall A. & Beadling, Carol
APPLICANT: Smith, Kendall A. & Beadling, Carol
                                                                            TELEFAX: (213) 489-42: INFORMATION FOR SEQ ID NO:
                                    SEQUENCE CHARACTERISTICS:
LENGTH: 2406 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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STREET: 444 South Flower St. - Suite 1900
CITY: Los Angeles
STATE: California
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TYPE: nucleic acid
STRANDEDNESS: single
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US-08-461-379A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
FEATURE:
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Sequence 1, Application US/08461379A Patent No. 5871961
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Best Local Similarity 51.1
Matches 185; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: 1
TITLE OF INVENTION: 1
TITLE OF INVENTION: 1
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                       CITY: Valley Forge
STATE: Pennsylvania
                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, SOFTWARE: Version #1.25
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                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Smith, Kendall A. & Beadling, Carol
FENTION: Nucleic Acids Encoding CR5 Polypeptide,
FENTION: Vector and Transformed Cell Thereof, and
FENTION: Expression Thereof
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51.1%;
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Pred. No. 1.
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US-08-461-379A-1
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Best Local Similarity
Matches 185; Conserv
                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/08462390B Patent No. 5882894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (610)470-0700
TELEFAX: (610)470-0701
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Smith, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 2406 base pairs
TYPE: nucleic acid
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           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                           APPLICANT: Smith, K. A., & Beadling, C.
TITLE OF INVENTION: Nucleic Acids Encoding CR8 Polypeptide, Vector and
TITLE OF INVENTION: Transformed Cell Thereof, and Expression Thereof
NUMBER OF SEQUENCES: 35
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                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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                                                                                                                                                          CITY: Valley Forge
STATE: Pennsylvania
                                                                                                                        ZIP: 19482
                                                                                                                                           COUNTRY:
APPLICATION NUMBER:
                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                               ADDRESSEE: Ratner & Prestia
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116..722
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Pred. No. 1.6e-08;
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GENERAL INFORMATION:

APPLICANT:

NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:

ADDRESSEE: ADDRESSEE:

PRETTY,

SCHROEDER & POPLAWSKI

(B) STREET

444 South Flower St.

Suite

Angeles

TITLE OF INVENTION:

Smith, Kendall A. & Beadling, Carol VENTION: Nucleic Acids Encoding CR1 EQUENCES: 35

Fusion

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; NAME/KEY:
; LOCATION:
US-08-462-390B-1
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                              RESULT 14
US-08-463-074B-1
Sequence 1, Application US/08463074B Patent No. 6020155
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Matches
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EILING DATE: 20-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: DART
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610)407-0700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PILING DATE: 5-JUND TRIBLE PRIOR APPLICATION NUMBER: USSN APPLICATION NUMBER: USSN PAPEL 27-CCT-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                             61 ttcctggagagggagaaatgtgtggatacgctggacttctggtttgcttgttaatgggttc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 2406 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 10-AU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 tggaccaagtotttacactocttgttgggtgaccaggatggtgcatacctcttccggact
                                                                                                                                                                                                                                                                                                     tacattgagaacaacagcgttgtctccaagcagctgaagcccgccaccaagacctacata 240
                                                                                            GA
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                                                                                                                                                                                                                                                 cgagatggcatcaagaagcaacagatcggctcggtcatgtttgaccaggcacagaccgag
                                                                                                                                                                                                                                                                                 TTCATTTG-----CAGTGAGGCCCCTAAAGAGGTCAACATTGACCATGAGACCCGCGAG
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(700 TD NO: 1:
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51.1%;
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STATE: California

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Best Local Similarity 51.1%;
Matches 185; Conservative
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FILING DATE: 20-NOV-91
ATTORNEY_AGENT INFORMATION:
NAME: VIVIANA AMZe1, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: 966 38143 (DART-020)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08 FILING DATE: 10-AUG-1993 PRIOR APPLICATION DATA:
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FILING DATE: 5-JUN-1995
FRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, SOFTWARE: Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                       tacattgagaacaacagcgttgtctccaagcagctgaagcccgccaccaagacctacata 240
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                                                                                                                                                                                                                                                           cgagatggcatcaagaagcaacagatcggctcggtcatgtttgaccaggcacagaccgag 300
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                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66 38149 (DART-050)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 5-JUNE-:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE: 27-OCT--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Smith, K. A., & Beadling, C.
TITLE OF INVENTION: Nucleic Acids Encoding CR6 Polypeptide, Vecto
TITLE OF INVENTION: Transformed Cell Thereof, and Expression Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
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                          241 cgagatggcatcaagaagcaacagatcggctcggtcatgtttgaccaggcacagaccgag 300
530 CTGACGAGGATGAACCTGCAGACTGCCACAGCCACATGCTTTGATGCGGCTCAGGGGAAG
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LOCATION:
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APPLICATION NUMBER:
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STATE: Californiaa
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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. (B) STREET:
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51.1%;
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Pred. No. 1.6e-08;
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649	590 ACACGTACCCTGATGGAGGAGTCCTACCCACGCTTCCTGAAGTCGCCTGCTTACCGG 649	DЪ
360	301 atccaggcagtgatggaggaaaatgcctaccaggtgttcttgacttctgacatttacctg 360	Qу

Search completed: June 7, 2001, 00:26:30 Job time: 19733 sec

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Title:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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seq length:
       June 6, 2001, 23:00:39 ; Search time 3054.04 Seconds (without alignments)
1055.527 Million cell updates/sec
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gb_est6:*
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gb_est9:*
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gb_est11:*
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gb_est3:*
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em\_esthum28: em\_estin1:\* em\_estin2:\* em\_estin3:\* em\_estin4:\* em\_estin5:\*

em\_estom1:\*
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em\_esthum20:\*
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em_gss_pln2:*
em_gss_pro:*
em_gss_rod1:*
em_gss_rod2:*
em_gss_rod3:*
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em_gss_vrt1:*
    231 CNS03YWO
230 CNS01YDU
231 CNS03GZD
140 BEB772155
230 CNS033J4
141 BEB54108
150 BF582324
3 AA196606
147 BF406997
169 BF802488
106 AL526136
105 AL645145
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105 AL64879
150 BF59312
232 CNS05IXC
109 AV138493
170 BF892872
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AL266841 Tetraodon
AL172875 Tetraodon
AL172875 Tetraodon
AL243521 Tetraodon
BE872155 601446262
AL266201 Tetraodon
BE894571 601433182
BE854108 ux27903.y
BF582324 602101153
AA198606 mu15d04.r
BF406997 UI-R-BJ2-BF802488 CMO-CI009
AL526136 AL526136
AL044145145 DKF2p4340
AL044479 DKFZp434C
BF559312 UI-R-E1-F
AL339465 Tetraodon
AV138493 AV138493
BF892872 QV1-MT013
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gb\_est102:\*
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gb\_est67:\*
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gb\_est99:\*
gb\_est100:\*
gb\_est101:\*

gb\_est89:

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gb\_est84:\*
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gb\_est97:\*
gb\_est98:\*
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JOURNAL
REFERENCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Meopterygii; Teleostei; Eureleostei; Neoteleostei;
Eurypterygii; Ctenosquamata; Acanthomorpha; Euacanthomorpha;
Holacanthopterygii; Acanthopterygii; Percomorpha;
Tetraodontiformes; Tetraodontoidei; Tetraodontidae; Tetraodon.
1 (bases 1 to 1068)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C.,
                                  Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of a lar scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                    2 (bases 1 to 1068)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottler, P., Quetier, F., Saurin, W. and Weissenbach, J.
Human gene number estimate provided by genome wide analysis usin
                                                                                                                                                                                                                                                                                                                                                                                                                              CNS03YWO 1068 bp DNA GSS 18-MAY-2000
Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
069C20 of library G from Tetraodon nigroviridis, genomic survey
                                                                                                                                                                                                                          Charaterization and repeat analysis of the compact freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                     GSS; genome survey sequence.
Tetraodon nigroviridis.
                                                                                                       Genoscope.
                                                                                                                            Unpublished
                                                                                                                                                                                                                                                 Bouneau, L., Billault, A., Weissenbach, J.
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                                                                                             Direct Submission
                                                                                                                                           Tetraodon nigroviridis
                                                                                                                                                                                                             Unpublished
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/organism-"Tetraodon nigroviridis"
                       Location/Qualifiers
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AI885075 w189001.x
AI769888 wj30a08.x
BF304996 601888511
BE795291 601592385
AU122006 AU122006
BF896301 RC1-WF014
AW199671 xm29b11.x
AW193671 xm29b11.x
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AA497296 fa03e12.r
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BF802233 CM1-CIOC
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BE798461 60158332
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BE932286 IL3-HT061
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                                  Bernot, A., Fizames, C., Wincker, P., Brottier, P., Saurin, W. and Weissenbach, J.
Human gene number cottain.
                                                                                                                                                                                                                                      GSS; genome survey sequence. Tetraodon nigroviridis. Tetraodon nigroviridis
                       Human gene number estimate Tetraodon nigroviridis DNA
                                                                   2 (bases 1 to 830)
Roest-Crollius, H., Jaillon, O.,
                                                                                          freshwater pufferfish Unpublished
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Roest-Crollius, H., Jaillon, O.,
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                                                                                                                                          Bouneau,L., Billault,A.,
                                                                                                                                                                            Holacanthopterygii; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontoidei; Tetraodontida
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/clone_lib="G"
/note="Genoscope sequence ID : COBG069BB10SP1-end
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Pred. No. 8.7
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                                                                                                                                                                                              sequence.
AL243621.1 GI:7964633
AL243621.1 GI:7964633
GSS; genome survey sequence.
Tetraodon nigroviridis.
                                                                                               Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostei;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei
Eurypterygii; Ctenosquamata; Acanthomorpha; Euacanthomorpha;
Holacanthopterygii; Acanthopterygii; Percomorpha;
Tetraodontiformes; Tetraodontoidei; Tetraodontidae; Tetraodon.
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025B16 of
                                            1 (bases 1 to 902)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fi
Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A.
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               Charaterization and repeat analysis of the
                                     Weissenbach,J.
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/note="Genoscope sequence
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/db_xref="taxon:99883"
/clone="218017"
 pufferfish
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Tetraodon nigroviridis
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Pred. No. 7.6e-60;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 798).
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collec Unpublished (1999)
                                                                                                                                                                      BE872155 798 bp
601446262F1 NIH_MGC_65
                                                                                                     human.
                                                                                                                              BE872155
BE872155.1
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2 (bases 1 to 902)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
                                                                                      Homo sapiens
                                                                                                                                                          mRNA sequence.
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/db_xref="taxon:99883"
/clone="025B16"
/clone_lib="G"
/note="Genoscope sequence ID : COB
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                                               AUTHORS
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GSS; genome survey sequence.

Tetraodon nigroviridis.

Tetraodon nigroviridis

Tetraodon nigroviridis

Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei;; Neoteleostei;

Eurypterygii; Ctenosquamata; Acanthomorpha; Euacanthomorpha;

Holacanthopterygii; Acranthopterygii; Percomorpha;

Tetraodontiformes; Tetraodontoidei; Tetraodontidae; Tetraodon.

1 (bases 1 to 975)

Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C.,

Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and

Weissenbach, J.
                                                                                                                                                                                                                                                                                                         CNS033J4 975 bp DNA GSS 15-N
Tetraodon nigroviridis genome survey sequence PUC-Ori
209G17 of library G from Tetraodon nigroviridis, genom
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Tissue Procurement: ATCC
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AL226201.1 GI:7885113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     369
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/db_xref="IMAGE:3850502"
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/lab_host="NH10B (phage-resistant)"
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Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.8 kb. Library constructed by Life
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                            BE894571
BE894571.1
EST.
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This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
Location/Qualifiers
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Homo
                                                                          mRNA sequence.
                                                                                      601433182F1 NIH_MGC_72
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/db_xref="taxon:99883"
/clone="209G17"
/clone_lib="G"
/clone_Tib="G"
/note="Genoscope sequence ID : COA
PUC-Ori"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: Robert_Strausberg@nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9746 row: c column: 22
High quality sequence stop: 649.
Location/Qualifiers
             ux27g03.y1 Soares_NMMAX_maxillary_process Mus musculus cDNA IMAGE:3511540 5' similar to TR:070239 070239 RAXIN. ;, mRNA
                                               BE854108
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1 (bases 1 to 651)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
   sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
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/clone_lib="NIH_MGC_72"
/tisue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo of Average insert size 2 kb. Library constructed by Life Technologies."

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/db_xref="taxon:9606"
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68.3%;
                                             585 bp
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Pred. No. 3e-37;
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                           Mus musculus cDNA
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                                                              gcacagaccgagatccaggcagtgatggaggaaaatgcctaccaggtgttcttgacttct
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                                                                                                                                                                                                                                                   AGGAAGCTTGAGCCCTGTGACTCAAATGAGGAAAAGAGGCTGAAGCTGGCAAGAGCCATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Possible reversed clone: similarity Seq primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tumor Gene Index
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
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Mammalia; Eutheria;
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/clone="IMAGE:3511540"
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Pred. No. 3.7e-33;
0; Mismatches 116; 1
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gcacagaccgagatccaggcagtgatggaggaaaatgcctaccaggtgttcttgacttct 348
                                                                                                               abgacctacatacgagatggcatcaagaagcaacagatcggctcggtcatgtttgaccag 288
                                                                                                                                                              tataagaggtaca---ttgagaacaacagcgttgtctccaagcagctgaagcccgccacc 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | tggaccaagtctttacactccttgttgggtgaccaggatggtgcatacctcttccggact 60
                                                                                                                                                                                                                                                      AGGAAGCTTGAGCCCTGTGACTCAAATGAGGAAAAGAGGCTGAAGCTGGCAAGAGCCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM9814 row: i column: 14
High quality sequence start: 5
High quality sequence stop: 688.
Location/Qualifiers
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Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Tel: (301) 496-1550
Tel: (301) 496-1550
Temail: Robert_Strausberg@nlh.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 956)
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/clone="IMAGE:4224469"
/clone="lb="NCI_CGAP_CO24"
/clone=lb="NCI_CGAP_CO24"
/lab_host="DH10B (T1 phage resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sali; Cloned unidirectionally. Primer: Oligo dT.
Site_2: Sali; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
a 234 c 288 g 176 t
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/strain="FVB/N"
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Pred. No. 4.3e-33;
0; Mismatches 116; Indels 12; Gaps
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuc Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. La
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA198606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The WashU-HHMI Mouse EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: mouseest@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                          118
                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                          3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Bertrand Jordan. Library went through two rounds of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH10B"
/lab_host="DH10B"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
/note="Vector: pH7T3D-Pac (Pharmacia) with a modified
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/clone="IMAGE:639463"
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/strain="C57BL/6J"
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                                                                                                              Score 143.6; DB 3; 
Pred. No. 4.9e-32; 
0; Mismatches 119;
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97044477
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                                                                                                                                                                             Email: msoares@blue.weeg.uiowa.edu
Oligo-dT track not found, Not I site shown in beginning of seque
is likely internal to the message. cDNA Library Preparation: M.J
Soares Lab Clone distribution: colones will be available through
                                                                                                                                                                                                                        451 Eckstein Medical Research Building Towa
Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                               Contact: Soares, MB Program for Rat Gene Discovery and Mapping
                                                                                                                                                                                                                                                                                                                                          Rattus.
                                                                                                                                                                                                                                                                                                                                                                              Norway rat.
Rattus norvegicus
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Seq primer: M13 Forward
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                                                                                                                                                                                                                                                                                                          discovery
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                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 475)
Bonaldo, M.F., Lenno
                                                                                                                                                      POLYA-No.
                                                                                                                                                                                                                                                                                                                                                                    Eukaryota;
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Res. 6 (9),
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                                                                                                                       organism="Rattus norvegicus"
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Sciurognathi;
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thi; Muridae; Murinae;
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Seq_primer: puc 18 forward
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1 (bases 1 to 406)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
                                                                                                                                                                                                                          Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar,
                                                                                                                                                                                                                                                                                                                                                                                                            Simpson, A.J
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                                                                                                                                     Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
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205; Conser
                                                                                                                                            L1,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Location/Qualifiers
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               /db_xref="taxon:9606"
/clone="CS0DC015YE11"
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                                            /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           916 C-CAGACCGAAATCCAGGCA 934
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                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 491)

Wambutt, R., Heubner, D., Mewes, H.W., Gassenhuber, J. and Wiemann, S. EST (Wambutt, et al.)

Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AL045145 491 bp mRNA
DKFZp4340084_r1 434 (synonym: htes3)
DKFZp4340084 5', mRNA sequence.
AL045145
consortium of the German Genome Project.

No sl sequence available.

This clone (DKFZp4340084) is available at the RZPD in Berlin.

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 140

Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
                                                                                                                                                       Clone from S. Wiemann, Molecular Genome Analysis, German Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg sequenced by AGOWA (Berlin/Germany) within the cDNA sequenced by AGOWA (Berlin/Germany)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST
                                                                                                                                                                                                                                                 Am Klopferspitz 18a D-82152 Martinsried, Germany This is the 5' sequence of the clone insert
                                                                                                                                                                                                                                                                                                                                           Contact: Wambutt R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="neuroblastoma cells"
/lab_host="DH10B"
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66.2%;
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Pred. No. 2.1e-23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99 ctggtttgcttgtaatgggttcaggcagatg-----aacctgaaggataccaaaac 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGATCCTGCCATGTTTGACCAGGCCCAGACCGAAATCCAGGCCACTATGGAGGAAAACAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       189;
                                                                                                                                                                                                                                                                                                                                                                                                                                AL044979 364 bp mRNA ES
DKFZp434C044_r1 434 (synonym: htes3) Homo
DKFZp434C044 5', mRNA sequence.
                                                                                                                                               Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de; sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing consortium of the German Genome Project.
                                                                                                                                                                                                                                                     EST (Wambutt, et al.)
Unpublished (1999)
Contact: Wambutt R
                                                                         No sl sequence available.
This clone (DKFZp434C044) is available at the RZPD in Please contact the RZPD: Ressourcenzentrum, Heubnerweg Berlin-Charlottenburg, GERWANY; Email: clone@rzpd.de.
                                                                                                                                                                                                           Am Klopferspitz 18a D-82152 Martinsried, Germany This is the 5' sequence of the clone insert
                                                                                                                                                                                                                                                                                              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 364)

Wambutt,R., Heubner,D., Mewes,H.W., Gassenhuber,J. and Wiemann,S
                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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Mammalia; Eutheria; Primates;
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/clone_lib="434 (synonym:
/tissue_type="testis"
/dev_stage="adult"
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKFZp434C044"
/clone_lib="434 (synonym:
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/note="Vector: pSport1;
127 c 139 g
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/db_xref="taxon:9606"
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Pred. No. 6e-22;
0; Mismatches
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Bonaldo, M.F., Lenno
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                                                                                                                                                                                                                                                                                                      Soares, MB
                /dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                       Eutheria;
       'lab_host="DH10B
                                                                                                                                                                                                                                                                                                                                                                                                                                     Metazoa;
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                                                                                                                                                                                                                                                                                                                            Email: msoares@blue.weeg.ulowa.edu
cDNA Library Preparation: M.B. Soares Lab Clone distribution:
clones will be available through Research Genetics (www.resgen.
This clone is also available through the I.M.A.G.E. Consortium
LLNL (info@image.lln1.gov). IMAGE ID- 1779287
Seq primer: M13 Forward.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BF559312 217 bp mRNA
UI-R-E1-fa-e-06-0-UI.rl UI-R-E1 Rattus
UI-R-E1-fa-e-06-0-UI 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Program for Rat Gene Discovery and Mapping University of Iowa 451 Eckstein Medical Research Building Iowa City, Tel: 319 335 8250
Fax: 319 335 9565
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1. .217
                                                                                                                                                                                            organism="Rattus norvegicus"
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Matches 111; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-E1 library is a subtracted library derived from the UI-R-E0 library. The UI-R-E0 library consisted of a mixture of individually tagged normalized libraries constructed from 8, 12 and 18-day embryo. The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dT track which allows identification of the library of origin of a clone within the mixture. The subtracted library (UI-R-E1) was constructed as follows: PCR amplified cDNA inserts from a pool of UI-R-E0 clones from which 3' ESTs had been derived was used as a driver in a hybridization with the UI-R-E0 library in the form of single-stranded circles. The remaining single-stranded circles subtracted library was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporate into DH10B bacteria (Life Technologies) to generate the UI-R-E1 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6: 791-806, 1996);
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1996) "
70 c
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

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                                               162;
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A98523
                                                                                                               Patent: WO 9911780-A 8 11-MAR-1999;
BIRCHMEIER WALTER (DE); BEHRENS JUERGEN (DE)
Location/Qualifiers
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CONDUCTINE PROTEIN AND A RELATED AGENT FOR DIAGNOSING AND TREATING TUMOR ILLNESSES
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1241 GCCAATGGCCAAGTGTCTCTACCTCATTTTCCGAGAACCCACCGCCTGCCCAAGGAGATG
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                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 2825)
Behrens, J., Jerchow, B.-A., Wurtele, M., Grimm, J., Asbrand, C., Wirtz, R., Kuhl, M., Wedlich, D. and Birchmeier, W. Functional interaction of an axin homolog, conductin, with beta-catenin, APC, and GSK3beta Science 280 (5363), 596-599 (1998)
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Sequence 6 from Patent WO9911780.
A98521
                    Behrens,J., Jerchow,B.-A. and Birchmeier,W.
Direct Submission
Submitted (22-JUN-1998) Cellular Biology, Max Delbrueck Center
Molecular Medicine, Robert-Roessle 10, Berlin 13122, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus conductin AF073788
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BIRCHMEIER WALTER (DE); BEHRENS JUERGEN (DE)
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CONDUCTINE PROTEIN AND A RELATED AGENT FOR DIAGNOSING AND TREATING
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                                                                         Direct Submission
Submitted (16-NOV-1999) Genetics & Development, Columbia
University, 701 W168th St. HHSC 1416, New York, NY 10032,
Location/Qualifiers
                                                                                                                                                                                                                           Zhang, T., Fagotto, F., Hsu, W., Zeng, L., Gilbert, D., Copeland, N.G., Jenkins, N.A., Warburton, D. and Costantini, F. Properties of mouse Axin2 and human AXIV2: chromosomal location, expression pattern, interaction with Axin and effects on embryoni
                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus Axin2 (Axin2) mRNA, complete cds. AF205889
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/db_xref="taxon:10090"
215. .2737
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GCQSFGYGRYSRSRSDHHHQHHHQCHTLLSTGGKLPPVAKELLGGKSFLTKQT
TKHVHHYIHHAVPKYKEELEAEATQRVKCLLCPGGTDYYCYSKCKSHSKAPEDLPGE
QFCGSRGGTLPKRNAKGTEPGLALSARDGGMSSAAGGPQLPGEEGDRSQDVWQWMLES
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KVLCCYLPTLNEEEEMTCADLKCKLSFTVYGLSSKTLAATASVKSTETAENGFRSFKR
SDPVNPYHVGSGYVFAATSANDSELGSDALTDDSMSMTDSVTGVFPYHMGSKKQLA
REMHRSVKANGQVSLPHFPRTHRLPKEMTPVEPAAFAAELISRLEKLKLELESRHSLE
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PPLTPPNTLAQLEEACRRLAEVSKPQKQRCCVASQQRDRNHSAAGQAGASPFANPSLA
PEDHKEPKKLASVHALQASELVVTYFFCGEEIPYRRMLKAQSLTLGHFKEQLSKKGNY
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STKPMPVSSNARRNEDGLGEPEGRASPDSPLTRWTKSLHSLLGDQDGAYLFRTFLERE
KCYDTLDFWFACNGFRQMNLKDTKTLRYAKAIYKRYIENNSVYSKQLKPATKTYIRDG
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                                 /db_xref="taxon:10090"
                                                   /organism="Mus musculus"
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and Kikuchi, A.
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Location/Qualifiers
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Yamamoto,H., Ikeda,S., Murai,H., Kishida,S. and Kikuchi,A. Direct Submission
Submitted (08-AUG-1997) Biochemistry, Hiroshima University, of Medicine, 1-2-3 Kasumi, Minami-ku, Hiroshima, Hiroshima
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="AAF22800.1"
/db_xref="GI:6653586"
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Pred. No. 6.2e-32;
Pred. No. 6.2e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Uochi,T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ikeda,S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                 inhibits axis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Koyama, S., Asashima, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Euteleostomi;
Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
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TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      acgcctgtggaacctgctgccttcgccgccgagctcatctccaggctggagaaactgaaa 120
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                                                                            Fernandez,C., Ferraguto,D., Forcum-Tansey,J., Gill,R.,
Gorrell,J.H., Gunaratne,P., Haller,G., Hernandez,J., Hogues,M.,
Hosak,H., Hou,X., Huber,J., Jackson,L., Jia,Y., Kelly,J., Kelly,S.,
Kovar,C., Liu,J., Liu,W., Loulseged,H., Lozado,R.J., Martin,R.,
Kovar,C., Liu,J., Liu,W., Loulseged,H., Lozado,R.J., Martin,R.,
Massey,E., McLeod,M.P., Mei,G., Moore,S., Morgan,M., Morris,S.,
Neal,D., Nelson,A., Nguyen,R., Nguyen,N., Oguh,M., Parish,B.,
Perez,L., Relter,D., Say,J., Shen,H., Vasquez,L., Watlington,S.,
Williamson,A., Wrensford,G., Zhou,X., Bouck,J., Hodgson,A.,
Milliamson,A., Wrensford,G., Zhou,X., Bouck,J., Hodgson,A.,
                                                                                                                                                                                                                                                                                                                                       Metzker, M.L., Lewis, L.R., Hume, J., Edwards, C., Harris, C., Dederich, D., Thomas, S., Okwuonu, G., Carlock, C., Garner, T., Addison, S., Pace, A., Williams, G., Bonnin, D., Brows, Buhay, C., Bunac, C., Burkett, C., Chacko, J., Chen, G., Chen, Z., Cox, C., Davis, C., Delgado, O., Ding, Y., Dugan-Rocha, S., Cox, C., Davis, C., Delgado, O., Ding, Y., Dugan-Rocha, S.,
                                                        Williamson, A., Wrensford, Muzny, D.M., Rives, M., Sch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 191041)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC024114 191041 bp DNA HTG 06-NOV-201 MUS musculus chromosome 11 clone RP23-278J12, WORKING DRAFT SEQUENCE, 30 unordered pieces.
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REMHRSVKANGQVSLPHFPRTHRLPKEMTPVEPAAFAAELISRLEKLKLELESHSLE
ERLQQIREDEEKEGSEQALSSRDGAPVQHPLALLPGSGYEEDPQTILDDHLSRVLKTF
GCOSPGVGRYSSPSRSSDHHHHHHQQCHALLPTGGKLPPEAACPLLGGKSFLTRQTTK
HVHHHYIHHAVPKTKEEIEAEATQRVRCLCPGGTDYYCYSKCKSHSKPPEPLPGEQF
CGSRGGTLPKRNTKGTEPGLALPAREGGMSSAAGAPQLPGEEGDRSQDVWQWMLESER
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DHKEPKRLASVHALQASELIVTYFFCGEEIPYRRMLKAQSLTLGHFKEQLSKKGNYRY
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/protein_id="Ac40089.1"
/protein_id="A080759"
/db_xref="G1:3080759"
/translation="MSSAVLVTILLPDPSSSFREDAPRPPVPGEEGETPPCQPSVGKVQ
/translation="MSSAVLVTILLPDPSSSFREDAPRPVPGDGGGTPPCQPSVGKVQ
STKPMPVSSNARRNEDGIGEPEGRASPDSPLTRWTKSLHSLLGQDGAYLFRTFTLERE
STKPMPVSSNARRNEDGIGEPEGRASPDSPLTRWTKSLHSLLGQDGAYLFRTFTLERE
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IKKQQIGSVMFDQAQTEIQAVMEENAYQVFLTSDIYLEYVRSGGENTAYMSNGGLGSL
KVLCGYLPTLNEEEEWTCADLKCKLSPTVVGLSSKTLRATASVRSTETAENGFRSFKR
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/db_xref≈"taxon:10116"
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Pred. No. 3.1e-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 191041)
Worley, K.C.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently
consists of 30 contigs. The true order of the pieces
is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      be preserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTE: Estimated insert size may differ from sequence length
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Chemistry: Dye-terminator Big Dye: 5% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 158769 bases at least Q40
Consensus quality: 172780 bases at least Q30
Consensus quality: 172780 bases at least Q30
Estimated insert size: 180377; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; sqarose-fp estimation
Quality coverage: 3.2x in Q20 bases; sum-of-contigs estimation
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                              150789
150889
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113342
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of 10232 bp in length
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Best Local
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                                                                                         AUTHORS
                AUTHORS
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Kawabata,A., Hikiji,T., Kobatake,N., Inagaki,H., Ikema,Y., Okamoto,S., Okitani,R., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S. NEDO human cDNA sequencing project upublished (2000)
2 (bases 1 to 2104)
Sugano,S., Suzuki,Y., Ota,T., Obayashi,M., Nishi,T., Isogai,T., Shibahara,T., Tanaka,T. and Nakamura,Y.
                                                                                                                                                                AK025718.1 GI:10438327
oligo capping; fis (full insert sequence).
Homo sapiens hepatoma cell_line:HepG2 cDNA
                                                                                                                                                                                                                   AK025718 2104 bp mRNA
Homo sapiens cDNA: FLJ22065 fis,
AF078165 Homo sapiens conductin
                                                                                                                 Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                           Homo sapiens
                                                                                                                                                        clone: HEP10566.
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43523 c 42989 g !
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/db_xref="taxon:10090"
/chromosome="11"
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191041: contig of 1307
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95.8%;
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Pred No. 6.7e-25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       143;
                                                 Mai,M., Qian,C., Smith,D.I. and Liu,W.
Direct Submission
Submitted (15-JUL-1998) Lab Medicine and Pathology, Mayo clinic,
200 First Street SW, Rochester, MN 55905, USA
Location/Qualifiers
                                                                                                                                                                                                                           Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3072)

1 (bases 1 to 3072)

Mai,M., Qian,C., Yokomizo,A., Smith,D.I. and Liu,W.

Cloning of the human homolog of conductin (AXIN2), a gene mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (29-AUG-2000) to the DDBJ/EMBL/GenBank databases. Submitted (29-AUG-2000) to the DDBJ/EMBL/GenBank databases. Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure Analysis, Human Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- 6 3'-end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology
                                                                                                                                                                       to chromosome 17q23-q24
Genomics 55 (3), 341-344 (1999)
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/clone_lib="HEP"
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/cell_type="hepatoma"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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Pred. No. 4.4e-24;
D; Mismatches 19
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                                                                                    Submitted (16-NOV-1999) Genetics & Development, Columbia University, 701 W168th St. HHSC 1416, New York, NY 10032, USA
                                                                                                                                Zhang, T. and Costa
Direct Submission
                                                                                                                                                                                                                                                    Jenkins, N.A., Warburton, D. and Costantini, F. Properties of mouse Axin2 and human AXIN2: chromosomal location,
                                                                                                                                                                                              Unpublished
                                                                                                                                                                                                                       axis formation
                                                                                                                                                                                                                                         expression pattern, interaction with Axin and effects on embryonic
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2538)
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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1 838 c 883 g 582 t
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SLAPEDHKEPKKLAGVHALQASELVVTYFFCGEEIPYRRMLKAQSLTLGHFKEQLSKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KVVCCYLPTLMEEEBYTCÄDFKCKLSPTVVGLSSKTLRATASVRSTETVDSGYRSFKR
SDPVNPYHIGSGYVFAPATSANDSEISSALTDDSMSWTDSSVDGIPPYRVGSKKQLQ
REMHRSVKANGQVSLPHPPRTHRLPKEMTPVEPATFAAELISRLEKLKLESSHSLE
REMLOQUSLPHEPRTHRLPKEMTPVEPATFAAELISRLEKLKLESSHSLE
RELOQUREDEREGSELTLNSREGAPTQHPLSLLPSGSYEEDPQTILDDHLSRVLKTP
GCQSPGVGRYSPRSRSPDHHHHHHSQYHLSLLPGGSLLPDAASSECPLLGGKGFVKR
QTYKHYHHYLHHHAVPKTKEEIEABATQRVPCFCPGGSEYCYSKCKSHSKAPETM
KOTKHYHHHYLHHHAVRKEEIFBAATGRVFCPGGAGALQLPREEGDRSQDVWQWML
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                                                                  ocation/Qualifiers
                                                                                                                                                                                                                                                                                                  Fagotto, F., Hsu, W., Zeng, L., Gilbert, D., Copeland, N.G.,
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KCVDTLDFWFACNGFRQMNLKDTKTLRVAKAIYKRYIENNSIVSKQLKPATKTYIRDG
IKKQQIDSIMFDQAQTEIQSVMEENAYQMFLTSDIYLEYVRSGGENTAYMSNGGLGSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product-"conductin"
/protein_id="AAD20976.1"
/db_xref="G1:4454791"
/translation="MSSAMLVTCLPDPSSSFREDAPRPPVPGEEGETPPCQPGVGKGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="AXIN2"
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Submitted (09-SEP-1999) to the DDBJ/EMBL/GenBank databases. Toshio Hirano, Biomedical research center, Osaka Univ. Med. scool, Department of Molecular Oncology; 2-2, Yamadaoka, Suita, Osaka 565-0871, Japan (E-mail:hirano@molonc.med.osaka-u.ac.jp, URL:http://www.med.osaka-u.ac.jp/pub/molonc/www/index.html, Tel:81-6-879-3880, Fax:81-6-879-3889)
                                                                                                                                                 Hirano,T., Hibi,M. and Shimizu,T. Direct Submission
                                                                                                                                                                                                                                            Shimizu,T., Yamanaka,Y., Ryu,S.L., Hashimoto,H., Yabe,T., Hirata,T., Bae,Y.K., Hibi,M. and Hirano,T. Cooperative roles of Bozozok/Dharma and Nodal-related proteins the formation of the dorsal organizer in zebrafish mech. Dev. 91 (1-2), 293-303 (2000)
                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes; Cyprinidae; Rasborinae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Danio rerio
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724 c 724 q 473 t
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CQSPGVGRYSPRSRSPDHHHHHHSQYHSLLPPGGKLPPAAASPGACPLLGGKGFVTKQ
TTKHVHHHYIHHHAVPKTKEEIEAEATQRVHCFCPGGSEYYCYSKCKSHSKAPETMPS
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EPKKLAGVHALQASELVVTYFFCGEETPYRRMLKAQSLTLGHFKEQLSKKGNYRYYFK
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DPVNPYHIGSGYVFAPATSANDSEISSDALTDDSMSMTDSSVDGIPPYRVGSKKQLQR
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/db_xref="GI:6653584"
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/note="similar to ESTs 823683 and
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87.0%;
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Pred. No. 2.9e-23;
0; Mismatches 21;
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AF009674
                               Two dominant mutations in the mouse Fused gene are the result transposon insertions genetics (1997) In press genetics (1997) In press 2 (bases 1 to 3411)
2 eng, L., Fagotto, F., Zhang, T., Hsu, W., Vasicek, T.J., Perry, W., 3rd, Lee, J.J., Tilphman, S.W., Gumbiner, B.M. and Costantini, F. The mouse Fused locus encodes Axin, an inhibitor of the Wnt signaling pathway that regulates embryonic axis formation (2011 90 (1), 181-192 (1997)
                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo. 1 (bases 1 to 3411)
                                                                                                                                                                                                                                    vasicek, T.J., zeng, \dot{L}., Guan, X.-J., zhang, T., Costantini, F. and Tilghman, S.M.
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(bases 1 to 3411)
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RDNIKRQUIDSAMFDQAQMEIQTAMEERAYQWFLTSDIYLEYVFTGCERPSHVAPNGL
GGLKLVGGYLFTLNEEEERSCNDFKAKALAITVGLSAKTLRSPPLRAVEALEKGYRSY
RRSDPGNPNRFTSGYSFAPATSANDSEVSSDALTDDSNSMTDSSVDAIPPYKLGSKKO
LQREMQRNMRNNGQVSLPPFPRTRPPKEMTPVFPAAFRAQLLARLERLKREDGETMSS
LEERLQQIQEEEERDESEMSSSASHSLPLLPPGTCEEDPQAILDEHLSRVLKTBGCQ
SPGLLRHSPRSRSPEORPLPRGGISTRSQSSNNGYVPAKTFISRQSTKHIHHYIHH
HAGPKSKEQITVEATORVQCLCHGTSECCTAYYIRSRSLGRDQCASPAEVALGHSSTL
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MYEGKILGKVDRMD"
1 839 c 864 g 796 t
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/protein_id="sayin240.1"
/protein_id="sayin240.1"
/db_xref="Gi:7229080"
/translation="murtLTDDMVSSFREDDPRPPVPGEEGETTCHHPSKLAMMRPKD
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HSLEPTRTHTWGGGGSSGHLRAHQPAHPFVQDPAMPPLPPNTLAQLEEARRRLEEVS
KPSKQRHSTSSLQRDKSHPVPVQNGSSAFPMDERKDPKKMSGCHSSLGSETVVTYFFC
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                                                                              Xenopus laev
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AF140243.1
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Submitted (22-JUN-1997) Biological Technology, Millennium
Pharmaceuticals, Inc., 640 Memorial Drive, Cambridge, MA (
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               \label{local_variance} Vasicek, T.J., \ Tilghman, S.M., \ Costantin1, F., \ Zeng, L., \ Perry, W.L. \\ and \ Zhang, T. \\
                       Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
                                        African clawed frog
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="GPGSRHHRARDRLIHEGAVSTDVLGCSAHCSLTQSPKMNIQEOG
FPLDLGASTTEDAPRPPVPGEBGELVSTDPRASYSFCGKGVGIKGETSTATPRRSD
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MQESAQVNGRVPLPHIPTYTKYPXEVRYEPQKFAEELHRLEAVQRTREAEEKLEERL
KRVRMEEEGEDGDPSSGPPGPCHKLPPAPAWHHFPPRLCWTWACAGLRDAHEENPESI
LDEHYQRVLRTTGROSSGPBGPCHKLPPAPAWHHFPPRLCWTWACAGLRDAHEENPESI
LDHHRHVHHYHHSTARPKEOVEAEATRRAQSSFAWGLEPHSHGARSGCYSEVGAAP
NASDGLAHSGKVGVACKRNAKKAESGKSASTEVPGASEDAEKNOXIMOWIIEGEKEIS
RHRRTGHGSSGTRKPQPHENSRPLSLEHPWAGPQLRTSVQPSHLFIQDDTMPPHPAPA
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LSETETRSQRKVGGGSAQPCDSIVVAYYFCGEPIPYRTLVRGRAVTLGQFKELLTKKG
SYRYYFKKVSDEFDCGVVFEEVREDEAVLPVFEEKIIGKVEKVD"
1 1010 c 1066 g 582 t 1 others
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adults"
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may inhibit embryonic axis formation"
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mutation due
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/note="contains RGS domain and Daughterless similarity;
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/map="16p13.3"
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/db_xref="GI:2252820"
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Danio rerio Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi Cypriniformes; Cyprinidae; Rasborinae; Danio.
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95; Conserv
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                                                                                                     Danio rerio
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                                                                                                                                                                   Danio rerio mRNA for axin1, complete cds. AB032262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antipova, A., Itoh, K. and Sokol, S. Direct Submission
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                                                                                                                                                                                                           AB032262
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HLKHKEDFNREAEGCVAHDSRFSRWGRSLNLLLDDQDGATLFRWYLEGEGLGDLLTFW
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VFDQAQQEIQRAMEQEAFTSFLQSDICKEYARGVEDSPTPESPGPGLPTLTEDEEFGG
LHHFSSGMKINRAFSRIPFRKORSHFRKLEGTYQYEAPAASINDSEISSDALTEDSM
SMTDGSVDGIPPYRSKKQREIHRSVSANGKVSLLFFVPRTMRPPAEMMTSPAEFAAKL
TIALEKVKKQRDAEEKLEEKLQRLKEEEEIADVDIPSSSHETVPGAALEDDPQSILDD
HVSRVLKTPANLSPRSQSPTVQRKGKFQPAFSKGOTSTSCHLRKVPQGMEATSTLAS
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EVSEEDAVLPLFEEKIICKVERAC"
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AKLMKKHHRETASVTPCPELKKATHRAASQPAHLFLQDTSMPPLTAPNTLDQLEEARR
RLVEDKRVPKLHKSRCVQSTTLKEKGKTAESVPSSGFSTLKLSEEQKTAKKPSSECPG
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/protein_id="AAF22574.
/db_xref="GI:6652991"
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/db_xref="taxon:8355"
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Gallus ga
AF009012
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Department of Molecular Oncology; 2-2, Yamadaoka, Suita,
565-0871, Japan (E-mail:hirano@molonc.med.osaka-u.ac.]p,
                                                          chicken.
                                                                                                AF009012.1
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Tel:81-6-879-3880, Fax:81-6-879-3889)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (09-SEP-1999) to the DDBJ/EMBL/GenBank
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Similarity 62.3%;
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KVSYEFDCGVVFEEVREDDAILPIFEEKIIGKVEKVD"
1769 c 874 g 564 t
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RQIKPATKSFIKDCVMKLHIDPAMFDQAQTEIQTMMEENTYPLFLKSDIYLEYTRTGG
ESPKLFSDQSSVSGNCKVLPCYLPTVIEDVEWRCDQEEEQIAESDPTPSNRLTQKLLL
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/protein_id="BAA92439.1"
/db_xref="GI:7229078"
/translation="MSMSVNEKGICYLPDLGSSFTEDAPRPPVPGEEGDLVSSDGRQY
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Pred. No. 0.0014;
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                                                                                                                                                                                                                                                                                             --CCACGTTGAACCAGAAAAGTTTGCTGCAGAACTGATCAATCGTTTGGAAGAAGTACAG 1457
    Human DNA sequence from cosmid 419C1 from the short arm of chromosome 16, spanning 7 299754 299754.1 GI:30767°.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                93;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zeng, L., Zhang, T.
Direct Submission
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LKQRLKPQKRPGSGASQPCENITVAYYEGGEPIPYRTLYKGRVYTLGQFKELLTKKGN
YRYYFKKVSDEFDCGVYFEEVREDDTILPIFEEKIIGKVEKID*
1 825 c 858 g 598 t
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KIYSDPSSGSGTGKGLPGYLPTLNEDEEWKCDQDTEPEASRDSAPSSRLTQKLLLETA
TQRATSTRRYSEGREFRHGSWREPVNPYYVNTGYAMAPATSANDSEQQSMSSDADTMS
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/db_xref="GI:2252818"
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/db_xref="taxon:9031"
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419C1 from a contig from the t.
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TITLE
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ORGANISM
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The true left end of Clone 419Cl is at 1 in this sequence. The true right end of clone 314C4 is at 104.
The true left end of clone 333BlO is at 21926.
The true left end of clone 333BlO is at 21926.
419Cl is from a 400kb clone contig on 16p.
Higgs D.R., Flint J. unpublished. MRC Molecular Haematology Unit, Institute of Molecular Medicine, Oxford.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clonerequest@sanger.ac.uk
on Apr 8, 1998 this sequence version replaced gi:2465054.
IMPORTANT: This sequence is not the entire insert of clone 419C:
It may be shorter because we only sequence overlapping sections
once, or longer because we arrange for a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (27-OCT-1997) Chromosome 16 Project Group (http://www.sanger.ac.uk/HGP/Chr16/) Sanger Centre, Wellcome Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Smye,
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1 (bases 1 to 22029)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               libraries constructed by Norman Doggett (unpublished).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   419C1 came from the Los Alamos,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        enquires: humquery@sanger.ac.uk Clone requests:
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incomplete repeat"
4653. .4914
                                                        /note-"/
                                                                                                                                               6389.
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/db_xref="taxon:9606"
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/note="AluJo repeat:
incomplete repeat"
                                         7656.
                                                                                                                                                                                                                                  5804.
                                                                                                                                                                                                                                                                         5508.
                                                                                                                                                                                                                                                                                                                                /note="AluJo repeat:
incomplete repeat"
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incomplete repeat"
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/clone_lib="LA16"
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                                                                                                  /note="AluJb repeat:
incomplete repeat"
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                                                          Alux repeat: matches 15. .301 of consensus
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                     matches
                                                                                                                         matches 247.
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    .124 of consensus;

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.44 of consensus;

of consensus;

of consensus"

of consensus;

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of

consensus;

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BASE COUNT
ORIGIN
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Best Local Similarity
Matches 84; Conserv
10598 TCCCTCGCAGCGCACGTACCGGGGTGCCGAAGGAGGT---CCGCGTGGAGCCTCAGAAGTT 10542
                                                                            10541 CGCGGAGGAGCTCATCCACCGCCTGGAGGCTGTGCAGCGCACGCGGGAGGAGGAGGAGAA 10482
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                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="MCRIB repeat: matches 333...139 of consensus"
14879. 14912
/note="17 copies of 2 mer 82 % conserved"
15202...15422
/note="Alux repeat: matches 7...227 of consensus;
incomplete repeat"
16542...16847
/note="Alux repeat: matches 301...1 of consensus"
17178...17476
/note="Alux repeat: matches 301...1 of consensus"
17178...17476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Alusq repeat: matches 297..1 of consensus"
9967. .10175
/note="match: 5' EST AA085320"
10450. >16291
/note="match: mouse 5' EST AA238939"
10683. .10981
/note="Alusx repeat: matches 299..1 of consensus"
11335. .11635
                                                                                                                                                                                                                                                                                                                                                          incomplete repeat" 6217 c 5887 g 4780 t
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/note="AluSx/g repeat: matches 82. .111 of consensus;
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/note="AluJb repeat: matches 267. .1 of consensus;
incomplete repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                          note="AluY repeat: matches 1. .301 of consensus" 1999. .22028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="4 copies of 44 mer 88 % conserved"
21693. .21994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note-"AluJo repeat: matches 2. .302 of consensus" 0549. .20724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="AluJo repeat: matches 2. .124 of consensus;
nocomplete repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            orte "AluY repeat: matches 301. .1 of consensus" (003. .12110 tote "AluSg repeat: matches 123. .1 of consensus; complete repeat"
                                                                                                                                                                                                                                                             24.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         e="AluY repeat: matches 1. .300 of consensus" 4. .19163

    12. .12248
    12. .1814 of consensus
    11. .12508
    12. .12508
    13. .1186 of consensus
    13. .1186 of consensus
    12. .12743

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Murine axin gene.
Mouse brain CNG-2
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Human porphobilino	X87633	20	1035	7.	28.8	45	
Human porphobilino	X87632	20	1035	17.8	28.8	44	
Human porphobilino	x87630	20	1035	?	28.8	43	
Human porphobilino	X87638	20	1035	.7	. 28.8	42	
Human porphobilino	X87637	20	1034	.7	28.8	41	
2	X40107	20	751	•	28.8	40	C
	C79115	21	550		28.8	39	C
Human lung tumour	07	20	550	•	28.8	38	C
Membrane-bound pro	649	21	3531	٠	29.2	37	
Human PRO290 nucle	583	21	3531	18.	29.2	36	
Human heart tissue	209496	20	4751	18.3	29.6	35	O
Bovine retina Ih i	0948	20	1820	•	29.6	34	O
brain	X84445	20	1790	18.	29.6	33	C
Mouse brain CNG-3	X84446	20	1507		.29.6	32	O
cycli	X25488	20	1307		29.6	31	C
Human secreted pro	F33247	22	1246	•	29.6	30	O
Human porphobilino	X87634	20	1034	18.3	29.6	29	
Human	C00205	21	372	•	29.6	28	
Eucalyptus grar	C56489	21	537	•	29.8	27	
Human secr	A42312	21	533	18.	30.2	26	
Human MIF1	Z58958	21	1914	18.	4	25	C
Human MIF1 prote	Z58953	21	1553	•	30.4	24	C
hGDF-1 and l	Q20690	13	2510	19.0	30.8	23	
Mouse GDF-1	239482	21	1247	٠	30.8	22	
Human GDF-1	V19538	19	1247	•	30.8	21	
Human GDF-1	V32588	19	1247		30.8	20	
cDNA sequence enco	T97883	18	1247	٠	30.8	19	
÷	ၾ	18	1247	•	30.8	18	
Human GDF-1( $fx$ ) mo	-	15	1247		30.8	17	
GDF-1(fx)	12	15	1247	٠	30.8	16	
Human GDF-1(fx) mo	731	15	1247	٠	30.8	15	
~	Q58055	15	1247	٠	30.8	14	
ogen GD	œ	14	1247	19.0	30.8	13	
Human GDF-1 coding	13	14	1247		30.8	12	

## ALIGNMENTS

RESULT X23370 Tumor-suppressing protein conductin diagnosis of tumors Conductin; tumour; diagnosis; treatment; beta-catenin; anti-tumour; therapy; cytoplasmic degradation; blockade; wnt signalling pathway; Mingless signalling pathway; Adenomatous Polyposis Coli; APC; tumour suppressor; ss. 17-JUN-1999 X23370 standard; cDNA; WPI; 1999-214706/18. P-PSDB; W93570. 02-SEP-1997; 01-SEP-1998; WO9911780-A2 Human conductin cDNA Behrens J, Birchmeier W; (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN 11-MAR-1999 Homo sapiens suppressor; (first entry) 97DE-1038205 98WO-DE02621 2523 ВP . used for treatment and MAX

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PD 113 369 PD 213 369 PD 115 P
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Matches 162; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1147
                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conductin; tumour; diagnosis; treatment; beta-catenin; anti-tumour; therapy; cytoplasmic degradation; blockade; Wnt signalling pathway; Wingless signalling pathway; Adenomatous Polyposis Coli; APC;
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                                                                                                                                                                                                                                                                                             protein_bind
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                                                                                                                                                                                     /bound_moiety= beta-catenin
/note= "as described in Claim
2561..2713
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/note= "as described in
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described
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                                                                                                               "Dishevelled homology region Claim 22"
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Pred. No. 1.2e-38;
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APC;
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Best Local (
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                                                                                                                                                                                                                                                                                                                                         1361
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 09-JUL-1998;
                                             WO9902179-A1
                                                                                                                             Homo
                                                                                                                                                    beta-catenin; ss.
                                                                                                                                                                           gastrointestinal cancer;
                                                                                                                                                                                      Axin; cancer; breast cancer; colorectal cancer;
                                                                                                                                                                                                            Human axin gene.
                                                                                                                                                                                                                                   14-JUN-1999
                                                                                                                                                                                                                                                          X09012;
                                                                                                                                                                                                                                                                               X09012 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes a novel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Behrens J,
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                                                                                                                                                               diagnosis; treatment;
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 98WO-US14414.
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/product=
                                                                                                     Location/Qualifiers
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                                                                                                                                                               therapy; thyroid carcinoma;
                                                                                                                                                                                                                                                                                 3411
                                                                                                                                                               esophageal cancer; carcinoma; melanoma;
erapy; thyroid carcinoma; tumorigenesis;
                                                                      Axin
                                                                                                                                                                                                                                                                                 ВP
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Pred. No. 1.2e-38;
; Mismatches 0;
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                     1313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           who are likely to develop cancer (thyroid carcinomas). The nucleic acids are also useful for diagnosing cancer and for detecting mutations in cancerous cells. Wild type Axin, its antisense molecule and identified compounds form pharmaceutical compositions in the treatment of cancer. The compositions are also useful for treating cancer by inhibiting tumorigenesis (by inducing degradation of beta-catenin). The nucleic acid encoding Axin acts through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding mutant and wild type Axin and oligonucleotides derived from them are useful for detecting mutations in the Axin gene and for determining whether a subject is
                                                                                                                                                Axin; cancer; breast cancer; colorectal cancer; gastrointestinal cancer; esophageal cancer; carcindiagnosis; treatment; therapy; thyroid carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   likely to develop cancer (including breast, colorectal, gastrointestinal, esophageal, carcinomas or melanomas). The wild type Axin and homologues of Axin are useful for treating subjects
WO9902179-A1
                                                                                                                                                                                                              Murine axin gene.
                                                                                                                                                                                                                                            14-JUN-1999
                                                                                                                                                                                                                                                                             x09013;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              negative regulation of the Wnt pathway in the Nieuwkoop Center.
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                                                                                                                                    beta-catenin;
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                                                                                                                                    88.
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                                                                      Location/Qualifiers
                           /product-
                                                                                                                                                                                                                                                                                                         DNA;
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                                                                                                                                                                                                                                                                                                         3761 BP
                            Axin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 56.4; DB 2
Pred. No. 1.6e-07
D; Mismatches 5
                                                                                                                                                                   carcinoma; melanoma;
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Best Local S
Matches 92
                                               BCNG; brain cyclic nucleotide gated ion channel; epilepsy; hyperalge Alzheimer's Disease; Parkinson's Disease; long QT syndrome; dyslexia sick sinus syndrome; age-related memory pystic fibrosis; sudden death syndrome; pacemaker rhythm dysfunction; sensory disorde auditory disorder; respiratory disorder; attention deficit disorder; learning disability; drug addiction; therapy; mBCNG-2; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                           1533
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3761 BP; 890 A; 1012 C; 1088 G; 771 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 7; Figure 9A-9B; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Newly isolated nucleic acid encoding "axis inhibition" protein (Axin) - useful for detecting, diagnosing and treating cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Constantini F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-JUL-1997;
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                                                                                                                                                                        Mouse brain
                                                                                                                                                                                                         10-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                     1590
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                                                                                                                                                                                                                                                                                 X84444 standard; cDNA; 1584 BP
                                                                                                                                                                                                                                                                                                                                                                                                      121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 gccaatggccaagtgtctctacctcattttccgagaacccaccgcctgcccaaggagatg 60
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              зp
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                                                                                                                                                                                                                                                                                                                                                                                        ctggagctggaaagccgccatagtctggaggagcggctgcag
                                                                                                                                                                                                                                                                                                                                                                  cgcactcgagaggctgaagaaaagttggaggaacggctgaag 1631
                                                                                                                                                                                                                                                                                                                                                                                                                                         ---cgggtagagccacagaaatttgctgaagagcttattcaccgtctagaggctgtccag 1589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gtcaatgggcgggtacctctacctcacattcctcgcacttaccgaatgccaaaggagatc 1532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                      CNG-2 coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 38.8;
Pred. No. 0
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. 026;
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                                                                                                                                                                                                                                                                                                                                                                                                          162
                                                                                                                                       epilepsy; hyperalgesia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 3761;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                       dyslexia;
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Z09482/c
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XX
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DE Huma
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KW Ih i
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CC (BCNG) of the invention, designated mBONG-2. BCNG and BCNG-related CC proteins are useful in screening for compounds that modulate, interact or CC affect expression. Compounds, e.g. antagonists and agonists, identified CC in the methods are useful for modulating BCNG or BCNG-related protein CC activity. Modulation is increased or decreased ion permissivity or ion CC flow rate. Modulators of BCNG, can be used to treat a neurological, renal, CC pulmonary, hepatic or cardiovascular condition. Such conditions include epilepsy, Alzheimer's Disease, Parkinson's Disease, long OT syndrome, CC epilepsy, Alzheimer's Disease, Parkinson's Disease, long OT syndrome, CC death syndrome or pacemaker rhythm dysfunction. BCNG or BCNG-related CC protein can also be used to treat sensory disorders, e.g. blindness, loss of vision, loss of smell, numbness and lack of ability to taste. Also central nervous system areas that control respiration or defects in the drugs, dyslexia, attention deficit disorder or learning disabilities, cc drug addiction and regulation of cell secretions. The proteins are useful targets for screening for drugs that are effective in the control of pain
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Best Local
Ih ion channel; human; sea urchin; fruit fly; rat; bovine; analgesi cardioactive; pacemaker; cardiac muscle; ion channel modulator; treatment; diagnosis; ion channel-related disease; cardiac disease; circulatory disorder; sinus ganglion regulation; sleep disorder; cortico-thalamic neuron; pain; detection; mutation; ss.
                                                                                                                                                                                                                                                                                                          1177
                                                                                                              Human Ih ion channel DNA fragment.
                                                                                                                                                   02-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                               1237
                                                                                                                                                                                                                      Z09482 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1584 BP; 351 A; 456 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleotide-gated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-418922/35
P-PSDB; Y22193.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYCO ) UNIV COLUMBIA NEW YORK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-MAY-1998;
23-DEC-1997;
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                                                                                                                                                                                                                                                       6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 isolated nucleic acid encoding a brain or heart cyclic
                                                                                                                                                                                                                                                                                                                              ctccaggctggagaaactgaaactggagct 128
                                                                                                                                                                                                                                                                                                                                                                                                       ccaccgcctgcccaaggagatgacgcctgtggaacctgctgccttcgccgccgagctcat 98
                                                                                                                                                                                                                                                                                                          CTCCAGGCTGGAAGACCTCAAATTTGAGCT 1148
                                                                                                                                                                                                                                                                                                                                                                          CCACCCCATGCTGGATGAAGTACATCTTCTTCCCGATGGTCCCCTCTCGGATGATGTAAT 1178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence encodes the brain cyclic nucleotide-gated ion channel of the invention, designated mBCNG-2. BCNG and BCNG-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                 54; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page 192-193;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                 (first entry)
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97US-0997685.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 32.4;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               437 G; 340 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             .6;
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                                                                        analgesic;
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Best Local
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                                                                     cardioactive; pacemaker; cardiac muscle; ion channel modulator; treatment; diagnosis; ion channel-related disease; cardiac disectirculatory disorder; sinus ganglion regulation; sleep disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acid and its encoding protein is used to identify substances (A) that modulate activity of ion channels; to treat and/or diagnose ion channel-related diseases, particularly cardiac or circulatory disorders and to prevent and/or treat cardiac/circulatory disorders (especially faulty regulation of the sinus ganglion), sleep disorders (particularly abnormal function of cortico-thalamic neurons) and/or pain. Fragments of the Ih ion channel nucleic acid are used to detect mutations e.g. for differential diagnosis. This sequence encodes a human Ih channel fragment isolated from human thalamus tissue.
                            Homo sapiens
                                                           cortico-thalamic neuron; pain;
                                                                                                                       In ion channel; human; sea urchin; fruit fly; rat; bovine; analgesic;
                                                                                                                                                          Human
                                                                                                                                                                                                                                                      Z09492 standard; DNA; 2029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1342 BP; 252 A; 451 C; 390 G; 240 T; 9 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes a novel Ih ion channel, isolated from human, sea urchin, bovine, rat, and fruitfly. The ion channels of the invention have analyesic and cardioactive activity. The Ih ion channel participates in the pacemaker function in cardiac muscle. The Ih ion channel nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 3; Page 57; 82pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            specific modulators, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                            792 CCACGCCGTGCTGGATGAAGTACATCTTCTTCCCGATGGTGCCTTCGCGGATGATGTAGT 733
                                                                                                                                                                                                                                                                                                                                  732 CACCCGGCTGGAAGACCTCGAACTTGAGCTTG 701
                                                                                                                                                                                                                                                                                                                                                   99 ctccaggctggagaaactgaaactggagctgg 130
                                                                                                                                                                                                                                                                                                                                                                                                                          39 ccaccgcctgcccaaggagatgacgcctgtggaacctgctgccttcgccgccgagctcat 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1999-527472/44.
                                                                                                                                                     heart tissue Ih ion channel DNA fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19.3%;
58.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g an Ih ion channel, used to identify for treatment, prevention and diagnosis of
                                                                                                                                                                                                                                                      ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 31.2; D
Pred. No. 3.5;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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                                                           detection; mutation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DВ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           38;
                                                                         e; cardiac disease;
sleep disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1342;
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RESULT C10491/C ID 209491/C ID 2094 AZ 2094 AZ 2094 Huma DT 02-N DT C1rd KW Card KW Ctreak KW Ct
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes a novel Ih ion channel, isolated from human, sea urchin, bovine, rat, and fruitfly. The ion channels of the invention
                                                                                                                                                                                                                         Ih ion channel; human; sea urchin; fruit fly; rat; bovine; analgesi cardioactive; pacemaker; cardiac muscle; ion channel modulator; treatment; diagnosis; ion channel-related disease; cardiac disease; circulatory disorder; sinus ganglion regulation; sleep disorder; cortico-thalamic neuron; pain; detection; mutation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      differential diagnosis. This sequence encodes a human Ih channel fragment isolated from heart tissue.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid encoding an specific modulators, and for
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Seifert R;
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  12-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                Human Ih ion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    209491 standard; DNA; 2886 BP
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                                                       26-AUG-1999.
                                                                                                               WO9942574-A1
                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cardiac disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                             channel DNA fragment #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP; 338 A; 774 C; 509 G;
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  99WO-EP00942.
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58.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
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Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        treatment, prevention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kaupp B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 356 T; 52 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scholten
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38;
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                                                                                                                                                                                                                                                                                                                                        analgesic;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             acid and its encoding protein is used to identify substances (A) that modulate activity of ion channels; to treat and/or diagnose ion channel related diseases, particularly cardiac or circulatory disorders and to prevent and/or treat cardiac/circulatory disorders (especially faulty regulation of the sinus ganglion), sleep disorders (particularly abnormal function of cortico-thalamic neurons) and/or pain. Fragments of the Ih ion channel nucleic acid are used to detect mutations e.g. for differential diagnosis. This sequence encodes a human Ih channel fragment isolated from human thalamus tissue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1249
                                                                                                                                                                         Human; METH1; METH2; anti-anglogenic; metalloprotease thrombospondin; cancer; diagnosis; hyperproliferative disorder; autoimmune disease; anglogenesis inhibitor; abnormal wound healing; inflammation; rheumatoid arthritis; psoriasis; endometrial bleeding disorder; diabetic retinopathy; macula degeneration; haemangioma; detection; arterial-venous malformation; immune deficiency; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes a novel Ih ion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 67-68; 82pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-527472/44
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23-JAN-1998;
28-AUG-1998;
                                                22-JAN-1999;
                                                                                                              WO9937660-A1
                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                           Human METH1 related
                                                                                                                                                                                                                                                                                                                         10-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                        232028 standard; DNA; 38186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2886 BP; 605 A; 774 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes a novel Ih ion channel, isolated from human, sea urchin, bovine, rat, and fruitfly. The ion channels of the invention have analyesic and cardioactive activity. The Ih ion channel participates in the pacemaker function in cardiac muscle. The Ih ion channel nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              specific modulators, and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ccaccgcctgcccaaggagatgacgcctgtggaacctgcttcccttcgccgccgagctcat 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cardiac disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CACCCGGCTGGAAGACCTCGAACTTGAGCTTG 1218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCACGCCGTGCTGGATGAAGTACATCTTCTTCCCGATGGTGCCTTCGCGGATGATGTAGT 1250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                         (first entry)
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98US-0072298.
98US-0098539.
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                                                                                                                                                                                                                                                                                           EST AC004449.
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for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ih ion channel, used to identify treatment, prevention and diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 31.2;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   940 G; 558 T; 9 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kaupp
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RESULT 10
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Best Local
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                                                                METH; metalloprotease; thrombospondin; angiogenesis inhibition; cancer therapy; benign tumour; coular angiogenic disease; rheumatoid arthritis; psoriasis; wound healing; endometriosis; vasculogenesis; granulation; hypertrophic scar; nonunion fracture; scleroderma, trachoma; vascular adhesion; myocardial angiogenesis; coronary collateral; cerebral collateral; arteriovenous malformation; ischaemic limb angiogenesis; Osler-Webber syndrome; wound granulation; plaque neovascularisation; telanglectasia; haemophiliac joint; EST; angiofibroma; fibromuscular dysplasia; expressed sequence tag; angiofibroma; fibromuscular dysplasia; expressed sequence tag;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer and other disorders related to angiogenesis including abnormal wound healing, inflammation, rheumatoid arthritis, psoriasis, endometrial bleeding disorders, diabetic retinopathy, some forms of macula degeneration, haemangiomas, and arterial-venous malformations. They may be useful in treating deficiencies or disorders of the immune system, by activating or inhibiting the proliferation, differentiation, or mobilisation (chemotaxis) of immune cells. The etiology of these immune deficiencies or disorders may be genetic, souch as cancer or some autoimmune disorders, acquired (e.g. by chemotherapy or toxins), or infectious. They can also be used for detection and diagnosis. 232002 to 232080, and Y49503 to Y49511 represent sequences given in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                  C90085 standard;
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               Unidentified
                                                     Crohn's disease;
                                                                                                                                                                                                                                                      AC004449 cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                         2432 CACCCGGCTGGAAGACCTCGAACTTGAGCTTG 2401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        metalloprotease thrombospondin (METH) proteins METH1 and METH2 respectively. METH1 and METH2 have been found to be potent inhibitors anglogenesis both in vitro and in vivo. They can be used for treating
                                                                                                                                                                                                                                                                                          19-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 38186 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 363-387; 457pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      treating hyperproliferative disorders, cancers or autoimmune disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (IRUE/) IRUELA-ARISPE
(HAST/) HASTINGS G A.
(RUBE/) RUBEN S M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       isolated metalloprotease thrombospondin polypeptides, useful for
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| || || || || | | | | | | | | | |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCACGCCGTGCTGCATGAAGTACATCTTCTTCCCGATGGTGCCTTCGCGGATGATGTAGT 2433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19.3%;
nilarity 58.7%;
Conservative
                                                     atherosclerosis;
                                                                                                                                                                                                                                                                                                                                                                  DNA;
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                                                                                                                                                                                                                                                                                                                                                                  38186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 31.2; DE Pred. No. 7.7; O; Mismatches
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                                                      birth
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                                                     control;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38;
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                                                     sequence
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RESULT 1
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22-DEC-1999;
22-FEB-2000;
                                                                                                                                                                              2492
                                                                                                                                                                                                                                                                                                                              ischaemic limb angiogenesis, Osler-Webber syndrome, plaque neovascularisation, telangiectasia, haemophiliac joints, angiofibroma, fibromuscular dysplasia, wound granulation, Crohn's disease or atherosclerosis. METH can also be used in birth control. METH can also used in diagnostic methods for the prognosis of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                  arthritis, psoriasis, delayed wound healing, endometriosis, vasculogenesis, granulations, hypertrophic scars, nonunion fractures, scleroderma, trachoma, vascular adhesions, myocardial angiogenesis, coronary collaterals, cerebral collaterals, arteriovenous malformations,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          metalloprotease and TH for thrombospondin; see B50002 and B50003). present sequence is an expressed sequence tag (EST) for METH. METH used for inhibiting angiogenesis in an individual, and for treating cancer, benign tumours, an ocular angiogenic disease, rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to human METH1 and METH2, metalloprotease and TH for thrombospondin; see B50002 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     METH1 and METH2 polynucleotides and encoded polypeptides, used to inhibit angiogensis in the treatment of disorders such as cancer, rheumatoid arthritis and psoriasis - {\sf res}
                                                   Z09494 standard;
                                                                                                                       2432 CACCCGGCTGGAAGACCTCGAACTTGAGCTTG 2401
                                                                                                                                                                                                                                                                                                       Sequence 38186 BP; 7571 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 7; Pages 663-687; 768pp; English.
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Fornwald JA,
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20-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) RUBEN S M.
) JONAK Z L.
) TRULLI S H.
) FORNWALD J A.
                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMITHKLINE BEECHAM CORP
BETH ISRAEL DEACONESS MI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HASTINGS G A.
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                                                                                                                                                                                                                                     Conservative
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Terrett JA;
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99US-0373658.
99US-0171503.
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99US-0144882.
                                                     DNA;
                                                                                                                                                                                                                                               19.3%;
                                                      794
                                                      ВP
                                                                                                                                                                                                                                                                                                       11502 C; 12194 G;
                                                                                                                                                                                                                                   Score 31.2; D
Pred. No. 7.7;
0; Mismatches
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                                                                                                                                                                                                                                                                DB
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                                                                                                                                                                                                                                     38;
                                                                                                                                                                                                                                                                                                        6919 T; 0 other;
                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                      Indels
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02-NOV-1999

(first entry)

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RESULT
Q41354
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AC Q41
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Best Local S
Matches 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                         acid and its encoding protein is used to identify substances (A) that modulate activity of ion channels; to treat and/or diagnose ion channel-related diseases, particularly cardiac or circulatory disorders and to prevent and/or treat cardiac/circulatory disorders (especially faulty regulation of the sinus ganglion), sleep disorders (particularly abnormal function of cortico-thalamic neurons) and/or pain. Fragments of the Inction of cortico-thalamic neurons) and/or pain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes a novel Ih ion channel, isolated from human, sea urchin, bovine, rat, and fruitfly. The ion channels of the invention have analyesic and cardioactive activity. The Ih ion channel participates in the pacemaker function in cardiac muscle. The Ih ion channel nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   In ion channel; human; sea urchin; fruit fly; rat; bovine; analgesicardioactive; pacemaker; cardiac muscle; ion channel modulator; treatment; diagnosis; ion channel-related disease; cardiac disease; circulatory disorder; sinus ganglion regulation; sleep disorder;
                                                                                          Q41354;
                                                                                                                     Q41354 standard; cDNA; 1247 BP
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 794 BP; 179 A; 230 C;
                                                                                                                                                                                                                                                                                                                                                                                                                              differential diagnosis. This sequence encodes a rat Ih channel fragment isolated from olfactory tissue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 71; 82pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           e.g. cardiac disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             specific modulators, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-527472/44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Baumann A,
Selfert R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W09942574-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cortico-thalamic neuron; pain; detection; mutation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rat olfactory Ih ion channel DNA fragment #4
 Human brain; Growth/Differentiation factor;
                           Human GDF-1 coding sequence
                                                            15-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (KERJ ) FORSCHUNGSZENTRUM JUELICH GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-FEB-1998;
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                                                                                                                                                                                                558
                                                                                                                                                                                                                                                            618
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                                                                                                                                                                                                                                                                                                                       Local Similarity
les 53; Conserv
                                                                                                                                                   12
                                                                                                                                                                                                                 ctccaggctggagaaactgaaactggagct 128
                                                                                                                                                                                                                                                                            ccaccgcctgcccaaggagatgacgcctgtggaacctgctgccttcgccgccgagctcat 98
                                                                                                                                                                                                CTCCAGGCTGGAAGACCTCAAATTTGAGCT
                                                                                                                                                                                                                                                            CCACCCCGTGCTGGATGAAGTACATCTTCTTCCCGATGGTCCCCTCTCGGATGATGTAGT
                                                                                                                                                                                                                                                                                                                       Conservative
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                                                          (first
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                                                          entry)
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Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ih ion channel, used to identify treatment, prevention and diagno:
                                                                                                                                                                                                                                                                                                                                                                                                224 G;
                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                529
                                                                                                                                                                                                                                                                                                                                                                                                161 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                     BB
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                                                                                                                                                                                                                                                                                                                       37;
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Best Local Similarity
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30-AUG-1991;
30-AUG-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Morphogen-induced modulation of inflammatory response resulting tissue damage, e.g. in autoimmune diseases, asthma, ischemia reperfusion injury, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         morphogenic protein; developmental cascade; morphogen; inflammation; anti-inflammatory;
 Morphogen GDF-1 coding sequence.
                                             Q38862
                                                                  Q38862
                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 26; Page 138-140; 165pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-MAR-1993
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                       13-JUL-1993
                                                                                                                                                                                                                                                                                                                   Sequence 1247 BP; 127 A; 497 C;
                                                                                                                                                                                                                                                                                                                                                 damage in e.g. inflammatory disease, autoimmune disease, arthritis, psoriasis, dermatitis, diabetes and emphysema. Proteins having at least 70% homology with GDF-1 amino acid sequences can also be used "GDF-1(fx)" (see R33407) refers to protein sequences encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cohen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9304692-A.
                                                                                                                                                                                                                                                                                                                                         human GDF-1 gene and defining the seven cysteine skeleton
                                                                                                                                                                                                                                                                                                                                                                                               GDF-1 is a preferred morphogen for use in treating tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1993-100652/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CREA-) CREATIVE BIOMOLECULES INC.
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                                                                                                                         831
                                                                                                                                                                                                                711
                                                                                                                                                                    771
                                                                                                                                            151 gagcggctgc 160
                                                                                                                                                                                          91
                                                                                                                                                                                                                           31 cogagaacccaccgcctgcccaaggagatgacgcctgtggaacctgctgccttcgccgcc 90
                                                                                         13
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                                                                                                                       cggccgcggc 840
                                                                                                                                                                  ctggccgaggcctcgctgctgctggtgaccctcgacccgcgcctgtgccaccccctggcc
                                                                                                                                                                                        gageteateteeaggetggagaaactgaaactggagetggaaageegeeatagtetggag 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sapiens
                                                                                                                                                                                                                                                           68;
                                                                   standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kuberasampath T,
Rueger DC, Smar
                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Growth Factor;
                       (first entry)
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91US-0752861.
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/note= "contains
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                                                                   DNA;
                                                                                                                                                                                                                                                                     19.0%;
                                                                   1247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       th T, Oppermann Smart JE;
                                                                   ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGF-beta super-family; ss
                                                                                                                                                                                                                                                           0;
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Pred.
                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                   448 G; 175 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cysteine skeleton
                                                                                                                                                                                                                                                             62;
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                                                                                                                                                                                                                                                                                  Length 1247;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      diabetes,
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RESULT
Q58055
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                                                                                                                                                                                                                                                                                                                                                                                                    This sequence encodes the morphogen growth/differentiation factor 1 (GDF-1) isolated from human brain. This morphogen is inactive when reduced but is active as an oxidised homodimer and when oxidised in combination with other morphogens. These morphogens are capable of stimulating proliferation of progenitor cell, stimulating the differentiation of progenitor cells, stimulating the proliferation of
                          Q58055;
                                                                                                                                                                                                                                                                                                                                                       differentiated cells and supporting the growth and maintenance of differentiated cells, including the redifferentiation of transform cells. These morphogens may also be capable of inducing redifferentiation of committed cells under appropriate environmental
  25-AUG-1994
                                                  Q58055 standard; cDNA; 1247
                                                                                                                                                                                                                                                                                                                      Sequence 1247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Screening cpds. to determine ability to modulate effective concn of a morphogen - by assaying test tissue type cells for parameter indicative of a prodn. level change of morphogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Morphogen; homodimer; stimulate; proliferation; progenitor of differentiation; growth; redifferentiation; transformation; mouse; Drosophila; Xenopus; committed cells; hippocampus; growth/differentiation factor 1; GDF-1; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 116-118; 132pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1993-100993/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cohen CN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-AUG-1991;
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                                                                                                            cggccgcggc
                                                                                                                                                            ctggccgaggcctcgctgctgctggtgaccctcgacccgcgcctgtgccaccccctggcc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Smart JE;
  (first entry)
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Pred. No. 4.5;
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                                                                                                                                                                                                                                                          62;
                                                                                                                                                                                                                                                                                                                      other;
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RESULT
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04-MAR-1993;
31-MAR-1993;
31-JUL-1992;
16-SEP-1992;
                                                                                                                                                                                                                                      Human GDF-1 (fx) morphogen and proteins having at least 70% homology with it are preferred morphogens for inclusion in new morphogen-enriched nutritional formulations. The formulations are dietary compositions suitable for people at risk for tissue damage due to protein energy malnutrition or to altered metabolism function and infant formulations to enhance tissue development in an infant or juvenile.
                                                                                                                                                                                                                                                                                                                                                                  Morphogen enriched dietary compositions and infant formula capable of enhancing tissue morphogenesis, development and viability, e.g. in infants, aged individuals and metabolic disorders, e.g. anorexia nervosa, etc
                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1994-065304/08
P-PSDB; R46750.
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                                                                                                                                                                                                                 Sequence 1247 BP;
                                                                                                                                                                                                                                                                                                                                           Disclosure and Claims 25-26; Page 139-141; 160pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jones WK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human morphogenic protein; GDF-1(fx); morphogen; infant food formulation; tissue morphogenesis; tissue debone growth; morphogen-enriched nutritional product; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human morphogenic protein GDF-1(fx)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rueger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CREA-) CREATIVE BIOMOLECULES INC
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 831
                         151
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                                                                                                             31 ccgagaacccaccgcctgcccaaggagatgacgcctgtggaacctgctgccttcgccgcc
                       gagcggctgc
                                                ctggccgaggcctcgctgctgctggtgaccctcgacccgcgcctgtgccaccccctggcc
                                                                        gageteateteeaggetggagaaactgaaactggagetggaaageegeeatagtetggag
cggccgcggc
                                                                                                  ccgcgcagcctccgcctggcgctggcgctacgccccgggcccctgccgcctgcgcgc
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                                                                                                                                                                Similarity
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                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92US-0923780.
93US-0029335.
93US-0040510.
92US-0922813.
92US-0946235.
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 840
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/note= "GDF-1(FX) cDNA"
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                                                                                                                                                                                                                 127 A; 494 C; 451 G; 175 T; 0 other;
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52.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cohen
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                                                                                                                                                   Score 30.8; D
Pred. No. 4.5;
0; Mismatches
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n CM, Pang RHL;
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                                                                                                                                                                5;
                                                                                                                                                                            DB 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ozkaynak E;
                                                                                                                                                      62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tissue development;
                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                             English.
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Q67315 standard; DNA; 1247

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                                                                                                                                                    Query Match
Best Local Similarity
Matches 68; Conserv
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04-MAR-1993;
31-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Cohen CM,
Pang RHL,
                                                                                                                                                                                                                                        Morphogens comprising an amino acid sequence sharing at least 70% homology with OP-1, OP-2, CBMP2, Vg1(fx), Vgr(fx), DPP(fx), GDP-1(fx), 60A(fx) and at least 80% homology with BMP3(fx), BMP5(fx) and BMP6(fx) are useful for integrating an implanted tooth in a tooth socket and for inhibiting tissue loss associated with periodontal disease or injury.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OP-1; OP-2; CBMP2; Vgl(fx); Vgr(fx); DPP(fx); GDF-1(fx); 60A(fx); BMP3(fx); BMP5(fx); BMP6(fx); tooth socket; alveolus; osteogenic protein; morphogen; morphogenic protein; periodontal tissue; regeneration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key
                                                                                                                                                                                                                 Sequence 1247 BP; 127 A; 494 C; 451 G; 175 T; 0 other;
                                                                                                                                                                                                                                                                                                                                 Claim 28-29; Page 114-116; 132pp; English.
                                                                                                                                                                                                                                                                                                                                                       Morphogen-induced periodontal tissue regeneration - used in integrating as implanted tooth in tooth socket or to inhibit tissue loss associated with periodontal disease or injury
                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1994-118107/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-MAR-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human GDF-1(fx) morphogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-OCT-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CREA-) CREATIVE BIOMOLECULES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-SEP-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tooth
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                                                 771 ctggccgaggcctcgctgctgctggtgaccctcgacccgcgcctgtgccaccccctggcc 830
                                                                                                    711
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                                                                gagctcatctccaggctggagaactggaaactggagctggaaagccgccatagtctggag 150
                                                                                                 cogagaacccaccgcctgcccaaggagatgacgcctgtggaacctgctgccttcgccgcc 90
cggccgcggc 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              implant; integration; inhibition; ss.
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Rueger DC, Smart
                                                                                                                                                    19.0%;
milarity 52.3%;
Conservative
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93US-0029335.
93US-0040510.
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84..1202
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/label= GDF-1
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Pred. No. 4.5;
0; Mismatches 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ozkaynak E;
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Search completed: June

7, 2001, 00:31:54

Job time: 8632 sec

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OM nucleic - nucleic search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Perfect score:
  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed; and is derived by analysis of the total score distribution.
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length: 2000000000
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Match
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US-08-155-743A-32
US-08-643-563A-32
US-08-643-563A-32
US-08-4451-953A-32
US-08-4451-953A-32
US-08-4451-953A-32
US-08-461-397A-32
US-08-912-088-32
US-08-912-088-32
US-08-912-088-32
US-08-912-088-32
US-08-912-088-32
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US-08-913-088-32
US-08-913-088-32
US-08-913-088-32
PCT-US93-0742-32
PCT-US93-0885-32
US-08-365-913-3
US-08-365-913-5
US-08-365-913-5
US-08-315-913-5
US-08-315-913-3
US-08-315-913-3
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US-08-278-729A-32
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28	28	28	28	28.2	28.2		28.2					28.2				28.2	28.2
17.3	17.3	17.3	17.3	17.4	17.4	17.4	17.4	17.4	17.4	17.4	17.4	17.4	17.4	17.4	17.4	17.4	17.4
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US-09-248-026-3	US-08-136-742A-3	US-07-853-913-3	US-09-071-434-2	US-09-427-048A-3	US-08-836-022A-3	5240846-4	US-08-469-617-16	US-08-030-081-1	US-07-890-609-1	US-08-469-461-1	US-08-604-488-1	US-08-466-886-16	PCT-US93-11667-1	US-09-248-026-1	us-08-691-605-1	US-08-951-912-5	US-08-951-912-1
Sequence 3, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 2, Appli	Sequence 3, Appli	Sequence 3, Appli	Patent No. 5240846	Sequence 16, Appl	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 16, Appl	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 5, Appli	Sequence 1, Appli

## ALIGNMENTS

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US-08-278-729A-32
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                                                                                                          TELEFAX: (508) 435-6951
INFORMATION FOR SEQ ID NO: 32
SEQUENCE CHARACTERISTICS:
LENGTH: 1247 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/278,729A
FILING DATE: 20-JUL-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESq., EDMUND R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-058CPFW
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 435-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIF: 01748
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: MORPHOGENIC PROTEIN SCREENING METHOD NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATEMY ADMINISTRATOR, CREATIVE BIOMOLECULES STREET: 45 SOUTH STREET
                FEATURE:
NAME/KEY: CDS
LOCATION: 84..1199
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                                                                                          MOLECULE TYPE: cDNA
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RUEGER, DAVID C.
PANG, ROY H.L.
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OZKAYNAK, ENGIN
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                /product= "GDF-1"
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; NAME/KEY: CDS
; LOCATION: 84..1199
; OTHER INFORMATION:
US-08-155-343A-32
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US-08-155-343A-32
                                    Query Match
Best Local Similarity
Matches 68; Conserv
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Best Local Similarity
Matches 68; Conserv
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                                                                                                                                                                                                                                                                                    TELEFAX: (617) 248-7100 INFORMATION FOR SEQ ID NO: 32:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                              NAME: FENTON ESQ., GILLIAN M.
REGISTRATION NUMBER: 36,508
REFERENCE/DOCKET NUMBER: CRP-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7560
                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION UMBER: U$5.08/155,343A FILING DATE: 15-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                         MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
31 ccgagaacccaccgcctgcccaaggagatgacgcctgtggaacctgctgccttcgccgcc 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: UZIP: 01748
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45 SOUTH STREET
                                      Conservative
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                                                                                                                                                                                                           linear
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                                                 19.0%;
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                                 Score 30.8; DB 1;
Pred. No. 0.82;
0; Mismatches 62;
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US-08-406-672-32
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            Query Match
Best Local Similarity
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    Matches
                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 752,857
FILING DATE: 30-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 667,274
FILING DATE: 11-MAR-1991
ATTORNEY_AGENT INFORMATION:
NAME: FENTON ESG., GILLIAN M.
                                                                                                                                    FEATURE:
                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: CR
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION UNIMBER: US 752,857
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MEDIUM TYPE: Floppy disk
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                                                                                        OTHER INFORMATION:
                                                                                                      LOCATION:
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                                                                                                                     NAME/KEY:
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OZKAYNAK, ENGIN
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                                                                                                                                                                                                                                                                 (617) 248-7560
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                                                                                      /product= "GDF-1"
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 Score 30.8; DB Pred. No. 0.82; 0; Mismatches
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                            DB 1;
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC COMPBILIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/643,56:
FILING DATE: 06-MAY-1996
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ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES STREET: 45 SOUTH STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 1247 base pairs
                                                                                                                                                                                                                                                                                                                                                                                        NAME: TWOMEY ESq., MICHAEL J.
REGISTRATION NUMBER: 38,349
REFERENCE/DOCKET NUMBER: CRP-058CN2
TELECOMMUNICATION INFORMATION:
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                                                      y Match 19.0%;
Local Similarity 52.3%;
nes 68; Conservative
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LOCATION: 84..1199
OTHER INFORMATION:
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gageteateteeaggetggagaaactgaaactggagetggaaageegeeatagtetggag 150
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OZKAYNAK, ENGIN
KUBERASAMPATH, TI
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                                                                                        Score 30.8; DB Pred. No. 0.82; O; Mismatches
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                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (617) 248-71 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: FENTON ESQ., GILLIAN M. REGISTRATION NUMBER: 36,508
REFERENCE/DOCKET NUMBER: CRP-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7560
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APPLICATION NUMBER: US
FILING DATE: 06-MAY-19
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NUMBER OF SEQUENCES: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 01748
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TOPOLOGY: lir
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                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
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45 SOUTH STREET
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N: 514
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Pred. No. 0.82;
0; Mismatches 62
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APPLICANT: COHEN, CHARLES M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 0)
FILING DATE: 22-MAY-1995
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy
   831
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                              151 gagcggctgc 160
                                                                                                                            711 CCGCGCAGCCTCCGCCTGGCGCTGGCGCTACGCCCCGGGCCCCTGCCGCCTGCCGCGCGC 770
                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: CRP-074CN FELECOMMUNICATION INFORMATION:
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                                                            771 CTGGCCGAGGCCTCGCTGCTGCTGGTGACCCTCGACCCGCGCCCTGTGCCACCCCCTGGCC 830
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                                                                                         91 gagotoatotocaggotggagaaactgaaactggagotggaaagcogccatagtotggag 150
                                                                                                                                           31 ccgagaacccaccgcctgcccaaggagatgacgcctgtggaacctgctgctgccttcgccgcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ITLE OF INVENTION: MORPHOG ITLE OF INVENTION: ULCERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPLICANT:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
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ceecceceec 840
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                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                      1247 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES 45 SOUTH STREET
                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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OZKAYNAK, ENGIN
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                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (508)
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                                                                                                                                                                                                                                                                                         /product= "GDF-1"
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                                                                                                                                                                                                          Score 30.8; DB Pred. No. 0.82;
                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                            62;
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US-08-451-953A-32
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                                                                                                                                                                                      Matches
                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (508) 435-6951 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: CF
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 435-9001
                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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831 CGGCCGCGGC 840
                             151 gagcggctgc 160
                                                           771 CTGGCCGAGGCCTCGCTGCTGCTGGTGACCCTCGACCCGCGCCTGTGCCACCCCCTGGCC
                                                                                                                         31 ccgagaacccaccgcctgcccaaggagatgacgcctgtggaacctgcttcgccgtcc 90
                                                                                       91 gagotoatotocaggotggagaaactgaaactggagotggaaagcogcoatagtotggag 150
                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                             NAME/KEY: CDS
LOCATION: 84..1199
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 45 SOUT CITY: HOPKINTON STATE: MA
                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: PITCHER ESQ., EDMUND R. REGISTRATION NUMBER: 27,829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/0 FILING DATE: 26-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE:
COMPUTER: IE
                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 01748
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                                                                                                                                                                                                                                                                                                                                                                 H: 1247 base pairs
nucleic acid
NDEDNESS: single
                                                                                                                                                                                                     Similarity
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OZKAYNAK, ENGIN
KUBERASAMPATH, TH
RUEGER, DAVID C.
                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                         linear
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                                                                                                                                                                                                                                                                                                                                           CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ROY H.L.
, CHARLES M.
                                                                                                                                                                                                   19.0%;
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                                                                                                                                                                                                                                                                            /product= "GDF-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US/08/451,953A
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                                                                                                                                                                                    0;
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                                                                                                                                                                                                   Score 30.8; DB Pred. No. 0.82;
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US-08-445-468A-32; Sequence 32, Application US/08445468A

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RESULT

Patent No. 5849686

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RESULT 9
US-08-461-397A-32
US-08-461-397A-32
; Sequence 32, Application US/08461397A
; Patent No. 5972884
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Best Local Similarity
Matches 68; Conserv
                                GENERAL INFORMATION:
APPLICANT: COHEN,
APPLICANT: CHARET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: FENTON ESQ., GILLIAN M.
REGISTRATION NUMBER: 36,508
REFERENCE/DOCKET NUMBER: CRP-072FW2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/445,468A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: CDNA
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                   PPLICANT:
                                                                                                                                                                                        831 CGGCCGCGGC 840
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: CDS
LOCATION: 84..1199
OTHER INFORMATION:
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CLASSIFICATION:
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ZIP: 01748
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STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1247 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                     gagctcatctccaggctggagaaactgaaactggagctggaaagccgccatagtctggag 150
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COHEN, CHARLES M.
CHARETTE, MARC F.
KUBERASAMPATH, THANGAVEL
RUEGER, DAVID C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPPERMANN, HERMAN PANG, ROY H.L.
                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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; LOCATION: 84..1199
; OTHER INFORMATION: /product= "GDF-1"
US-08-461-397A-32
                                                                                                                                                                                    RESULT 10
US-08-912-088-32
                                                                                                                                                    Sequence 32, App
Patent No. 59941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                  GENERAL INFORMATION:
APPLICANT: SMART, JOHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 617/248-7100 INFORMATION FOR SEO ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 1247 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-074FW2
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
STREET: 45 SOUTH STREET
                                                   APPLICANT:
                                                                                APPLICANT:
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                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/0
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
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                 APPLICANT:
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                                                                                                                                                                                                                                                        831 CGGCCGCGGC 840
                                                                                                                                                                                                                                                                                         151 gagcggctgc 160
                                                                                                                                                                                                                                                                                                                            771 CTGGCCGAGGCCTCGCTGCTGCTGGTGACCCTCGACCCGCGCCTGTGCCACCCCCTGGCC
                                                                                                                                                                                                                                                                                                                                                                                               91 gagctcatctccaggctggagaaactgaaactggagctggaaagccgccatagtctggag 150
                                                                                                                                                                                                                                                                                                                                                                                                                  31 ccgagaacccaccgcctgcccaaggagatgacgcctgtggaacctgctgccttcgccgcc 90
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: sing
TOPOLOGY: linear
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 INVENTION:
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                                                                                                                                                        Application US/08912088
994131
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                                            OPPERMANN, HERMAN
OZKAYNAK, ENGIN
KUBERASAMPATH, THANGAVEL
RUEGER, DAVID C.
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OZKAYNAK, ENGIN
                                PANG,
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                                ROY H.L.
                CHARLES M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19.0%;
52.3%;
MORPHOGENIC PROTEIN SCREENING METHOD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 30.8; DB Pred. No. 0.82; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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NUMBER OF SEQUENCES: 3

ADDRESSEE:

B: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES 45 SOUTH STREET

STREET: 45 SOUTH CITY: HOPKINTON

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USA

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Best Local Similarity 52.3
Matches 68; Conservative
                                                                                                                                                                                     Sequence 32, Application US/08278730A Patent No. 6022853
                                                                                                                                                                                                                     -08-278-730A-32
                                                                                                                                                                     GENERAL INFORMATION:
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                                                                                                     APPLICANT: KUBEKASA.....
APPLICANT: COMEN, CHARLES M.
APPLICANT: RUEGER, DAVID C.
APPLICANT: RUEGER, DAVID C.
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APPLICATION NUMBER: I
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MEDIUM TYPE: Floppy disk
                              NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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                                                                 TITLE OF INVENTION: MORPHOGENIC-ENRICHED DIETARY COMPOSITION
                                                                                     APPLICANT:
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LOCATION: 84..1199
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: PITCHER ESQ., EDMUND R. REGISTRATION NUMBER: 27,829 REFERENCE/DOCKET NUMBER: CRP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE:
 STREET:
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                   ADDRESSEE:
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2: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES 45 SOUTH STREET
                                                                                 OPPERMANN, HERMAN PANG, ROY H.L.
                                                                                                                                                     KUBERASAMPATH, THANGAVEL
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; OTHER INFORMATION: /product= "GDF-1"
US-08-278-730A-32
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                                                                                                                                                                                                                                                                 Sequence 32,
Patent No. 6(
GENERAL INFO
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 1247 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: FENTON ESQ., GILLIAN M.
REGISTRATION NUMBER: 36,508
REFERENCE/DOCKET NUMBER: CRP-
TELECOMMUNICATION IMPORMATION:
TELLEPHONE: (617)*248-7560
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MEDIUM TYPE: Floppy disk
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                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                         APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
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                                                                                                             NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                         151 gagcggctgc 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: MA
COUNTRY: USA
ZIP: 01748
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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ZIP: 01748
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                                                            STREET:
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STRANDEDNESS: sing
                                                CITY:
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                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGGCCGAGGCCTCGCTGCTGCTGACCCTCGACCCGCGCCTGTGCCACCCCCTGGCC
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                                            HOPKINTON
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                                                                                                                                                                    RUEGER, DAVID C
COHEN, CHARLES M
OZKAYNAK, ENGIN
                                                                                                                                                                                                                                                                                                Application US/08445467
                                                            35 SOUTH STREET
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                                                                                                                                                         SMART, JOHN E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                      PANG, ROY HL
                                                                                                                                                                                                                       OPPERMANN,
                                                                                                                                                                                                                                                   KUBERASAMPATH, THANGAVEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDS
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                                                                               CREATIVE BIOMOLECULES, INC
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52.3%;
                                                                                                             INFLAMMATORY RESPONSE 33
                                                                                                                                            MORPHOGEN-INDUCED MODULATION
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                                                                                                                                                                                                                         HERMANN
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Gaps

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OTHER INFORMATION: /F.
OTHER INFORMATION: /F.
OTHER INFORMATION: /n
US-08-445-467-32
                                                                                   RESULT 13
US-08-480-515A-32
; Sequence 32, Application US/08480515A
; Patent No. 6090776
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Best Local Similarity
Matches 68; Conserv
                               GENERAL INFORMATION:
APPLICANT: KUBERA
APPLICANT: PANG,
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INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 1247 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 07/752
FILING DATE: 30-AUG-1991
ATTORNEY_AGENT INFORMATION:
NAME: PITCHER ESQ, EDMUND R
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 61/248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 07/667,274
FILING DATE: 11-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/753,059
FILING DATE: 30-AUG-1991
PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                 APPLICANT:
                                                                                                                                                                                        831 CGGCCGCGGC 840
                                                                                                                                                                                                               151 gagcggctgc 160
                                                                                                                                                                                                                                                            771 CTGGCCGAGGCCTCGCTGCTGCTGGTGACCCTCGACCCGCGCCTGTGCCACCCCCTGGCC 830
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LOCATION: 84..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE TYPE: BRAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: HOMO SAPIENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
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               KUBERASAMPATH, THANGAVEL PANG, ROY H.L. OPPERMANN, HERMANN
                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
RUEGER, DAVID C
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/note= "GDF-1 CDNA"
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RESULT 14
PCT-US93-07190-32
Sequence 32, Application PC/TUS9307190
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (617) 248-7100 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
                                                                                                      TITLE OF INVENTION: MORPHOGEN-ENRICHED I NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS: ADDRESS: CREATIVE BIOMOLECULES, INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: MORPHOGEN TREATMENT OF ORGAN TRANSPLANTS NUMBER OF SEQUENCES: 33
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NAME: FENTON ESQ., GILLIAN M.
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                         831 CGGCCGCGGC 840
                                                                                                                                                                                                                                                                                                                                  151 gagcggctgc 160
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                                                CITY: HOPKINTON
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: CDS
LOCATION: 84..1199
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/0 FILING DATE: 07-JUN-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: HOPKINTON
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                COUNTRY: UZIP: 01748
                                                                                      STREET:
                                                                                                                                                                                                                                                                                                                                                                                                              91 gageteatetecaggetggagaaactgaaactggagetggaaageegeeatagtetggag 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 36,508
REFERENCE/DOCKET NUMBER: CR
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SMART, JOHN E.
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                                                                                                                                                             MORPHOGEN-ENRICHED DIETARY COMPOSITION
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                                                                                                                                                                                                                                                                                                                                                            Sequence 32, Application PC/TUS9307231 GENERAL INFORMATION:
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Best Local Similarity
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                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: CRI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
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                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: cDNA ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                831 CGGCCGCGGC 840
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                              FILING DATE:
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OTHER INFORMATION:
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COMPUTER: II
                                APPLICATION NUMBER: POFILING DATE: 19930729
                                                                                                                                                                     COUNTRY: UZIP: 01748
                                                                                                                                                                                                         CITY: HOPKINTON
STATE: MASSACHU
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                 CLASSIFICATION:
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LOCATION: 84..1199
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/note= "GDF-1 CDNA"
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Search completed: June 7, 2001, 00:26:34 Job time: 19737 sec
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 1247 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                        831 CGGCCGCGGC 840
                                                                                                 151 gagcggctgc 160
                                                                                                                               771 CTGGCCGAGGCCTCGCTGCTGGTGACCCTCGACCCGCGCCTGTGCCACCCCCTGGCC 830
                                                                                                                                                                                       y Match 19.0%;
Local Similarity 52.3%;
                                                                                                                                                       91 gagotoatotocaggotggagaaactgaaactggagotggaaagcogcoatagtotggag 150
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                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE TYPE: BRAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: sing
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/note= "GDF-1 CDNA"
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em\_esthum10:\*
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Minimum DB
Maximum DB
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Listing first 45 summaries
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Perfect score:
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463.402 Million cell updates/sec
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162
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em\_estpl8:\*
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em\_esthum27:\*
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gb\_est48:\* gb\_est49:\*

gb\_est76 gb\_est77

gb\_est62

gb\_est80 gb\_est81

gb\_est87

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Result
No.
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
Score
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em_gss_pln1:*
em_gss_pln2:*
em_gss_pro:*
em_gss_rod1:*
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em_gss_rod4:*
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3 AA937585

8 AI3773864

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0 AI419942

7 AI220032

02 AI819109

03 AI858567

3 AA884421

19 AW762829

9 AI336613

AA915948

3 AA915948

3 AA915959

3 AI660139

52 AW3625

52 AW3656657

4 AI742962
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AA937585 Of71h02.s
AI272864 q143h03.x
AI307112 q189f01.x
AA489644 aa43d02.s
AI419942 tg40d11.x
AI280032 qg78h02.x
AI818109 wk27205.x
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AI832829 ur66f04.y
AI336613 q062c07.x
AA489748 aa43d02.r
AA489799 Oh86911.s
AA489798 ur61a09.x
R33823 yh78f12.r1
AW207598 UI-H-BI1-
AW207598 UI-H-BI1-
AW566657 fk03a11.y
AI13772962 wg76d09.x
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gb\_est74:\*
gb\_est91:\*
gb\_est92:\*
gb\_est93:\*
gb\_est94:\*
gb\_est96:\*
gb\_est96:\*

gb\_est69: gb\_est70:

gb\_est67:\*
gb\_est68:\*

gb\_est71 gb\_est72 gb\_est73

gb\_est98:\*
em\_gss\_tun1:\*
em\_gss\_hun1:\*
em\_gss\_hun2:\*
em\_gss\_hun3:\*
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em\_gss\_inv2:\*

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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                       Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 444)

NCI-GGAP http://www.ncbi.nlm.nih.gov/nclcgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                              CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                 Tumor Gene Index
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                                                                                                                              Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                              Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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/note-"Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from colon adenocarcinoma, and was then primed with a Not I -
                                             /organism-"Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1435827"
/clone_1lb="NCI_CGAP_CO8"
/tissue_type="adenocarcinoma"
                                    /lab_host-"DH10B"
                                                                                                                 Location/Qualifiers
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AI629343
BF812711
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BG169700
AZ484715
BF442400
BF120462
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AL223062 Tetraodon
D24290 RICR1662A R
AU173197 AU173197
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AI629343 fc10h02.y
BF812711 RC3-CI019
BE379078 601237710
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BG169700 602324691
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BF442240 259095 MA
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BG103866 RHIZ2_37_
AV642870 AV642870
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BF896910 CM2-MT015
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3900 601779134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCCCCGTGGAACCCGCCACCTTTGCAGCTGAGCTGGATCTCGAGGCTGGAAAAGCTGAAG
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similar to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AI272864.1 GI:3895132
EST.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Anote Torgan: colon; Vector: pT773D-Pac (Pharmacia) with a modified polylinker; lst strand cDNA was prepared from colon adenocarcinoma, and was then primed with a Not I coligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "
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                                                                                                                                                                                                   /clone="IMAGE:1875125"
/clone_lib="NCI_CGAP_Co8"
                                                                                                                                                                     /tissue_type="adenocarcinoma"
/lab_host="DH10B"
                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
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88.3%;
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RESULT 3
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 143;
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q189f01.x1
3' similar
                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: Robert_Strausberg@nih.gov
This clone is available royaltly free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
Insert Length: 534 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rei: (301) 496-1550
Email: Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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                Similarity
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   Conservative
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                                                                                      (Pharmacia) with a modified polylinker; Site_1: Not 1; Site_2: Eco R; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHPU, and fetal heart NbHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479.
                                                                                                                                                                                                                                                                                             pregnant uterus"
                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1879513"
                                                                                                                                                                                                                                                                                                          /clone_lib="Soares_NhHMPu_S1"
/tissue_type="Pooled human melanocyte,
                                                                                                                                                                                                                                                               /lab_host="DH10B"
/note="Organ: mixed (see below);    Vector: pT7T3D-Pac
                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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              81.2%;
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Matches Query Match Best Local

Similarity

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Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WashU-Merck EST Project 1997
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Contact: Wilson RK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MAGE Consortium (info@image.llnl.gov) for Possible reversed clone: polyT not found Seq primer: -41ml3 fwd. ET from Amersham High quality sequence stop: 389.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.
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                        /note="Organ: mixed (see below); Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHPU, and fetal heart NbHH19W) were mixed, and sc circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 3 consisted of I.M.A.G.E. clone
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note-"Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified CDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-68729, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo."
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/lab_host-"DH10B"
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/clone="IMAGE:2111253"
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                                                                                                                                                                                                                                                                                                              80.2%;
                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                             Score 130; DB 20;
Pred. No. 4.2e-27;
0; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                              Length 460;
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RESULT 6
AI220032/c
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RESULT 7
AI818109/c
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Best Local Similarity
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                                                                                                                                                                                                                                                           gccaatggccaagtgtctctacctcattttccgagaacccaccgcctgcccaaggagatg
                                                                                                                                                                               acgcctgtggaacctgctgccttcgccgcgagctcatctccaggctggagaaactgaaa 120
                                                                                                                                                          ACCACCGTGGAAGCCGCCACCTTTGCAGCTGAGCTGATCTCGAGGCTGGAAAAGCTGAAG
                                                                                                                                                                                                                                    GCCAATGGCCAAGTGTCTCTACCTCATTTCCCGAGAACCCACCGCCTGCCCAAGGAGATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq primer: -40UP from Gibco
High quality sequence stop: 224.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumor Gene Index
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National Cancer Institute, Cancer Genome Anat
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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1 (bases 1 to 543)
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                                                                                                                                                                                                                                                                                                                                                                                                                            /note-"Organ: pooled; Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed, and s circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified CDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. " 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1841331"
/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                   79.3%;
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                                                                                                                                                                                                                                                                                                                                   Score 128.4; DB 1
Pred. No. 1.2e-26;
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                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                  gccaatggccaagtgtctctacctcattttccgagaaccccaccgcctgcccaaggagatg
                                                                                                                                                                                           ACCCCCGTGGAACCCGCCACCTTTGCAGCTGAGCTGATCTCGAGGCTGGAAAAGCTGAAG
                                                                                                                                                                                                                                                                      GCCAATGGCCAAGTGTCTCTACCTCATTTCCCGAGAACCCACCGCCTGCCCAAGGAGATG 349
AI858567 418 bp mRNA EST 07-MAR-2000 w164d08.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2429679 3'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 591)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA Library Preparation: M. Bento Soares, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."

159 c 192 g 138 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
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/clone_lib="NCI_CGAP_Brn25"
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86.4%;
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298
                  124 gagctggaaagccgccatagtctggaggagcggctgcag 162
                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                          64 cctgtggaacctgctgccttcgccgccgagctcatctccaggctggagaaactgaaactg 123
                                                                                                                                                                                             4 aatggccaagtgtctctacctcattttccgagaacccaccgcctgcccaaggagatgacg
                                                                                                                                                                     AAGGGCGAAGTGTCTCTACCTCATTTCCCCGAGAACCCACCGCCTGCCAAGTGAGATGACC
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Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
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NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurola Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index
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Location/Qualifiers
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DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 541 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: Robert_Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AI858567.1 GI:5512183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA Library Preparation: M. Bento
                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                           62
                                                                                                                                                                                                                                                                                                                                                                                  T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."

115 c 149 g 89 t 3 others
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/clone_lib="NCI_CGAP_Brn25"
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/lab_host="DH10B"
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                                                                                                                                                                                                                                                                               72.5%;
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Primates;
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                                                                                                                                                                                                                                                                               Score 117.4; DB 103; Length 418; Pred. No. 1.7e-23;
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AA884421 391 bp mRNA EST 27-W am16b12.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone IMAGE:1466975 3' similar to TR:042400 042400 AXIN. ;, r

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VERSION
KEYWORDS
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Best Local
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                                                                                                                                                                                                                                                                                                                             331 CCCACCTTTGCAGCTGAGCTGATCTCGAGGCTGGAAAAGCTGAAGCTGGAGTTGGAGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                     16 tctctacctcattttccgagaacccaccgcctgcccaaggagatgacgcctgtggaacct 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                          cgccatagtctggaggagcggctgcag 162
                                                                                                                                                                                                                                                                                                                                              gctgccttcgccgagctcatctccaggctggagaaactgaaactggagctggaaagc 135
                                                                                                                                                                                                                                                                                                                                                                                                  TCTCTACCTCATTTCCCGAGAACCCACCGCCTCCCAAAGGAGATGACCCCCGTGAACCCCG 332
                                                                                                                                            AW762829
ur66f04.yl
Mus musculus
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: Robert_Strausberg@nih.gov
This clone is available royaltyfree through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
Possible reversed clone: similarity on wrong strand
Possible reversed clone: polyT not found
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 234.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                          EST.
                                                                                         AW762829
AW762829.1
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                              similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tumor Gene Index
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                                                        house mouse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHLIPW, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "
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/db_xref="taxon:9606"
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/clone_lib="Soares_NFL_T_GBC_S1"
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                                                                                                                     508 bp mRNA EST 04-MAY-2000 NCI_CGAP_Mam3 Mus musculus cDNA clone IMAGE:3155263 TR:088566 088566 CONDUCTIN. ;, mRNA sequence.
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                                                                                           GI:7694771
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83.0%;
   Chordata;
Rodentia;
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Pred. No. 1.5e-20;
D; Mismatches 25;
 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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103 aggctggagaaactgaaactggagctggaaagccgccatag 143
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                                                                                                                                                                                                                                                                                                                                                              qo62c07.x1
similar to
Mammalia; Eutheria; Primates; Catarrhin1; Hon 1 (bases 1 to 413)

NCI-CGAp http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat Tumor Gene Index Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-GGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Other_ESTs: ur66f04.x1
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="tumor, gross tissue"
/dev_stage="10 months"
/lab_host="DH10B"
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/clone_lib="NCI_CGAP_Mam3"
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/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                      413 bp mRNA EST 13-FEB-1999 NCI_CGAP_C08 Homo sapiens cDNA clone IMAGE:1913100 TR:042400 042400 AXIN. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                            GI:4073540
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                                                                                                                                                                                                            Euteleostomi;
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                                                                                 l (bases 1 to 399)

I (bases 1 to 399)

Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. and Wilson, R. and 
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aa43002:r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:823683

5', mRNA sequence.
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Seg primer: -40UP from Gibco.
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est@watson.wustl.edu
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/lab_host="DH10B"
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Pred. No. 5.1e-18;
0; Mismatches 18;
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         cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 524 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA915999 546 bp mRNA EST 29-APR-1998 oh86g11.s1 NCI_CGAP_CO8 Homo sapiens cDNA clone IMAGE:1473956 similar to TR:042400 042400 AXIN. ;, mRNA sequence.
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97; Conserv
                                                                                                                                                                                                                                                   Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael
                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                Tumor Gene Index
Unpublished (1997)
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1 (bases 1 to 546)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP ^~~~~ Institute, Cancer Genome Anatomy Project (CGAP),
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/tissue_type="Tooled human melanocyte, fetal heart,
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                                                                                                                                                                                                                                                                                                                        Tumor Gene Index
Unpublished (1997)
Contact: Robert Strau
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A1660139 408 bp mRNA EST 18-DEC-1999 we61a09.xl Soares_thymus_NHFTh Homo sapiens cDNA clone IMAGE: 2345560 3' similar to TR:088566 088566 CONDUCTIN. ;, mRNA
                                                                                                                                                                                                                                             NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                                                          quality sequence stop: 333.
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/Clone_11b-"Soares_thymus_NHFTh"
/dev_stage-"fetal"
/dev_stage-"fetal"
/lab_host-"DH10B (phage-resistant)"
/note-"Organ: thymus, pooled; Vector: pT7T3D-Pac
/Pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: Eco RI; 1st strand cDNA was primed with a Not
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/lab_host="DH10B"
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/clone_lib="NCI_CGAP_Co8"
                                                                                                                                    /organism="Homo sapiens"
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74.8%;
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                                                                                                                                                                                                                                                                                                   Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 445
High quality sequence stops: 235
Source: IMAGE Consortium, LLNL
                                                                                                                                                                                                             This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 445 Std Error: 0.00 Seq.primer: M13RP1
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1. (bases 1 to 361)
                                                                                                                                                                                                                                                                                                                                                                                                                                   Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1
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Location/Qualifiers
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'dev_stage="placenta obtained at birth (full term)"
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## SUMMARIES

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BIRCHMEIER WALTER (DE); BEHRENS JUERGEN (DE)
Location/Qualifiers
1. .207
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Birchmeier, W. and Behrens, J.
CONDUCTINE PROTEIN AND A RELATED AGENT FOR DIAGNOSING
                                                                                                                                                                                          Sequence 9 from Patent A98524
                                                                                                                                TUMOR ILLNESSES
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AC074322 Homo sapi
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Mus musculus
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1 (bases 1 to 2825)
Behrens,J., Jerchow,B.-A., Wurtele,M., Grimm,J., Asbrand,C., Wirtz,R., Kuhl,M., Wedlich,D. and Birchmeier,W.
Functional interaction of an axin homolog, conductin, with beta-catenin, APC, and GSK3beta
Science 280 (5363), 596-599 (1998)
                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                   Mus musculus
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Sequence 6 from Patent WO9911780.
A98521
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BIRCHMEIER WALTER (DE); BEHRENS JUE
Location/Qualifiers
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Birchmeier, W. and Behrens, J.
CONDUCTINE PROTEIN AND A RELATED AGENT
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Zhang, T., Fagotto, F., Hsu, W., Zeng, L., Gilbert, D., Copeland, N.G., Jenkins, N.A., Warburton, D. and Costantini, F.
Properties of mouse Axin2 and human AXIN2: chromosomal location,
                                                                                                                                                                                                                                       Mus musculus Axin2
AF205889
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expression pattern,
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QFCGSRGGTLFKRNAKGTEFGLALSARDGGMSSAAGGPQLPGEEGDRSQDVMQWMLES
ERQSKKSHFISAQSIRKSYFEEGLALSARDGGMSSAAGGPQLPGEEGDRSQDVMQWMLES
ERQSKKPHSAQSIRKSYFEEGLALSARDGGMSSAAGGPALSASHFFTQDPAM
PPLTPNTLAQLEEACRLAEVSKFQKORCCVASQQNBRNHSAAGQAGASFFANPSLA
PEDHKEPKLASVHALQASELVVTYFFCGEEIIYRRMLKAQSLTLGHFKEQLSKKGNY
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IKKQQIGSYWFDQAQTEIQAVMEENAYQVFLTSDIYLEFYRSGGENTAXHSNGGLGSL
KVLCGYLPTLNEEEEWTCADLKCKLSPTVVGLSSKTLRATASVRSTETAENGFRSFKR
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                                                                                                       AC024114.8 GI:11094615
HTG; HTGS_PHASE1; HTGS_DRAFT
                                                                                                                                                                                         Mus musculus chromosome 11 clone RP23-278J12, WORKING DRAFT
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QFCGSRGGTLPKRNAKGTEPGLALSARDGGMSSAAGAPQLPGEEGDRSQDVWQWMLES
ERQSKSKPHSAQSIRKSYPLESARAAPGERVSRHHLLGASGHSRSVARAHPFTQDPAM
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stkpmpvssnarrnedolgebeggaspdsplirmtkslhslldgdgarverffeke
kcvdtldemfacngfromikdtkrakenjtrktikryienusvvskolkpratktyird
ikkooigsvmfdaggelgarverakenjtykryienusvvskolkpratktyird
ikkooigsvmfdaggelgarverakenjtyvelissivilevrsgebraamsneglgsl
kvlcgvlptlneeeemtcadlkcklsptvvglssktlratasvrstetaengfrsfkr
sdpvnpyhvgsgvvfapatsandselssdaltdbsmsmtdssvgvpppvrmgsrkglo
remhrsvkanggvslpfppthhlpksmytpepafaaelisrleklkleesrksle
erlooiredeberegsbalssrdgapvqhplallpsgsveedpotilldhlsrvlktp
cosseverygrysprsrspdhhqdyyhdgchtllpsgsveedpotildbckskvlktp
cosseverygrysprsrspdhhqdyyhdgchtllpsgsklepvaceplogkssltkot
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55. .2577
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/chromosome="11"
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/db_xref="GI:6653586"
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AUTHORS

TITLE JOURNAL REFERENCE

TITLE JOURNAL AUTHORS

COMMENT

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Direct Submission

Direct Submission

Submitted (24-FEB-2000) Human Genome.Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 4, 2000 this sequence version replaced gi:9929587.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center project Information
Center project name: MACA
Center clone name: MACA
Center clone name: MACA
Center clone name: MACA
Center clone name: RP23-278J12

Sequencing vector: M13; L08821
Chemistry: Dye-primer Bodipy: 95% of reads
Chemistry: Dye-terminator Big Dye: 5% of reads
Chemistry: Dye-terminator Big Dye: 5% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 178769 bases at least Q40
Consensus quality: 172780 bases at least Q40
Consensus quality: 179030 bases at least Q20
Estimated insert size: 180377; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 3.2x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fernandez,C., Ferraguto,D., Forcum-Tansey,J., Gill,R.,
Gorrell,J.H., Gunaratne;P., Haller,G., Hernandez,J., Hogues,M.,
Hosak,H., Hou,X., Huber,J., Jackson,L., Jia,Y., Kelly,J., Kelly,S.,
Kovar,C., Liu,J., Liu,W., Loulseged,H., Lozado,R.J., Martin,R.,
Massey,E., McLeod,M.P., Mei,G., Moore,S., Morgan,M., Morris,S.,
Meal,D., Nelson,A., Nguyen,R., Nguyen,N., Oguh,M., Parish,B.,
Perez,L., Reiter,D., Say,J., Shen,H., Vasquez,L., Watlington,S.,
Williamson,A., Wrensford,G., Zhou,X., Bouck,J., Hodgson,A.,
Muzny,D.M., Rives,M., Scherer,S., Sodergren,E., Weinstock,G.,
Morley,K. and Gibbs,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dederich,D., Thomas,S., Okwuonu,G., Carlock,C., Garner,T., Addison,S., Pace,A., Williams,G., Bonnin,D., Brooks,A., Brown,J., Buhay,C., Bunac,C., Burkett,C., Chacko,J., Chen,G., Chen,Z., Cox,C., Davis,C., Delgado,O., Ding,Y., Dugan-Rocha,S.,
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                                                                                                                                                                                                                                                                                                          NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 30 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence
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of unknown length
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/db_xref="taxon:10090"
/chromosome="11"
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                  gtgggtcgctacagcccacggtcccgc 207
                                                                                              accattttggacgaccacctctccagggtcctcaagacccccggctgtcaatcccctggt 180
                                                                                                                                                                         gcaccggtccagcacccctggccctcctaccctccggcagctatgaagaggacccacaa 120
                                                                                                                                                                                                                                                       | cagatccgggaggatgaagaaaaggagggtctgagcaggccctgagctcacgggatgga
                                                                                                                                                         GCACCGGTCCAACACCCCCTGGCCCTCTTACCCTCTGGCAGCTATGAAGAGGACCCACAA
                                                                             ACCATCTTGGACGACCACCTGTCCAGGGTCCTCAAGACCCCCGGCTGCCAGTCCCCTGGT
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Direct Submission
Submitted (08-AUG-1997) Biochemistry, Hiroshima University, School of Medicine, 1-2-3 Kasumi, Minami-ku, Hiroshima, Hiroshima 734,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Axil, a member of the Axin family, interacts with both glycogen synthase kinase 3beta and beta-catenin and inhibits axis formation of Xenopus embryos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AF017757 3216 bp mRNA ROD 24-APR-1998 RATTUS norvegicus GSK-3beta interacting protein Axil mRNA, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and Kikuchi, A.
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Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AF017757
AF017757.1
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus.
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1. Cell. Biol. 18 (5), 2867-2875 (1998)
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DHKEPKRLASVHALQASELIVTYFFCGEEIPYRRMLKAQSLTLGHFKEQLSKKGNYRY
YFKKASDEFACGAVFEEIWDDETYLPMYEGRILGKVERID"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TEANALATION - "MSSAVLVTLLPDPSSSFREDAPRPPVPGEEGETPPCQPSVGKVQ
STKPMPVSSNARRNEDGIGEPECRASPDSPLTRWTKSLHSLLGODGAYLFRTELERE
KCYDTLDFWFACNGFRGNMLKDTKTLEVAKAYKRYLENNSVVSKQLKGAYKFYTELERE
KCYDTLDFWFACNGFRGNMLKDTKTLEVAKAYKYKRYLENNSVVSKQLKGAYKFYTELERE
IKKQQIGSVMFDQAQTEIQAVMEENAYQVFLTSDIYLEYVRSGGENTAYMSNGGLGSL
KKQQGSVLFTLABEEEBWTCADLKCKLSPTVVGLSSKTLBATASVRSTETAENGFRSFKR
SEPVNPYHVGSGYVFAPATSANDSELSSDALTDDMSMSMDSSVDGIPPYRNGSKKQLQ
REMHRSVKANGGVSLPHFPRTHRLPKEMTPVEPAAFAAELISRLEKLKLELESRHSLE
ERLQQIREDEEKEGSEQALSSRDGAFVQHPLALLPSGSYEEDPQTILDDHLSRVLKTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCQSGOVGRYSPRSRSPDHHHHHHQQCHALLPTGGKLPPEAACPLLGGKSFLTKQTTK
HVHHHYIHHHAVPKTKEEIEABATTQRVRCLAGGTGKLGKSGKSKSHSKPPEPLEGEGF
CGSRGGTLPKRNTKGTEPGLALPAREGGMSSAAAPQLPGEEGDRSQDVWQWMLESEGF
QSKSKPHSTQSIRKSYPLESARAPPGERVSRHHLLGASGHPRSAARAHPFTQDPAMPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Rattus norvegicus"
/db_xref="taxon:10116"
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/db_xref="GI:3080759"
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                                                                                                                                                                                                                                                                                                                                 93.0%;
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                                                                                                                                                                                                                                                                                                            Score 192.6; DB 9
Pred. No. 1.2e-38;
0; Mismatches 9
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Query Match
Best Local Similarity
Matches 161; Conser
                                                                                                                                                                                                                                                                                         500 CAGATCCGAGAGGATGAAGAGAGAGAGGGCTCCGAGCTCACACTCAATTCGCGGGAGGGG 559
                                                                                           gcaccggtccagcacccctggccctcctaccctccggcagctatgaagaggacccacaa 120
                                                                                                                                                                                                                                                                                                                   cagatccgggaggatgaagaaaaggagggtctgagcaggccctgagctcacgggatgga 60
GTAGGCCGCTATAGCCCTCGCTCCCGC
                      gtgggtcgctacagcccacggtcccgc 207
                                                                                                                                                                                         GCGCCCACGCAGCCCCCCCTCCCCTACTGCCCTCCGGCAGCTACGAGGAAGACCCGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA ilbrary construction, 5'-& 3'-end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (29-AUG-2000) to the DDBJ/EMBL/GenBank databases. Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure Analysis, Human Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kawabata,A., Hikiji,T., Kobatake,N., Inagaki,H., ikema,r., Okamoto,S., Okitani,R., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S. NEDO human cDNA sequencing project
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Homo sapiens hepatoma cell_line:HepG2 cDNA to mRNA, clone_lib:HEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2000)
2 (bases 1 to 2104)
Sugano,S., Suzuki,Y., Ota,T., Obayashi,M.,
Shibahara,T., Tanaka,T. and Nakamura,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="HepG2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="highly similar to AF078165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="HEP"
/note="cloning vector pME18SFL3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cell_type="hepatoma"
/clone="HEP10566"
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77.88;
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Pred. No. 9.3e-24;
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121 accattttggacgaccacctctccagggtcctcaagacccccggctgtcaatcccctggt 180
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                                                                                         gcaccggtccagcaccccctggccctcctaccctccggcagctatgaagaggacccacaa 120
                                                                                                                                                                                GCGCCCACGCAGCACCCCCTCTCCCTACTGCCCTCCGGCAGCTACGAGGAAGACCCCGCAG 1414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (16-NOV-1999) Genetics & Development, Columbia University, 701 W168th St. HHSC 1416, New York, NY 10032, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zhang, T., Fagotto, F., Hsu, W., Zeng, L., Gilbert, D., Copeland, N.G. Jenkins, N.A., Warburton, D. and Costantini, F. Properties of mouse Axin2 and human AXIN2: chromosomal location,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zhang, T., Fagotto, F., Hsu, W.,
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AF205888
AF205888.1 GI:6653
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AF205888
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                                                                                                                                                                                                                                                                                                                                                                               617
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                                                                                                                                                                                                                                                                                                                                                                            KASDEFACGAVFEEIWEDETVLPMYEGRILGKVERID"
1724 c 724 g 473 t
                                                                                                                                                                                                                                                                                                                                                                                                                PNTLAHLEEACRRLAEVSKPPKORCCVASOORDRNHSATVQTGATPFSNPSLAPEDHK
EPKKLAGVHALQASELVVTYFFCGEEIPYRRMLKAQSLTLGHFKEOLSKKGNYRYYFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMHRSYKANGRYSLPHFPRTHRLPKEMTPVEPATFAAELISRLEKLKLELESRHSLEE
RLQQIREDEEREGSELTLNSRGAPTQBLSLLESGSYEEDPQTILDDHLSRYLKTPG
CQSFGVGRYSSPRSRSPHHHHHHSYVHSLLPPGGKLPPAAASPGACPLLGKGFPYKD
TTKHYHHHYIHHHAVPKTKEEIEAEATQRYHCFCPGGSEYYCYSKCKSHSKAPETMPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KKQQIDSIMFDQAQTEIQSVMEENAYQMFLTSDIYLEYVRSGGENTAYMSNGGLGSLK
VVCGYLPTLNEEEEWTCADFKCKLSPTVVGLSSKTLRATASVRSTETVDSGYRSFKRS
DPVNPYHIGSGYVFAPATSANDSEISSDALTDDSMSMTDSSVDGIPPYRVGSKKQLQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                           EQFGAQSTKKAYPLESARSSPGERASRHHLWGGNSGHPRTTPRAHLFTQDPAMPSLTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CVDTLDFWFACNGFROMNLKDTKTLRVAKAIYKRYIENNSIVSKOLKPATKTYIRDGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="mssamlytclpdpsssfredaprppypgeegetppchhggggpg
HQTHYCLFQHQAERRWYGEPEGRASPDSPLTRWTKSLHSLLGDQDGAYLFRTFLEREK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="AAF22799.1"
/db_xref="GI:6653584"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="AXIN2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "tissue_type="brain; lymphoblast"
note="similar to ESTs 823683 and 446378"
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                                                                                                                                                                                                                                                                 Score 133.4; DB 8 Pred. No. 8.9e-24;
                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                             46;
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64 da da

121 accattttggacgaccacctctccagggtcctcaagacccccggctgtcaatcccctggt 180

61 gcaccggtccagcaccccctggccctcctaccctccggcagctatgaagaggacccacaa 120

CAGATCCGAGAGGATGAAGAGAGAGAGGGCTCCGAGCTCACACTCAATTCGCGGGAGGGG 1337

GCGCCCACGCACCCCCTCTCCCTACTGCCCTCCGGCAGCTACGAGGAAGACCCGCAG 1397

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BASE COUNT
ORIGIN
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181
                                                                                       Local Similarity
1 cagatoogggaggatgaagaaaaggagggtotgagcaggcootgagotoacgggatgga 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTAGGCCGCTATAGCCCTCGCTCCCGC 1501
                                                                161;
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Submitted (15-JUL-1998) Lab Medicine and Pathology, Mayo clinic,
Submitted (15-JUL-1998) Rochester, MN 55905, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mai,M., Qian,C., Yokomizo,A., Smith,D.I. and Liu,W. Cloning of the human homolog of conductin (AXIN2), to chromosome 17q23-q24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens conductin mRNA, complete cds. AF078165
AF078165.1 GI:4454790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genomics 55 (3), 341-344 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia; Eutheria; Primates; 1 (bases 1 to 3072)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                      PAMPPLTPPNTLAQLEEACRRLAEVSKPPKQRCCVASQQRDRNHSATVQTGATPFSNP
SLAPEDHKEPKKLAGVHALQASELVVTYFFCGEEIPYRRMLKAQSLTLGHFKEQLSKK
                                                                                                                                                                                                                        GNYRYYFKKASDEFACGAVFEEIWEDETVLPMYEGRILGKVERID"
                                                                                                                                                                                                                                                                                      {	t ESERQSKPKPHSAQSTKKAYPLESARSSPGERASRHHLWGGNSGHPRTTPRAHLFTQD}
                                                                                                                                                                                                                                                                                                              SEQFGGSRGSTLPKRNGKGTEPGLALPAREGGAPGGAGALQLPREEGDRSQDVWQWML
                                                                                                                                                                                                                                                                                                                              QTTKHVHHHYIHHHAVPKTKEEIEAEATQRVHCFCPGGSEYYCYSKCKSHSKAPETMP
                                                                                                                                                                                                                                                                                                                                                     GCQSPGVGRYSPRSRSPDHHHHHHSQYHSLLPPGGKLPPAAASPGACPLLGGKGFVTK
                                                                                                                                                                                                                                                                                                                                                                       REMHRSVKANGQVSLPHFPRTHRLPKEMTPVEPATFAAELISRLEKLKLELESRHSLE
ERLQQIREDEEREGSELTLNSREGAPTQHPLSLLPSGSYEEDPQTILDDHLSRVLKTP
                                                                                                                                                                                                                                                                                                                                                                                                                        SDPVNPYHIGSGYVFAPATSANDSEISSDALTDDSMSMTDSSVDGIPPYRVGSKKQLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                          IKKQQIDSIMFDQAQTEIQSVMEENAYQMFLTSDIYLEYVRSGGENTAYMSNGGLGSL
KVVCGYLPTLNEEEEWTCADFKCKLSPTVVGLSSKTLRATASVRSTETVDSGYRSFKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="mssamlyTclpdpsssfredaprppypgeegetppcqpgygkgq
VTKPMSVSSNTRRNEDGLGEPEGRASPDSPLTRWTKSLHSLLGDQDGAYLFRTFLERE
KCVDTLDFWFACNGFRQMNLKDTKTLRYAKAIYKRYIENNSIVSKQLKPATKTYIRDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="conductin"
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/db_xref="GI:4454791"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="AXIN2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  codon_start=1
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                                                                                   64.48;
77.88;
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caccccctggccctcctaccctccggcagctatgaagaggacccacaaaccattttggac 132
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2 (bases 1 to 3485)
2 (bases 1 to 3485)
4 (bases 1 to 3485)
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Danio rerio mRNA for axin2, complete cds.
AB032263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes; Cyprinidae; Rasborinae; Danio.
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Danio rerio
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1 839 c 864 g
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LEERLQQIQEEEERDESEMSSSSASHSLPLLPPGTCEEDPQAILDEHLSRVLKTPGCQ
SPGLLRHSPRARSPERQRPLPRGGLSTRSQSSSASNGYVPAKTFISRQSTRHIHHYHHH
HAGPKSKEQIEVEATQRVQCLCHGTSECCTAPYIRSRSLGRDQCASPAEVALGHSSTL
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/protein_io="BAA92440.1"
/protein_io="BAA92440.1"
/db_xref="01:7229080"
/translation="MNRTLTDDMVSSFREDDPRPPVPGEEGETTCHHPSKLAMMRPKD
/translation="MNRTLTDDMVSSFREDDPRPPVPGEEGETTCHHPSKLAMMRPKD
PVKTIMADLRCSTARRDEDGLGEPEGSASPDSPLARWTKSLHFTLGDDDGAQLERAYL
                                                                                                                                                                                                                                                                                                                                                                                                                                   GEEIPYRRMMKTHSLTLGHFKEQLRKKGNYRYFFKRASDEFECGAVFEEVWDDCTVLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSLEPTRTHTWGGGGSSGHLRAHQPAHPFVQDPAMPPLPPPNTLAQLEEARRRLEEVS
KPSKQRHSTSSLQRDKSHPVPVQNGSSAFPMDERKDPKKMSGCHSSLGSETVVTYFFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RDNIKRQQIDSAMFDQAQMEIQTAMEENAYQMFLTSDIYLEYYRTGCENPSHVNPNGL
GGLKLVCGYLPTLNEEEEMSCNDFKAKALATVVGLSAKTLRSPPLRAVEALEKGYRSY
RRSDPGNPNRFTSGYSFAPATSANDSEVSSDALTDDSMSMTDSSVDAIPPYKLGSKKQ
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/db_xref="taxon:7955"
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                                                                                                                  Score 72.6; DI
Pred. No. 1.5e
0; Mismatches
                                                                                                                                                      6; DB 8;
1.5e-08;
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                                                                                                                  Gaps
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Matches Query Match

Local Similarity 64.4 hes 67; Conservative

21.68;

Score 44.8; DB Pred. No. 0.15;

8;

Length 3066; Indels

0

Gaps

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0;

Mismatches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hirano, Biomedical research center, Osaka Univ. Med. scool, bepartment of Molecular Oncology; 2-2, Yamadaoka, Suita, Osaka 565-0871, Japan (E-mail:hirano@molonc.med.osaka-u.ac.jp, URL:http://www.med.osaka-u.ac.jp/pub/molonc/www/index.html, Tel:81-6-879-3880, Fax:81-6-879-3889)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (09-SEP-1999) to the DDBJ/EMBL/GenBank databases. Toshio Hirano, Biomedical research center, Osaka Univ. Med. scool,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hirano, T., Hibi, M. and Shimizu, T. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi Cypriniformes; Cyprinidae; Rasborinae; Danio.
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Danio rerio
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                            859
                                                                                                                                                        ROIKPATKSFIKDCVMKLHIDPAMFDQAĞTEIQTMMEENTYPLFLKSDIYLEYTRTGG
ESPKLESDQSSYSGNGKVLPGYLEFTYLEDVEWRCDGEEGQIAESDGTPSNRLTGOKLLL
ETYPQRYANSKRYQDMREYHHASMREPVNPYYNSGYALPATSANDSEQQSMSSDAD
TLSLTDSSYDGVPPYRYRKPHREIHESAKVNGRVPLPHIPRTNRIPKDIHVEPEKFA
AELISRLEGYLREREAQEKLEBERLKRYRLEEEGDDADISTGPSLANHRVPPAVHVQHY
GGRYSEMSYNGLQLRDAHEENPESILDEHYQRYMKTPGCQSPGTGRHSFKSRSPDGLF
GGRYSEMSYNGLQLRDAHEENPESILDEHYQRYMKTPGCQSPGTGRHSFKSRSPDGLF
AGKIPCLMMPLSGGQGKHQARQGPKGEAAHLHHKHIHTHYAAAGKREAEDAERAR
MIGGERMNTEDHYGPKSRNYADGMSYGFNTWDPMSYSSKGSTLSKRPVRKGEDGRNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Danio rerio"
/db_xref="taxon:7955"
25. .2532
                            KVSYEFDCGVVFEEVREDDAILPIFEEKIIGKVEKVD"
769 c 874 g 564 t
                                                                             EMREPLPADDMERNQKILQMMMEGEKEAGRYKRSPYGSISGPKKAQGHEPARPSSVER
LGAVHPWVTAQLRNNVQPSHPFIQDPTMPPNPAPNPLTQLEEARRRLEEERRKSGTLQ
AKQRHKNMKKQPCENITVAYYFCGEPIPYRTSVKGRIVTLGQFKELLTKKGSYKYYFK
                                                                                                                                                                                                                                                                                                                                                                                           NHSFYSSKSDSLKNEASIATPRRPDLDLGYEPEGSASPTPPYLKWAESLHSLLDDQDG
IHLFRTFLKQEECADMLDFWFACSGFRKQEANDGNEKMLKLAKAIYKKYILDNNGIVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="axin1"
25. .2532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="BAA92439.1"
/db_xref="GI:7229078"
                                                                                                                                                                                                                                                                                                                                                                                                                                               translation="MSMSVNEKGICYLPDLGSSFTEDAPRPPVPGEEGDLVSSDGRQY/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="axin1"
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104 atgaagaggacccacaaaccattttggacgaccacctctccagggtcctcaagacccccg 163
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Gallus ga
AF009012
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                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (13-JUN-1997) Genetics and Development, Columb University, 701 W. 168th Street, New York, NY 10032, USA
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                                                                                                                                                                                                                                                                                                                                 INRLEEVQKEREAEEKLEERLKRVRAEEEGGEDADISSGDSVISHKMPSAQPFHHFAPR
YSEMGCAGMQMRDAHEENPESILDEHVQRVMKTPGCQSPGPGRHSPKPRSPESGHLGK
LSGTLGTIPFCHGKHTTKSGMKLDAANLYHHKHVYHHIHHSMMKPKEQIEAEATQRV
                                                                                                                                                                                                                                                                                                                                                                                                       YSSKSDAVRNETSTATPRRSDLDLGYEPEGSASPTPPYLKWAESLHSLLDDQDGINLF
RTELKQEDCADLLDTWFACSGFRKLBECVSNEEKRLKLAKAIYKYILDNNGTYSRQI
KPATKSFIKDCVMKLQIDPDMFDQAQTEIQCMIEDNTYPLFIKSDIYLEYTRTGGESP
KIYSDPSSGSGTGKGLGYDTLYTLNEDDEEWKCDQDTEPEASRDSAPSSRLTQKILLETA
TQRATSTRRYSEGREFRHGSWREPVNPYYVNTGYAMAPATSANDSEQQSMSSDADTMS
LTDSSIDGIPPYRLKKQHRREMQESAKANGRVPLPHIPRTYRMFKDHYEPEKKPAAEL
                                                                                                                                                                                                                      YRYYFKKVSDEFDCGVVFEEVREDDTILPIFEEKIIGKVEKID"
                                                                                                                                                                                                                                                                     PVAVHPWVSAQLRNVVQPSHPFIQDPTMPPNPAPNPLTQLEEARRRLEEEEKRAGKLP
                                                                                                                                                                                                                                                                                                                     QNSFAWNVDSHNYATKSRNYSENLGMAPVPMDSLGYSGKASLLSKRNIKKTDSGKSDG
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/protein_id="AAC60245.1"
/db_xref="GI:2252818"
/db_xref="GI:2252818"
/translation="MNIQGKGFPLDLGRSFTEDAPRPPVPGEEGELVSTDPRPVSHGF
/translation="MNIQGKGFPLDLGRSFTEDAPRPPVPGEEGELVSTDPRPVSHGF
                                                                                                                                                                                                                                             LKQRLKPQKRPGSGASQPCENIVVAYYFCGEPIPYRTLVKGRVVTLGQFKELLTKKGN
                                                                                                                                                                                                                                                                                       ANYEMPGSPEDVERNQKILQWIIEGEKEISRHKKTNHGSSGVKKQLSHDMVRPLSIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mutation due to an iap insertion
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/db_xref="taxon:9031"
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                                                 Score 43.8; DB 8; Pred. No. 0.26; 0; Mismatches 37;
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AF097313
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                                                                                       1392 CCACGAGGAAAATCCGGAATCTATTCTGGATGAACACGTGCAGCGTGTTATGAAAAACCCC 1451
1452 GGGCTGCCAGTCCCCTGGGACTGGACGTCATTCCCCCAAAATCCCGC 1497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
                                     162 cggctgtcaatcccctggtgtgggtcgctacagcccacggtcccgc 207
                                                                                                             102 ctatgaagaggacccacaaaaccattttggacgaccacctctccagggtcctcaagacccc 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           164 gctgtcaatcccctggtgtgggttgcctacagcccacggtcccg 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCTGTCAGTCTCCAGGCCCCGGCCGCCACTCTCCCAAGCCACG 1753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATGAAGAAAACCCAGAAAAGCATCCTGGACGAACACGTGCAGCGTGTGATGAAAAACACCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 2529)
Hedgepeth,C.M., Deardorff,M.A. and Klein,P.S.
Xenopus axin interacts with glycogen synthase kinase-3 beta and
expressed in the anterior midbrain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          African clawed frog.
Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission Submitted (06-OCT-1998) Medicine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 (bases 1 to 2529)
Hedgepeth, C.M., Dear
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AF097313.1 GI:3834642
                                                                                                                                                                                                                                                                                                                         761
                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                    PQKQRLKPQKKNVSAPSQPCDNIVVAYYFCGEPIPYRTMVKGRVVTLGQFKELLTKKG
NYRYYFKKVSDEFDCGVVFEEVREDDMILPIYEEKIIGQVEKID"
1 602 c 635 g 531 t
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KPATKSFIKDCVLRQQIDPAMEDQAQMEIQSMMEDNITYPVFLKSDIIYLEYTTIGGESP
KNYSDQSSGSGTGKGPSGYLDFUNEDDEWRCDOGGEHERERGCIPSSLFSQKILALDSS
SHCAGSNRRLSDGREFRPGTWREPVNPYYVNTGYAGAPVTSANDSEQQSMSSDADTMS
LTDSSVDGIIPPYRLKKHYRREMQESANANGRGPLPHIPRTYHHAPDDHYDPEKKPAAEL
ISRLEGVLRDREAEQKLEERLKRVRAEEEGDDGDVSGFSVISHKLPSGPPMHFRISR
YSETGCVGMQIRDAHEENPESILDEHYQRVMKTPGCQSPGTGHHSPKSRSPDGHLSKT
LFGSLGTMQTGHGKHSSKSTAKVDSGNLHHHKHYVHHHGGVKPKEQIDESTQRV
                                                                                                                                                                                                                                                                                                                                                                                         PGAVHPWVSAQLRNVVQPSHPFIQDPTMPPNPAPNPLTQLVSKPGARLEEEEKKAAKM
                                                                                                                                                                                                                                                                                                                                                                                                                ASHEMPVVPEDSERHQKILQWIMEGEKEIIRHKKSNHSSSSAKKQPPTELARPLSIEF
                                                                                                                                                                                                                                                                                                                                                                                                                                   QTNFPWNVESHNYATKSRNYAESMGMAPNPMDSLAYSGKVSMLSKRNAKKADLGKSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="axin"
/protein_id="AAC71036.1"
/db_xref="GI:3834643"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YSLKNDGIKNETSTATPRRPDLDLGYEPEGSASPTPPYLKWAESLHSLLDDQDGIHLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Xenopus laevis"
/db_xref="taxon:8355"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              translation="MSVKGKGFPLDLGGSFTEDAPRPPVPGEEGELITTDQRPFSHTY"
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                                                                                                                                                                                                    20.3%;
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                                                                                                                                                                             Score 42; DB 8; Pred. No. 0.76; 0; Mismatches
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Philadelphia, PA 19104, USA
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                          162 cggctgtcaatcccctggtgtgggtcgctacagccc 197
                                                                                                                                                                                        Local
                                                                                                                ctatgaagaggacccacaaaccattttggacgaccacctctccagggtcctcaagacccc 161
TGGCTGCCAGTCACCTGGCCCAGGCCACCGCTCTCC 1867
                                                                                       CCATGAGGAGAATCCTGAGAGCATCCTGGATGAGCACGTGCAAAGGGTCATGAGGACACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zeng,L., Fagotto,F., Zhang,T., Hsu,W., Vasicek,T.J., Perry,W.L. 3rd, J., Tilghman,S.M., Gumbler,B.M. and Costantini,F. The mouse Fused locus encodes Axin, an inhibitor of the Wnt signaling pathway that regulates embryonic axis formation carrage (1), 181-192 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (13-JUN-1997) Genetics and Development, Columb University, 701 W. 168th Street, New York, NY 10032, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zeng,L., Zhang,T., Perry,W.L. III, Lee,J.J. and Costantini,F. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 3761)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
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KQRYVQAVMQRGRTCVRPACAPVLSVVPAVSDLELSETETKSQRKAGGGSAPPCDSIV
VGYYFCGEPIPYRTLVRGRAVTLGQFKELLTKKGSYRYYFKKVSDEFDCGVVFEEVRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="LGSGSrlreAlaAaAaAGACWGRAGAWFQRGLVRVSSRFWRRSAA
CLAPPPGHGSPSRRRRRDGGPPGPRPRRGPPAEPPLSAWASPGREPGPGPRLHSRRAL
ERLIPLGAVSTEVLGCSAHCSLWQSPKNNVQEQGFPLDLGASFTEDAPRPPVPGEEGE
                                                                                                                                                                                                                                                                                                                             DEPVLPVFEEKIIGKVEKVD"
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EIRVEPQKFAEELIHRLEAVQRTREAEEKLEERLKRVRMEEEGEDGEMPSGPMASHKL
PSVPAMHHFPPRYVDMGCSGLRDAHEENPESILDEHVQRVMRTPGCQSPGPGHRSPDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YILLSOQOGISLFRYFLKQEGCADLLDFWFACSGFRKLEPCDSNEEKRLKLARAIYRK
YILLSSGIVSRQTEPATKSFIKSCVMKQQIDPAMEDQAQTEIQSTMEERYYPSFIKSD
YILDSTRTGSESPKVCSDQSSGSGTKGMSGYLPTLMEDEWKCDQDADEDDGRDPLP
PSRLTQKLLLETAAPRAPSSRRYNEGRELRYGSWREPVNPYYVNSGYALAPATSANDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mutation due
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/db_xref="taxon:10090"
/chromosome="17"
                                                                                                                                                                                                                                                                                                                                                                                                              RRVQSSFSWGPETHGHAKPRSYSENAGTTLSAGDLPFGGKTSAPSKRNTKKAESGKNA
NAEVPSTTEDAEKNQKIMQWIIEGEKEISRHRKAGHGSSGLRKQQAHESSRPLSIERP
                                                                                                                                                                                                                                                                                                                                                                                                                                                      GHVAKTAVLGGTASGHGKHVPKLGLKLDTAGLHHHRHVHHHVHHNSARPKEQMEAEVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LVSTDSRPVNHSFCSGKGTSIKSETSTATPRRSDLDLGYEPEGSASPTPPYLRWAESL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="AAC53285.1"
/db_xref="GI:2252816"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /map="between Hba-ps4 and D17Leh54"
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                                                                                                                                                                                          18.6%;
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Consensus quality: 162326 bases at least Q40
Consensus quality: 165118 bases at least Q30
Consensus quality: 165125 bases at least Q20
Consensus quality: 166195 bases; agarose-fp estimation
Quality coverage: 4.78 in Q20 bases; sum-of-contigs estimation
Quality coverage: 4.78 in Q20 bases; sum-of-contigs estimation.
**NOTE: This is a 'working draft' sequence. It currently
**consists of 19 contigs. The true order of the pieces
**is not known and their order in this sequence record is
** arbitrary, Gaps between the contigs are represented as
**runs of N, but the exact sizes of the gaps are unknown.
**This record will be updated with the faished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center: Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (07-OCT-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On May 4, 2000 this sequence version replaced 91:6604364.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens chromosome SEQUENCE, 19 unordered paccol1505
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DOE Joint Genome Institute.
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DOE Joint Genome Institute.
Sequencing of Human Chromosome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HTG; HTGS_PHASE1; HTGS_DRAFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center Code:
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FEATURES
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Search completed: June 7, 2001, 00:36:12 Job time: 20986 sec
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                                                                                                        4416 CCAGTGCCCCACCAGGTCCCGTAACTCACCTAGCAGTGAAGAGCCTGCACTCACACCATG 4357
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1. 171415

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="19"

/clone="CTD-2081K17"

/clone_lib="CalTech human BAC library D"

43300 a 41368 c 40333 g 44601 t 1813 others
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101414: contig of 12857 bp in length
101514: gap of unknown length
115884: contig of 14370 bp in length
115984: gap of unknown length
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133510: contig of 17526 bp in length
131610: gap of unknown length
151017: contig of 17407 bp in length
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HCV NSZ-NS4 clone
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Human gene express	eryA region of S.	AML1-MTG16 fusion	MTG16	protein	MTG16b protein cod	ancreat	Nucleic acid seque	IVmac239 proviral	SIVmac239 nef-dele	e of r	d seq	DNA encoding a GDP	HCV NS2-NS4 clone			Human G-protein co		Human GPCR protein	Human G-protein co	Neisseria gonorrhe				EST clone EC302.	HCV antigen clone	AB005297 cDNA clon	Human BAI1 gene.	Human METH2 relate	Human ORFX ORF1991	HCV NS2-NS4 clone	Mouse Voltage-gate	HCV NS2-NS4 clone	HCV NS2-NS4 clone

## ALIGNMENTS

Tumor-suppressing protein conductin diagnosis of tumors Conductin; tumour; diagnosis; treatment; beta-catenin; anti-tumour; therapy; cytoplasmic degradation; blockade; Wnt signalling pathway; Wingless signalling pathway; Adenomatous Polyposis Coli; APC; tumour suppressor; ss. 17-JUN-1999 (first entry) WPI; 1999-214706/18. P-PSDB; W93570. Behrens J, Birchmeier 02-SEP-1997; 01-SEP-1998; 11-MAR-1999 W09911780-A2 Homo sapiens tumour suppressor; Human conductin cDNA. x23370; X23370 standard; cDNA; 2523 BP (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX 97DE-1038205 98WO-DE02621. Σ used for treatment and

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                               misc_feature
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                                                                    protein_bind
                                                                                                            protein_bind
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                                                                                                                                                                                                                                      Conductin; tumour; diagnosis; treatment; beta-catenin; anti-tumour; therapy; cytoplasmic degradation; blockade; Wnt signalling pathway; Wingless signalling pathway; Adenomatous Polyposis Coli; APC;
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                                                                                                                                                                                                                                tumour suppressor;
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                                                                                                                                                                                                                                                                                                                        x23369;
                                                                                                                                                                                                                                                                                                                                          X23369 standard; cDNA; 2825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This inventi
anti-tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2523 BP; 620 A; 728 C; 723 G; 452 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                             181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cagatccgggaggatgaagaaaggagggtctgagcaggccctgagctcacgggatgga 1248
                                                                                                                                                                                                                                                                                                                                                                                                                              accattttggacgaccacctctccagggtcctcaagacccccggctgtcaatcccctggt 1368
                                                                                                                                                                                                                                                                                                                                                                                                                                        accattttggacgaccacctctccagggtcctcaagacccccggctgtcaatcccctggt 180
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207; Conserv
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                            /bound_moiety= |
/note= "as desc:
2561..2713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        describes a novel human conductin protein which has
                                                                                                                                                   /product= "Conductin" 446..814
                                                                                                                                                                               Location/Qualifiers 215..2737
                                                                                                           1241..1402
                                                                   1403..1609
                                                                                                                 /note= "regulator of G-protein signalling described in Claim 19"
                    /*tag=
                                                                               /note-
                                                                                      bound_moiety= GSK-3beta
                                                                                                                                                                      /*tag=
                                                            *tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
 "Dishevelled homology region
Claim 22"
                                     ety= beta-catenin
described in Claim
                                                                              described
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 207; DB 20;
Pred. No. 1.7e-48;
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Best Local
CDS
                                                                                                                                                                Axin; cancer; breast cancer; colorectal cancer; gastrointestinal cancer; esophageal cancer; carcinoma; melanoma; diagnosis; treatment; therapy; thyroid carcinoma; tumorigenesis; beta catenin; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1523
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    anti-tumour activity. Detecting the presence or amount of conductin, at protein or nucleic acid levels, is used to diagnose tumours, while agents that (re)activate conductin are used for tumour therapy. Conductin binds to beta-catenin and induces its cytoplasmic degradation, resulting in blockade of the Wnt/Wingless signalling pathway in vertebrates. Conductin also binds to Adenomatous Polyposis Coli (APC)
                                                                                                 Mus musculus
                                                                                                                                                                                                                                                                                                                                 Murine axin gene
                                                                                                                                                                                                                                                                                                                                                                                                          14-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X09013 standard; DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2825 BP; 703 A; 815 C; 813 G; 494 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fragments and, in conjunction with APC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (DELB-)
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207; Conserv
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Location/Qualifiers
1..2981
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Pred. No. 1.8e-48;
; Mismatches 0;
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Best Local S
Matches 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding mutant and wild type Axin and oligonucleotides derived from them are useful for detecting mutations in the Axin gene and for determining whether a subject is likely to develop cancer (including breast, colorecta), gastrointestinal, esophageal, carcinomas or melanomas). The wild type Axin and homologues of Axin are useful for treating subjects who are likely to develop cancer (thyroid carcinomas). The nucleic acids are also useful for diagnosing cancer and for detecting mutations in cancerous cells. Wild type Axin, its antisense molecule and identified compounds form pharmaceutical compositions in the treatment of cancer. The compositions are also useful for treating cancer by inhibiting tumorigenesis (by inducing degradation of beta-catenin). The nucleic acid encoding Axin acts through negative regulation of the treatment of the first treatment acts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1772
Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiparkinic; immunosuppressant; cardiant immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; hypotensive; antibacterial; antifungal; antifheumatic; antithyroid; antianaemic; gene therapy; cancer; proliferative disorder; hypottension neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
                                                                                                                                                                                                                                                            C75493;
                                                                                                                                                                                                                                                                                            C75493 standard; cDNA; 402
                                                                                                                                                                                                                                                                                                                                                                                      1832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3761 BP; 890 A; 1012 C; 1088 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 7; Figure 9A-9B; 95pp; English.
                                                                                                                                                                                     Human ORFX ORF1048
                                                                                                                                                                                                                         08-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Newly isolated nucleic acid encoding "axis inhibition" protei (Axin) - useful for detecting, diagnosing and treating cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Constantini F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-JUL-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          negative regulation of the Wnt pathway in the Nieuwkoop Center.
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                                                                                                                                                                                                                                                                                                                                                                                                   162 cggctgtcaatcccctggtgtgggtcgctacagccc 197
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DB; W96265.
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/product= Axin
                                                                                                                                                                                   polynucleotide sequence SEQ ID NO: 2095
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62.5%;
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Pred. No. 0
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                                                                                                                                                                                                                                                                                                                                                                                                          CC C74446 to C77606 encode the proteins given in B40237 to B43397, which CC represent the human ORRX open reading frames I to 3161. The ORRX CC sequences have activities such as: cytostatic; hepatotropic; vulnerary; CC antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; CC cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; CC dermatological; immunosuppressive; antithripamatory; antibacterial; cc antiviral; antifungal; antirheumatic; antithromatory; antibacterial; cc sequences can be used for determining the presence of or predisposition CC to, or preventing or treating pathological conditions associated with an CC ORFX-associated disorder. The nucleic acids can be used to express ORFX CC proteins in gene therapy vectors. The proteins and nucleic acids may be CC used to treat cancers, proliferative disorders, neurodegenerative CC disorders, osteoarthritis, graft vs host disease, cardiovascular disease, CC diabetes mellitus, hypertension, hypothyroidism, cholesterol ester CC storage, systemic lupus erythematosus, severe combined immunodeficiency CC contense coamilation, to inhibit thrombosis, and as a contractive to contense coamilation, to inhibit thrombosis, and as a contractive to contense coamilation.
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Best Local
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02-APR-1999;
05-APR-1999;
30-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cholesterol ester storage; systemic lupus erythematosus; infection severe combined immunodeficiency; malaria; autoimmune disorder; as allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound bone damage; cartilage damage; antiinflammatory disease; coagulati
                                                                                                                                                                                                                                                                                                                                                           Sequence 402 BP; 77 A; 126 C; 107 G; 92 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                enhance coagulation; to inhibit thrombosis; and as a contraceptive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 5; Page 1573; 5507pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shimkets RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-MAR-2000; 2000WO-US08621.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CURA-) CURAGEN CORP.
                                                                                                                191
                                                                                                                                113 acccacaaaccattttggacgaccacctctccagggtcctcaagacccccgg 164
                                                                                                                                                                                                                           53
                                                                                                                                                                                                                                                                                  Local Similarity
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                                                                                                          ctcttgtgctgcaagtgaaagaagccctccccagtgtcctcaccaccatgg
                                                                                                                                                                                   gcgtgggttcagtgggcacccactccctggtactgctactgtccggccccaatgatgaac 190
                                                                                                                                                                                                       gggatggagcaccggtccagcaccccctggccctcctaccctccggcagctatgaagagg 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000-602362/57.
)B; B41284.
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99US-0127636.
99US-0127728.
2000US-0540763.
                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Leach
                                                                                                                                                                                                                                                                              17.0%;
57.1%;
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                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                  Score 35.2;
Pred. No. 0.
                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                48;
                                                                                                                                                                                                                                                                                                    Length 402;
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X09012 standard; DNA;

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X09012

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                                                                                                                                                                                                                                                                                                     Nucleic acids encoding mutant and wild type Axin and coligonucleotides derived from them are useful for detecting mutations in the Axin gene and for determining whether a subject is likely to develop cancer (including breast, colorectal, gastrointestinal, esophageal, carcinomas or melanomas). The wild type Axin and homologues of Axin are useful for treating subjects who are likely to develop cancer (thyroid carcinomas). The nucleic acids are also useful for diagnosing cancer and for detecting mutations in cancerous cells. Wild type Axin, its antisense molecule and identified compounds form pharmaceutical compositions in the treatment of cancer. The compositions are also useful for treating cancer by inhibiting tumorigenesis (by inducing degradation of beta-catenin). The nucleic acid encoding Axin acts through congestive regulation of the Wnt pathway in the Nieuwkoop Center.
                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                         Matches
                                                                                                                                               1503
            X28371 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Axin; cancer; breast cancer; colorectal cancer; gastrointestinal cancer; esophageal cancer; carcinoma; melanoma; diagnosis; treatment; therapy; thyroid carcinoma; tumorigenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-JUL-1998;
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                                                                                                                                                                                                                                                                               Sequence 3411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Figure 10A-10B; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Newly isolated nucleic acid encoding "axis inhibition" protein (Axin) - useful for detecting, diagnosing and treating cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Constantini F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JAN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  beta-catenin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-JUN-1999
                                                                                                   164 gctgtcaatcccctggtgtgggtcgctacagccc 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; W96264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYCO ) UNIV COLUMBIA NEW YORK.
                                                                                                                                                             104 atgaagaggacccacaaaccattttggacgaccacctctccagggtcctcaagacccccg 163
                                                                                                                                                                                                                     Local Similarity
                                          σ
                                                                                    gccgccagtcgcctgggcctggccatcgctcccc 1596
                                                                                                                                            acgaggagaaccctgagagcatcctggacgagcacgtacagcgtgtgctgaggacaactg 1562
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                                                                                                                                                                                                        56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         useful for detecting, diagnosing and treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene
                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                              BP; 752 A; 1010 C; 1066 G; 582 T; 1 other;
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             CDNA; 15202 BP
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                                                                                                                                                                                                                                     DВ
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ID F11514 standard;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                     This sequence encodes an imidazoline receptor of the invention. Host cells expressing the polypeptides are useful for screening for ligands of an imidazoline receptor. Restriction fragments of the polypucleotide are useful as labeled probes for isolating and identifying DNA material encoding polypeptides that are receptive to imidazoline compounds. The isolation of polypucleotides encoding the imidazoline receptive polypeptides have immunological and ligand binding properties, which enable identification of agents having greater potency and/or more selectivity for these receptors.
Multiple gene expression; filamentous fungal cell; EST;
                                                   13-MAR-2001
                                                                                                                                                                 9872
                                                                                                                                                                                                                   9932
                                                                                                                                                                                                                                                                    9992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polynucleotides encoding imidazoline receptive polypeptides useful for screening for ligands of imidazoline receptors, and isolating and identifying polynucleotides encoding imidazoline
                        Aspergillus niger EST SEQ ID NO:4037.
                                                                            F11514;
                                                                                                                                                                                                                                                                                                                                                                              Sequence 15202 BP; 2844 A; 4417 C; 4444 G; 3479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 72-79; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         receptive polypeptides
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                                                                                                                                                                                          121 acca 124
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                                                                                                                                                                GCCA
                                                                                                                                                                                                                   gcaccggtccagcaccccctggccctcctaccctccggcagctatgaagaggacccacaa 120
                                                                                                                                                                                                                                                                    cagatccgggaggatgaagaaaaggaggggtctgagcaggccctgagctcacgggatgga
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                                                                                                                                                                                                                                                                                                                   Conservative
                                                 (first entry)
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                                                                                                   cDNA; 438
                                                                                                                                                                                                                                                                                                                               15.8%;
                                                                                                                                                                                                                                                                                                                   0;
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Pred. No. 4.8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         CC expression of genes in a first filamentous fungal (FF) cell relative to cells. The method uses fluorescence-labeled nucleic acids isolated from the FF cells and a substrate of expressed sequence tags (EST). The ESTS CC are used in the methods for monitoring differential expression of genes CC in a first filamentous fungal (FF) cell relative to expression of genes CC in a first filamentous fungal (FF) cell relative to expression of genes CC in a first filamentous fungal (FF) cell relative to expression of the ESTS CC same genes in one or more second filamentous fungal cells. Monitoring CC potential of the microorganisms to be improved. New genes may be consisted function of genes from FF cells allows the production consisted and gene copy number variation and stability can be consisted and gene copy number variation and stability can be consisted and gene copy number variation and stability can be consisted and gene copy number variation and stability can be consisted and to changes in culture conditions, environmental stress, spore consisted and the companies over genomic or random cDNA CC consisted to changes in culture conditions, environmental stress, spore consisted one gene or open reading frame, and organisation of the collaboration of the gene products to facilitate consisted one gene or open reading frame, and organisation of the microarrays based on function of the gene products to facilitate consisted to F14878 represents ESTs from Aspergillus oryzae; and F14879 to E1337 represents ESTs from Aspergillus oryzae; and F14879 to E1337 represents ESTs from Aspergillus oryzae; and F14879 to consiste to consiste the first of the first 
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 438 BP; 84 A; 92 C; 91 G; 170 T; 1 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Monitoring differential expression of genes in filamentous fungal cells uses fluorescence-labeled nucleic acids isolated from the cells and a substrate of expressed sequence tags -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Berka RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200056762-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 specifically claimed in the present invention.
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                                                                                                                                         100
                                                                                                                                                                  160 cccggctgtcaatcccctggtgtgtgtcgctacagcccacggtcc 204
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                                                                                                                                                                                                                                                            agctatgaagaggacccacaaaaccattttggacgaccacctctccagggtcctcaagacc 159
                                                                                                                                         TCCGCATAAATAGCCTCTAATTTCCGGATCTGCAGTCCAAGACCC
                                                                                                                                                                                                                                     AGGAAAGAAAAGGATTAAAGAAGCATTTTGAACTAACACTTCTCCAACCGCTTCCTCTTC
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                                                                                                                                                                                                                                                                                                                                                        15.2%;
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Pred. No. 5.
                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                               Length 438;
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X86273 standard; DNA; 2326

ВP

22-FEB-2000

(first entry)

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                                                                                                                                                                                                                                                                                                                                                                                                                     The specification describes the use of p53 transcription tags for developing products to determine p53 status, to diagnose cancer and to evaluate cytotoxicity or carcinogenicity of a test agent. A method for diagnosing cancer or determining p53 status in a sample suspected for being neoplastic comprises comparing the level of transcription of an RNA transcript in a first sample (s1) of a first tissue (t1) to the level of transcription of the transcript in a second sample (s2) of a second tissue (s2), where s1 is suspected of being neoplastic and s2 is a normal human tissue (of the same type) and the transcript is identified by a tag; and categorizing s1 as neoplastic or as having a mutant p53 when transcription is found to be the same or lower in the first, than in s2. The methods and products can be used to determine p53 status, to diagnose cancer and to evaluate cytotoxicity or carcinogenicity of a test agent. X86265-75 encode human PIG proteins.
                             Z36256
                                                           236256 standard;
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2326 BP; 544 A; 635 C; 637 G; 510 T; 0 other;
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17-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         p53 transcription tag; p53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding a human PIG protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VIND ( OCYU)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neoplastic;
                                                                                                                                     121
                                                                                                                                                             143 ccagggtcctcaagacccccggctgtcaatcccctggtgtgggtcgctacag 194
                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                        23 aggaggggtctgagcacgcctgagctcacgggatggagcacccggtccagcaccccctgg
                                                                                        9
                                                                                                                                                                                                               ccctcctaccctccggcagctatgaagaggacccacatatttggacgaccacctct 142
                                                                                                                                cgcggcgcctgcagtggcacggattgctctgccctaccgtgacgcgctccgg
                                                                                                                                                                                              gccgccggcacacaaggcgctttctagctccctcccccgagcgcacagcccgcctccttc
                                                                                                                                                                                                                                                        aggccggagaggaggcggtgcggtggccgtgcggagaccccggtccagacgcctggcg
                                                                                                                                                                                                                                                                                                                    84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIG; ss
                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polyak K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOHNS HOPKINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0079817
97US-0059153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98WO-US19300
                                                           DNA;
                                                                                                                                                                                                                                                                                                                                15.1%;
                                                           10384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vogelstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tags to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           status;
                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                               Score 31.2; DB Pred. No. 9.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                determine p53 status in, e.g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ₽;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer; cytotoxicity; carcinogenicity;
                                                                                                                                                                                                                                                                                                                                                 DB
                                                                                                                                                                                                                                                                                                                    ; 88
                                                                                                                                                                                                                                                                                                                                                 20;
                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                Length 2326;
                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                         60
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Best Local S
Matches 69
 Hepatitis C virus
                         Clone; polypeptide; NS2-NS4;
transcriptase; cDNA; primer;
                                                                   HCV NS2-NS4 clone MX25-2.
                                                                                               26-APR-1993
                                                                                                                          Q32483;
                                                                                                                                                    Q32483 standard; DNA; 849
                                                                                                                                                                                                                         1912
                                                                                                                                                                                                                                                                                                                                    2032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents the human longevity assurance gene 1 (LAGI), designated LAGIHs. The LAGIHs cDNA was isolated from total brain mRNA. The LAGI protein, or proteins with at least 25-30% homology to the LAGIHs protein, is administered to increase the longevity of a human cell: Expression of these polypeptides is used to increase tolerance of human cells to cellular stresses, such as starvation or acidic pH (5-5.5). The LAGI proteins are also used for increasing reproductive capacity of human cells. LAGI polynucleotides can be used as probes for detecting LAGI from different species, as the LAGI gene is highly conserved across the spectrum of eukaryotes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10384 BP; 2135 A; 2839 C; 3598 G; 1812 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel human homologue for increasing longevity, tolerance and reproductive capacity of a cell -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-053098/04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jazwinski SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9958671-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cell reproductive capacity; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (RESE ) RESEARCH CORP TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-MAY-1999;
                                                                                                                                                                                                                                                  193
                                                                                                                                                                               10
                                                                                                                                                                                                                                                                                                                                                              73
                                                                                                                                                                                                                                                                                               gaccacctctccagggtcctcaagacccccggctgtcaatcccctggtgtgggtcgctac 192
                                                                                                                                                                                                                                                                                                                                              caccccctggccctcctaccctccggcagctatgaagaggacccacaaaccattttggac 132
                                                                                                                                                                                                                       AGCCCGAGGCCCC 1900
                                                                                                                                                                                                                                              agcccacggtccc 205
                                                                                                                                                                                                                                                                            AGGGGGCGCGCGGCCCGAGAGACCTTATCCTGGGGCTCCAACGTCCTGGGCCTCTCC
                                                                                                                                                                                                                                                                                                                                CTCACCCCAGCCCGGCCACACCCCCGCATCTACCCGGGTTCCCCCCACGCAGCACTGTCTGA 1973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tolerance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        longevity assurance gene 1; LAG1; LAG1Hs; cell longevity; olerance; cellular stress; starvation; acidic pH;
                                                                                                                                                                                                                                                                                                                                                                                       69; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page 92-99; 98pp; English.
                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kirchman P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0075014.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99WO-US10160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the human longevity assurance gene 1 (LAG1).
                                                                                                                                                                                                                                                                                                                                                                                                   14.8%;
                                                                                                                                                      BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jiang J;
                                                                                                                                                                                                                                                                                                                                                                                       0,
                           Hepatitis (
                                                                                                                                                                                                                                                                                                                                                                                                   Score 30.6;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                        ç;
                                                                                                                                                                                                                                                                                                                                                                                                      18;
                                                                                                                                                                                                                                                                                                                                                                                                                 DΒ
                                         Virus;
                                                                                                                                                                                                                                                                                                                                                                                      64;
                                                                                                                                                                                                                                                                                                                                                                                                                 21;
                                         HCV;
                                                                                                                                                                                                                                                                                                                                                                                     Indels · 0;
                                                                                                                                                                                                                                                                                                                                                                                                                Length 10384;
                                         serum;
                                         HC
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                            1913
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RESULT 11
Q32482/C
ID Q32482
XX Q32482
AC Q32482
XX 26-APR
XX Clone;
KW Clone;
KW transc
XX Hepati
XX EP5183
XX PN EP5183
XX PD 16-DEC
XX
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequences given in Q32483-501 are various clones which were used in the isolation of the NS2-NS4 regions of the Hepatitis C Virus (HCV) gene of the invention (see also Q32442 and Q32472-82). These sequences were isolated from the serum of a patient suffering from hepatitis C (HC). The isolated RNA sequences were converted into cDNA using transcriptase in the presence of one of the primer sequences given in Q32578-79. The sequences were then amplified using primer pairs. The cDNA sequences isolated represent different alleles of the same region of the HCV gene. Sequence comparisons of these clones showed that it is possible for a patient to carry more than one HCV strain at one time. See also Q32436.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-JUL-1991;
07-OCT-1991;
16-DEC-1991;
20-APR-1992;
             16-DEC-1992
                                      EP518313-A.
                                                              Hepatitis C
                                                                                       transcriptase; cDNA;
                                                                                        Clone; polypeptide; NS2-NS4;
transcriptase; cDNA; primer;
                                                                                                                                                                                Q32482;
                                                                                                                                                                                                        Q32482 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 849
                                                                                                                             HCV NS2-NS4 clone MX25-1.
                                                                                                                                                        26-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 147-49; 305pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New hepatitis C virus gene and its encoded protein - diagnosing and vaccinating against hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EP518313-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hayashi N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MITU ) MITSUBISHI KASEI CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-JUN-1991;
                                                                                                                                                                                                                                                                                                                          123
                                                                                                                                                                                                                                                                                                                                                  16
                                                                                                                                                                                                                                                                         63
                                                                                                                                                                                                                                                                         CACCAGGTTCTCCAAGGCGGCCTCAGCT
                                                                                                                                                                                                                                                                                          cccctggccctcctaccctccggcagct 103
                                                                                                                                                                                                                                                                                                                          GAAGAACACAAGGAAAGAGAGGATGCCATGCGCTCCCCCCCATGGATGCTGCATTGAGGAC
                                                                                                                                                                                                                                                                                                                                         gaagaaaaggagggtctgagcaggccctgagctcacgggatggagcaccggtccagcac
                                                                                                                                                                                                                                                                                                                                                                            52;
                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                virus
                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Honda Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                           ₿₽;
                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91JP-0332329.
92JP-0099957.
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91JP-0287008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91JP-0139268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92EP-0109812
                                                                                                                                                                                                        DNA; 849 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                         150 A; 250 C;
                                                                                                                                                                                                                                                                                                                                                                                        14.7%;
59.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Murakami T,
                                                                                                                                                                                                                                                                                                                                                                            0,:
                                                                                        Hepatitis C; Virus; HCV; serum;
allele; ss.
                                                                                                                                                                                                                                                                                                                                                                                        Score 30.4;
Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                         247 G;
                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                         36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seki M,
                                                                                                                                                                                                                                                                                                                                                                                                                                           202
                                                                                                                                                                                                                                                                                                                                                                                                    DB
                                                                                                                                                                                                                                                                                                                                                                                                                                           T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Takahashi
                                                                                                                                                                                                                                                                                                                                                                            36;
                                                                                                                                                                                                                                                                                                                                                                                                    13;
                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 used for infections
                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                            64
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RESULT 12
Q32494/c
Q32494 standard; DNA; 1280 BP.
XX
AC
Q32494;
XX
DT
26-APR-1993 (first entry)
XX
DE
HCV NS2-NS4 clone MX25026A-1.
XX
Clone; polypeptide; NS2-NS4; Hep
KW transcriptase; CDNA; primer; all
XX
OS Hepatitis C virus.
XX
FH
Key
FT
CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 52; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-JUN-1991;
12-JUL-1991;
07-OCT-1991;
16-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the invention. These sequences were isolated from the serum of a patient suffering from hepatitis C (HC). The isolated RNA sequences were converted into CDNA using transcriptase in the presence of one of the primer sequences given in 03253-64. The sequences were then amplified using primer pairs. The cDNA sequences isolated represent different alleles of the same region of the HCV gene. Sequence comparisons of these clones showed that it is possible for patient to carry more than one HCV strain at one time. See also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New hepatitis C virus gene and its encoded protein - used for diagnosing and vaccinating against hepatitis C virus infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequences given in Q32472-82 and Q32442 are various clones which encode the NS2-NS4 regions of the Hepatitis C Virus (HCV) gene of the invention. These sequences were isolated from the serum of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 146-47; 305pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1992-417213/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hayashi N,
Teranishi Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MITU ) MITSUBISHI KASEI CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cccctggccctcctaccctccggcagct 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gaagaaaaggagggtctgagcaggccctgagctcacgggatggagcaccggtccagcac 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CACCAGGTTCTCCAAGGCGGCCTCAGCT 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAAGAACACAAGGAAAGAGAGGATGCCATGCGCTCCCGCCATGGATGCTGCATTGAGGAC 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         849 BP; 146 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Honda Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91JP-0139268.
91JP-0172794.
91JP-0287008.
91JP-0332329.
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                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Murakami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         245 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                            Hepatitis C; Virus; allele; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 30.4;
Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seki M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         209 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Takahashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13;
                                                                                                                                                                                                                                                                                  HCV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
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                                                                                                                                                                                                                                                                                  serum;
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RESULT 13
Q32495/C
ID Q32495
XX Q32495
AC Q32495
AC Q32495
XX 26-APH
XX Clone;
KW Clone;
KW Clone;
KW transc
XX Hepati
XX Hepati
XX FT CDS
FT CDS
FT CDS
FT CDS
FT CDS
XX X I6-DEC
XX X EF518:
XX Y EF
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Best Local S
Matches 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-JUN-1991;
12-JUL-1991;
07-OCT-1991;
16-DEC-1991;
20-APR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA using transcriptase in the presence of one of the primer sequences given in Q32578-79. The sequences were then amplified using primer pairs. The cDNA sequences isolated represent different alleles of the same region of the HCV gene. Sequence comparisons of these clones showed that it is possible for a patient to carry more these clones showed that it is possible for a patient to carry more
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q32495
                                                                                                                                                                                                                                                                                                                                                    Hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                Clone; polypeptide; i
transcriptase; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q32495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New hepatitis C virus gene and its diagnosing and vaccinating against
                                                                                                16-DEC-1992
                                                                                                                                                         EP518313-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HCV NS2-NS4 clone MX25026B-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1280 BP; 222 A; 385 C; 376 G; 297 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       these clones showed that it is po
than one HCV strain at one time.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HCV) gene of the invention (see also Q32442 and Q32472-82). These sequences were isolated from the serum of a patient suffering from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequences given in Q32483-501 are various clones which in the isolation of the NS2-NS4 regions of the Hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 165-67; 305pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hayashi N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MITU ) MITSUBISHI KASEI CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hepatitis C (HC). The isolated RNA sequences were converted into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CACCAGGTTCTCCAAGGCGGCATCAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cccctggccctcctaccctccggcagct 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAAGAACACAAGGAAAGAGAGGATGCCATGCGCTCCCGCCATGGATGCTGCATTGAGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gaagaaaaggagggtctgagcaggccctgagctcacgggatggagcaccggtccagcac 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
52; Conserv
                                                                                                                                                                                                                                                                                                                                                       virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Honda Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91JP-0139268.
91JP-0172794.
91JP-0287008.
91JP-0332329.
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                                                                                                                                                                                                                                                      Location/Qualifiers
1..1278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA;
                                                                                                                                                                                                                                                                                                                                                                                                            NS2-NS4; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.7%;
59.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Murakami T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 30.4; D
Pred. No. 14;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                Hepatitis C; allele; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              See also Q32436.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               encoded protein - hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seki M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Takahashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    HCV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  used for infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                    serum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    were used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           These
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64
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11-JUN-1992;

92EP-0109812.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                            misc_feature
                                                                                                                                                                          resting potential; alpha subunit; modulator; hearing/vision problem; migraine; central nervous system; CNS; seizure; neuroprotective agent; psychotic disorder; reporter; treatment; detection; antibody; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequences given in Q32483-501 are various clones which were used in the isolation of the NS2-NS4 regions of the Hepatitis C Virus (HCV) gene of the invention (see also Q32442 and Q32472-82). These sequences were isolated from the serum of a patient suffering from sequences were isolated from the sequences were converted into cDNA using transcriptase in the presence of one of the primer cDNA using transcriptase in the presence of one of the primer sequences given in Q32578-79. The sequences were then amplified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-OCT-1991;
16-DEC-1991;
                                                                                                                                                              primer;
                                                                                                                                                                                                                                                                                 04-APR-2000
                                                                                                                                                                                                                                                                                                                                         Z49454 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1280 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    using primer pairs. The cDNA sequences isolated represent different alleles of the same region of the HCV gene. Sequence comparisons of these clones showed that it is possible for a patient to carry more than one HCV strain at one time. See also Q32436.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New hepatitis C virus gene and its encoded protein - diagnosing and vaccinating against hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hayashi N,
Teranishi
                                                                                      mat_peptide
                                                                                                                                 Mus sp.
                                                                                                                                                                                                                                                   Mouse Voltage-gated Potassium channel monomer, Kv6.2 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MITU ) MITSUBISHI KASEI CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-JUN-1991;
12-JUL-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16
                                                                                                                                                                                                                                                                                                                                                                                                                 63
                                                                                                                                                                                                                                                                                                                                                                                                                                            76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1992-417213/51.
                                                                                                                                                                                                                                                                                                                                                                                                                 CACCAGGTTCTCCAAGGCGGCATCAGCT 36
                                                                                                                                                                                                                                                                                                                                                                                                                                cccctggccctcctaccctccggcagct 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAAGAACACAAGGAAAGAGAGGATGCCATGCGCTCCCGCCATGGATGCTGCATTGAGGAC 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gaagaaaaggagggtctgagcaggccctgagctcacgggatggagcaccggtccagcac 75
                                                                                                                                                               ds
                                                                                                                                                                                                                      gated potassium channel; Kv6.2; mouse; excitability;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page 167-69; 305pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Honda Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91JP-0139268.
91JP-0172794.
91JP-0287008.
91JP-0332329.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92JP-0099957.
                           /label= Mouse_Kv6.2_polypeptide
/note= "Voltage gated potassium
1381..1389
                                                                                                    Location/Qualifiers
/note= "This region encodes the amino acid sequence
                                                                       /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         222 A; 385 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14.7%;
59.1%;
                                                                                                                                                                                                                                                                                                                                           1518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Murakami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 30.4;
Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      376 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seki M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         297 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Takahashi K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36;
                                            channel subunit"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
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RESULT 15
Q32501/c
ID Q32501 standard; D
XX
AC Q32501;
XY
DT 26-APR-1993 (firs
XX
DT 26-APR-1993 (firs
XX
Clone; polypeptide
XX
KW Clone; polypeptide
XX
CS Hepatitis C virus.
XX
                                                                                                                                                                                                                                                                                            ρy
                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                       Ω
                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                 Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is the gene encoding the mouse Kv6.2 monomer, which is an alpha subunit of heteromeric voltage-gated potassium channel. It is isolated from brain tissue and maintains the resting potential and controls the excitability of a cell. Kv6.2 polypeptide can be used to identify compounds, that modulate the ion flux through heteromeric voltage-gated potassium channels. Such modulators are used as neuroprotective agents and for treating CNS disorders, such as migraines, hearing and vision problems, psychotic disorders and seizures. It can also be used as reporter molecules in assays and to produce antibodies. Kv6.2 DNA sequence can be used to produce specific primers or probes
                                               Clone; polypeptide; NS2-NS4; Hepatitis C; transcriptase; cDNA; primer; allele; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New voltage-gated potassium channel alpha subunit, useful for identifying modulators of voltage-gated channel activity usefut treating central nervous system disorders e.g. migraines and neuroprotective agents
                 Hepatitis C virus
                                                                                            HCV NS2-NS4 clone N25N15-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1518 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jegla TJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200001811-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ICAG-) ICAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for detection purposes.
                                                                                                                                                                                                                                                                 296
                                                                                                                                                                                                                                                                                            122 ccattttggacgacca 137
                                                                                                                                                                                                                                                                                                                             236
                                                                                                                                                                                                                                                                                                                                                                                      176 agatectagtgaatgtgggtggeeageggtacetgetgeeetggageaceetggatgeet 235
                                                                                                                                                                                                                                                                                                                                            62 caccggtccagcaccccctggccctcctaccctccggcagctatgaagagggacccacaaa 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Loca L
                                                                                                                                                                                                                                                                                                                                                                                                                 2 agatccgggaggatgaagaaaaggaggggtctgagcaggccctgagctcacgggatggag
                                                                                                                                                                                                                                                                                                                            tcccgctgagccgcctgagcaggctccggctgtgccgcagccatgaggagatcacgcagc 295
                                                                                                                                                                                                                                                              tctgcgatgactacga 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000-126937/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <u>ن</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 Similarity 70; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page 65-66; 80pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   14.7%;
nilarity 51.5%;
Conservative
                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-US14945
                                                                                                                                                                                        DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             271 A; 467 C; 470 G;
                                                                                                                                                                                        3564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELK, which is represented in the specification as the typographical error KV6.2 (an insertion
                                                                                                                                                                                        ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the protein name) "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 30.4;
Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               310 T; 0 other;
                                                                 Virus; HCV; serum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB
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                                                                                                                                                                                Query Match
Best Local Similarity 59.1
Matches 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-JUN-1991;
12-JUL-1991;
07-OCT-1991;
16-DEC-1991;
20-APR-1992;
                                                                                                                                                                                                                                                                                                The sequences given in Q32483-501 are various clones which were used in the isolation of the NS2-NS4 regions of the Hepatitis C virus (HCV) gene of the invention (see also Q32442 and Q32472-82). These sequences were isolated from the serum of a patient suffering from hepatitis C (HC). The isolated RNA sequences were converted into CDNA using transcriptase in the presence of one of the primer sequences given in Q32578-79. The sequences were then amplified using primer pairs. The CDNA sequences isolated represent different alleles of the same region of the HCV gene. Sequence comparisons of these clones showed that it is possible for a patient to carry more than one HCV strain at one time. See also Q32436.
                                                                                                                                                                                                                                                                          Sequence 3564 BP; 668 A; 1064 C; 1046 G; 786 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 186-92; 305pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New hepatitis C virus gene and its encoded protein - used for diagnosing and vaccinating against hepatitis C virus infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1992-417213/51.
P-PSDB; R29870.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hayashi N,
Teranishi Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MITU ) MITSUBISHI KASEI CORP.
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                                                                                                                                    123 GAAGAACACAAGGAAAGAGGATGCCATGCGCTCCCGCTATGGATGCTGCATTGAGGAC 64
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                                                                                        76 cccctggccctcctaccctccggcagct 103
                                                                          CACCAGGTTCTCCAAGGCGGCCTCAGCT 36
                                                                                                                                                    gaagaaaaggaggggtctgagccaggccctgagctcacgggatggagcaccggtccagcac 75
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91JP-0172794.
91JP-0287008.
91JP-0332329.
92JP-0099957.
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59.18;
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Pred. No. 17;
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1: /cgn2_6/ptodata/2/1na/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/1na/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/1na/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/1na/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/1na/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/1na/backfiles1.seq:*
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US-08-439-009A-3
US-08-460-900C-42
US-08-460-900C-42
US-08-656-055-5
US-08-668-5
PCT-US95-13233-5
US-07-953-230A-2
US-09-036-997A-1
US-09-036-997A-1
US-09-131-818-14
US-09-231-818-14
US-09-231-818-14
US-09-131-818-14
US-07-918-953-3
US-08-081-661-12
US-07-918-953-12
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olication US/08937972 2443 AATION: Lal, Preeti Lal, Preeti	llarity 54.0%; P Conservative 0; sggsaggatgaagaaagg [	15.8%; 54.0%; Cive	lication US/08922635. y1	tion John Tina DNA	6 359 4 US- 6 359 4 US- 6 510 1 US- 6 515 3 US- 6 515 4 US- 6 2156 2 US- 6 4895 4 US- 6 4895 4 US- 5 6315 3 US- 5 6315 3 US- 5 8535 3 US- 5 8535 3 US- 5 8535 3 US- 5 8537 3 US- 5 8537 3 US- 6 2451 3 US- 6 2451 3 US- 7 US- 8 US-
972	algygtccgagcag algall         gaggcccgggggg tcctaccctccggc             CCCACACTAGCCGC	Score 32.8; DB Pred. No. 1.5; 0; Mismatches aggagggtctgagcag                 agganggcccccccccccccccccccccccccccccccc	CODING ENCODI 1sting 2,635A 66	ALIGNMENTS	3-08-784-582-3 3-08-785-271-3 3-07-918-953-7 3-08-081-661-7 3-08-589-028-1 3-08-784-582-1 3-08-785-271-1 3-08-785-271-1 3-08-99-514-1 3-08-913-0508-2 3-08-911-745-7 3-08-716-3518-1 3-08-820-1708-29 3-09-273-565-29 3-09-273-565-29 3-09-273-565-32 3-09-273-565-32
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CORRESPONDENCE ADDRESS

ADDRESSEE:

TITLE OF INVENTION: ANTIGENS UMBER OF SEQUENCES: 6

Corley, Neil C. Shah, Purvi

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Best Local Similarity
Matches 67; Conserv
                                                                                                                                            Sequence 3, Application US/07642734C Patent No. 5824513
                                                                                                                                                                          -07-642-734C-3
                                                                                                                            GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linea:
IMMEDIATE SOURCE:
LIBRARY: BLADNO'
CLONE: 1318190
                                            APPLICANT: Mcalpine, J B TITLE OF INVENTION: Recor
                                                                                                                                                                                                                                           1245 AGGCCCGGC 1253
                                                                                            APPLICANT: Katz, L
APPLICANT: Donadio, S
                                                                                                                                                                                                                                                                                                                                                                    1125 CAGGAGCTGAGGGCACCCAGCAACCTGGGCCTGCATTCCATCCGCTCTGCAGCCCCA 1184
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LENGTH: 1352 base pairs
TYPE: nucleic acid
                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                       1185 AGCATCTTTCCAGTGGGGCCCCCATTCACGTTGGTCCTCAGGGAAACCAGGGTCCGGGGC 124
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                                                                                                                                                                                                                                                                       157 acccccggc 165
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ELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
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ADDRESSEE:
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Edward H. Gorman
                ADDRESS:
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27
                                                           Recombinant DNA Method for Producing
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                                            Analogs
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TELEFAX: 708-938-2623 INFORMATION FOR SEQ ID NO: 3:
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ORIGINAL SOURCE:
ORGANISM: Sac
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TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
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OPERATING SYSTEM:
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    Saccharopolyspora erythraea
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4171..4428
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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acyltransferase domain module 3"
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beta-ketoreductase domain of module 3"
                              module
                                                                                                              acyl carrier
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beta-ketoacyl ACP synthase of module 3"
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/function= "gene eryA"
/product= "eryA ORF2 encoding modules 3 & 4
6-deoxyerythronolide B"
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acyl carrier domain of module 3"
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module 4"
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module 3"
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NAME/KEY: misc_feature LOCATION: 10831.12174
OTHER INFORMATION: /func OTHER INFORMATION: beta-FEATURE:
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LOCATION: 10723..20
OTHER INFORMATION:
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LOCATION: 14857..15114
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyl carrier domain of module 5
FEATURE:
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LOCATION: 10723..15165
OTHER INFORMATION: /fun
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LOCATION: 15166..20235
OTHER INFORMATION: /fur
OTHER INFORMATION: modu
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LOCATION: 14062..14610
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoreductase of module 5"
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OTHER INFORMATION:
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LOCATION: 6054..7026
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyltransferase domain of modul
                                                               NAME/KEY: misc_feature
LOCATION: 16768..17721
OTHER INFORMATION: /fur
OTHER INFORMATION: acyl
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LOCATION: 15172..1659
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoacylaCPsynthase domain of modul"
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LOCATION: 12379..13350
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LOCATION: 9433..9984
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OTHER INFORMATION: /
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18379..18921
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module 5"
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beta-ketoacylaCPsynthase domain of modul"
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/function= "gene -eryA"
/product= "orf3 encoding modules 5 & 6
6-deoxyerythronolide B formatio"
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module 6"
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Patent No. 6004787
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Best Local Similarity
                                                                                                                                                           TELEPHONE: 847-938-3137
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDLIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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NAME: CASULO, Dianne
REGISTRATION NUMBER: 40,943
REFERENCE/DOCKET NUMBER: 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Method of Directing Biosynthesis TITLE OF INVENTION: Specific Polyketides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Katz, L
APPLICANT: Mcalpine,
                  HYPOTHETICAL: NAME OF ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
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CLASSIFICATION: 435
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LOCATION: 19149..1939
OTHER INFORMATION: /function= "a
OTHER INFORMATION: acyl carrier
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                                                                                                        LENGTH: 20235 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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acyl carrier domain of module 6"
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Pred. No. 13;
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NAME/KEY: misc_feature
LOCATION: 7165..9216
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: dehydratase and encylreductase domains
FEATURE:
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OTHER INFORMATION:
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OTHER INFORMATION:
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LOCATION: 4471..10722
OTHER INFORMATION: /function= "approximate span
OTHER INFORMATION: module 4"
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LOCATION:
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LOCATION: 10225..10483
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OTHER INFORMATION: /fun OTHER INFORMATION: modu
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OTHER INFORMATION:
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LOCATION: 3406..3921
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10723..20235
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10723..15165
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/function="gene ==ryA"
/product="orf3 encoding modules
6-deoxyerythronolide B formatio"
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acyl carrier domain of module 4"
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acyltransferase domain of module
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module 3"
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beta-ketoreductase domain of module
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beta-ketoacyl ACP synthase of module
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/product= "eryA ORF2 encoding modules 3 & 4
6-deoxyerythronolide B"
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Best Local Similarity
Matches 53; Conserv
                                                                                                            3322
                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: 14857..15114
OTHER INFORMATION: /function= "approximate span c
OTHER INFORMATION: acyl carrier domain of module
FEATURE:
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LOCATION:
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LOCATION: 19492..20235
OTHER INFORMATION: /fur
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LOCATION:
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OTHER INFORMATION: module 6"
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19149..19398
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18379..18921
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15172..16569
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15166..20235
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12379..13350
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10831..12174
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thioesterase domain of module
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acyltransferase domain of module
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acyltransferase domain of module
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beta-ketoreductase domain of
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module 5"
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Pred. No. 13;
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RAL INFORMATION:

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Matches 55; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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NFORMATION FOR SEQ ID NO:
                                                                                                               APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,00
FILING DATE: 14-DEC-1994
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MEDIUM TYPE: Floppy
                                             TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing TITLE OF INVENTION: Proteins and Uses Related Thereto
                                                                                  APPLICANT:
                                                                                                  APPLICANT:
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FILING DATE: 30-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REGISTRATION NUMBER: HMI-006CI
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CITY: Boston
STATE: MA
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PRIOR APPLICATION DATA:
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                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                        124 attttggacgaccacctctccagggtcctcaagacccc 161
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                                                                                                                                                                                                                                                                                                                                                                                  64 ccggtccagcacccctggccctcctaccctccggcagctatgaagaggacccacaaacc 123
                                                                                                                                                                                                                                                                                       60 TTTCTCATCGACCACATCGCCGTGTGTGTCCGGAACGC 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 3900 base pairs
TYPE: nucleic acid
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                                                                               Bumcrot, David A.
Marti-Gorostiza, Elisa
                                                                                                             McMahon, Andrew
Tabin, Clifford
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                                                                                                               Ingham, Phillip W. McMahon, Andrew P. Tabin, Clifford J.
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HOAG & ELIOT LLP
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Pred. No. 17
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                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: SCOTT, I
APPLICANT: GOODRICI
APPLICANT: JOHNSON
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                                                                                                                                                                                                                                     Sequence
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LENGTH: 3900 base pair
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                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert STREET: Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US (FILING DATE: 4-MAY-1995 PRIOR APPLICATION DATA:
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                                                                                                                           NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US OF FILING DATE: 14-DEC-1994 PRIOR APPLICATION DATA:
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                                                                                                                                          TITLE OF INVENTION:
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COMPUTER READABLE FORM:
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CITY: E
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                                              STATE:
                                                           CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                            COUNTRY:
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TOPOLOGY: li
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55; Conserv
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                                                                                                                        GOODRICH, LISA V
JOHNSON, RONALD L
VENTION: Patched Genes and their Use
EQUENCES: 19
                                                                                                                                                                                       SCOTT, MATHEW P
                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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; Pred. No. 12;
0; Mismatches
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Matches 55; Conservative
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INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                            ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                  ATTORNEY/AGENT INFORMATION:

NAME: ROWLAND, BETTLAM I

REGISTRATION NUMBER: 20015

REFERENCE/DOCKET NUMBER: a60190-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: SCOTT, MATHEW P
APPLICANT: GODRICH, LISA V
APPLICANT: JOHNSON, ROMALD L
TITLE OF INVENTION: Patched Genes and their Use
                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
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LENGTH: 4434 base pairs
                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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MOLECULE TYPE:
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TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
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SOETWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
ELECOMMUNICATION INFORMATION: TELEPHONE: 415-781-1989
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                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                          FILING DATE:
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                                                                                                                                                                                                            APPLICATION NUMBER: US/08/656,059
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                                                                                                                                                                                                                                                                                                                                                            COUNTRY: US
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COMPUTER: II
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SYSTEM: PC-DOS/MS-DOS
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Pred. No. 12
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; TOPOLOGY: 1; MOLECULE TYPE: US-08-954-668-5
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US-08-954-668-5/c
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     Matches
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                                 Query Match
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Best Local Similarity
                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                             SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/954,668
FILLNG DATE: 20-Oct-1997
CLASSIFICATION: 530
                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 617-832-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: SCOTT, MATHEW F
APPLICANT: GOODRICH, LISA V
APPLICANT: JOHNSON, RONALD L
                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Patched Genes and their Use NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       261 TTTCTCATCGACCACATCGCCGTGTGTGTCCGGAACGC 224
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                    Local
                                                                                                                               LENGTH: 4434 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                            NAME: Vincent, Matthew P
REGISTRATION NUMBER: 3670
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                              TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: UZIP: 02109
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STREET: One Post Office Square
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TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
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                    Similarity
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     Conservative
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                  14.18;
56.18;
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                    Score 29.2;
Pred. No. 12;
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Pred. No. 12;
   Mismatches
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                                 DB 4;
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                                 Length 4434;
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Gaps
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64 ccggtccagcaccccctggccctcctaccctccggcagctatgaagaggacccacaaacc 123

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GENERAL INFORMATION:
                                                                                                                                                 Sequence 2, Application US/07953230A
Patent No. 5476779
                                                                                                                                    GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
                                                               APPLICANT: CHEN, Thomas T
APPLICANT: SHAMBLOTI, MICHAEL J
TITLE OF INVENTION: INSULIN-LIKE GROWTH FACTORS ISOLATED
TITLE OF INVENTION: FROM RAINBOW TROUT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 415-781-1989
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
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                                CORRESPONDENCE ADDRESS
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                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                 261 TTTCTCATCGACCACATCGCCGTGTGTGTCCGGAACGC
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                                                                                                                                                                                                                                                                                                                    321 CTGATCGAGCGCCACTTGGGCGTCCACCCAGCTGGTGCGTATGTAAAGATCCGAGAATAA 262
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REFERENCE/DOCKET NUMBER:
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FILING DATE: 06-OCT-1990
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OPERATING SYSTEM: PC-DOS/MS-DOS
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Four Embarcadero Center, Suite 3400
Burns, Doane, Swecker & Mathis
George Mason Bldg., Washington & Prince Sts.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     415-398-3249
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Pred. No. 12;
0; Mismatches
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Best Local Similarity
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                                                                                                                                                                                                                                                 TITLE OF INVENTION:
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                                                                                                                 ZIP: 46268
                                                                                                                                  COUNTRY:
                                                                                                                                                   STATE:
                                                                                                                                                                  CITY: Indianapolis
                                                                                                                                                                                                   ADDRESSEE:
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                                                                                                                                                                                                                                  OF SEQUENCES:
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                                                                                                                                                   Indiana
                                                                                                                                    USA
                                                                                                                                                                                                                                                                                Waldron,
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TELEFAX: (703) 836-20: INFORMATION FOR SEQ ID NO:
                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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LENGTH: 732 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 836-6620
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NAME: Crane-Feury, Sharon
REGISTRATION NUMBER: 36,1:
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MEDIUM TYPE: Floppy disk
                CURRENT APPLICATION DATA:
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STATE: Virginia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/09036987A 6143526
                                                                                                                                                                                                             E: Dow AgroSciences LLC Patent Department
9330 Zionsville Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           United States
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                Treadway, Patti J.
Turner, Jan R.
                                                                                                                                                                                                                                                                                                                                                                                             Merlo, Donald J.
                                                                                                                                                                                                                                                                                                                                                                                                              Crawford, Kathryn P. Madduri, Krishnamurthy
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Broughton, Mary C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Richard H
                                                                                                                                                                                                                                                                          Production: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13.9%;
                                                                                                                                                                                                                                                                                                               Biosynthetic Genes For Spinosyn Insecticide
                                                                                                                                                                                                                                                                                                                                      Clive
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38.
US/09/036,987A
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Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57;
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ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER:

Stuart,

50,608

0,

FILING DATE: 0
CLASSIFICATION:

09-MAR-1998

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RESULT 13
US-09-010-928B-3/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/09010928B Patent No. 5994099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           atent No. SOLUTION:
GENERAL INFORMATION:
APPLICANT: Lewis, Randolph V
APPLICANT: Hayashi, Cheryl Y
APPL
                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: NFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78772 CTCACCGGACACGACGCGGCGACCGTGCACCGCCTGCTCCAACTCCAGCCGGGGGGGAC 78713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78712 GCCGCCTACGACCGGGACAACCCGGCTGGACGCGACCTCGTCGTGGTCGACGAGGCGTCC 78653
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INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M
REGISTRATION NUMBER: 28977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 22-JAN-19
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                      HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 50
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317)337-4816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
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NAME/KEY:
                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                             STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: UZIP: 22042
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CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                      ENGTH:
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                                                                                                                                                                                                                                            nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: BIRCH, STEWART,
8110 GATEHOUSE RD.
                                                                                                                                                                                                                                                                                  2824 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                               linear
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                                                                                                                                                                                                                 not relevant
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Pred. No. 29;
0; Mismatches
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SUITE 500E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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RESULT 14
US-08-403-852D-14
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Best Local Similarity
Matches 55; Conserv
                                                                  TELEFAX: (202) 408-4400 INFORMATION FOR SEQ ID NO: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL
                                                                                                                REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                      FILING DATE: 10-MAI-1---
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: PCT/FR 93/00923
                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/
FILING DATE: 25-SEP-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow,
STREET: 1300 I Street, N.W., Suite 700
                                                                                                                                                                               FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               823 CTGGTCCAGCACCACCGGGTCCGGAACCTCCAGCACCAC 785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                883 CTGGTCCAGAACCTCCAGGTCCTACACCTCCTGGTCCGGAGCCACCAGGCCCTACACCTC 824
                                                                                                TELEPHONE:
 STRANDEDNESS:
                                                                                                                                                   REGISTRATION NUMBER:
                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/403,852D FILING DATE: 10-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 ccggtccagcaccccctggccctcctaccctccggcagctatgaagaggacccacaaacc 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: OTHER INFORMATION:
                                 ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Washington
              nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                         20005-3315
                                                                                                                                                                  Meyers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/08403852D
                               474 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Crouzet,
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1..2724
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                                                                                                   (202)
double
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                                                                                                408-4000
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Biosynthesis Of Streptogramins,
Coding For These Polypeptides Av
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                                                                                                                                                                                                                     FR 92/11441
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note- "Flagelliform DNA sequence taken from 3' region. Stop codon begins at position 2722.
                                                                                                                                 03806.0054-00000
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Pred. No. 16;
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ORIGINAL SOURCE:
ORGANISM: S.pristinaespiralis

ANTI-SENSE: MOLECULE TYPE:

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Crouzet, Joel
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Best Local Similarity
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REGISTRATION NUMBER:
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A1819942 tg40d11.x
A1858567 w164d08.x
AW207598 UJT-H-BII1-AI336613 qo62c07.x
AI376113 q189f01.x
AI37712 q189f01.x
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AA1363868 qy60a10.x
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AA141251 xs23a05.x
AA444251 xs23a05.x
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3 AA937585
11 AW172276
3 AA884421
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AUTHORS
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Unpublished (1997)
Contact: Robert Strausberg,
Tel: (301) 496-1550
                                                                                                                                                                          This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 457 Std Error: 0.00 Seq primer: -40UP from Gibco.
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Robert_Strausberg@nih.gov
/note-Torgan: pooled; Vector: pf7773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from five normalized libraries were mixed, and as circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and cloneIDs: Soares NbHSF pool 1:
                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2371025"
/clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"
/lab_host="DH10B"
                                                                                                                                                                Location/Qualifiers
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BF712351
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BE196680
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BF712351 MI-P-A3-a
A1873834 wm42c05.x
BF189495 235091 MA
AL053013 Drosophil
BF867287 963088C11
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BE427144
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R33823 yh78f12.r1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence stop: 333.
Location/Qualifiers
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Seg primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 788 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/lab_host="DHIOB (phage-resistant)"
/lab_host="DHIOB (phage-resistant)"
/note="Organ: thymus, pooled; Vector: pT7T3D-Pac
/note="Organ: thymus, pooled; Vector: pT7T3D-Pac
/note="Organ: thymus, pooled; Vector: pt15D-Pac
/note="Organ: thymus, pooled; Vector: pt16D-Pac
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                                                                                                                                                                                                                                                                                                          /clone="IMAGE:2345560"
/clone_lib="Soares_thymus_NHFTh"
/dev_stage="fetal"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                   This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 752 Std Error: 0.00 Seq primer: -400P from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 543)
NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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AI220032
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                                                                                                                                                                                                                                                                                                                                                                                                  quality sequence stop: 224.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (301) 496-1550
1: Robert_Strausberg@nih.gov
    /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NBHL19W, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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.M.A.u....
/26408-728711, and /_
and M. Fatima
                                                                                                                                                                                                                                                        /lab_host="DH10B"
                                                                                                                                                                                                                                                                   /clone="IMAGE:1841331"
/clone_lib="Soares_NFL_T_GBC_S1"
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/db_xref="taxon:9606"
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77.88;
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wk27c05.x1
similar to
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                                                                                                                                                                                                                             High quality sequence stop: 465
Location/Qualifiers
                                                                                                                                                                                                                                                             Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                             www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 700 Std Error: 0.00
                                                                                                                                                                                                                                                                                                             found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CGAP/BTGAP), Tumo
Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                              Bonaldo, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project
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                                                                                                                                                                                                                                                                                                                         cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
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        Ø
adaptors (Pharmacia), dig
                                                                                                             /tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
                                                                                                                                              /clone="IMAGE:2413544"
/clone_lib="NCI_CGAP_Brn25"
                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
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161; Conserv
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 740 Std Error: 0.00
Seq primer: -40UP from Gibco
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National Cancer Institute, Cancer Genome Anat
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67
                                                                                                                                                                                                                                                                                                                                                                                                        quality sequence stop: 421.
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                       /notes Organ: pooled; Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Scares and M. Fatima Bonaldo. "
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159 c 192 g 138 t
  Soares and M. Fatima Bonaldo.
1 124 c 162 g 107 t
                                                                                                                                                                                                                                                            /organism-"Homo sapiens"
/db_xref="taxon:9606"
/db_nce="IMAGE:2111253"
/clone_1ib="Soares_NFL_T_GBC_S1"
/lab_host-"DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AI858567 418 bp mRNA EST 07-MAR-2000 w164d08.xl NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2429679 3's similar to TR:088566 O88566 CONDUCTIN. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                   DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 541 Std Error: 0.00
Seq primer: -40UP from Gibco
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AI858567.1
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 418)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
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                                                                                                                                                                                                                                                                                                     High quality sequence stop: 402.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: Robert_Strausberg@nih.gov
Tissue Procurement: David N. Lou:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA Library Arrayed by: Greg Lennon, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA Library Preparation: M. Bento Soares, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (301) 496-1550
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/tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
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/clone_lib="NCI_CGAP_Brn25"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: NCI-CGAP clone distribution
information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      383 bp. mRNA EST 02-DEC-1999 UI-H-BII-afk-g-08-0-UI.sl NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722358 3', mRNA sequence.
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Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
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Mammalia; Eutheria;
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/Glone=TiMAGE:2723358"
/Clone=Lib="NCI_CGAP_Sub3"
/Clone=Lib="NCI_CGAP_Sub3"
/Lab_host="PH108 (Life Technologies)"
/lab_host="PH0108 (Life Technologies)"
/lab_host="Nector: pP773D-Pac (Pharmacia) with a modified
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1 115 c 149 g 89 t
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/db_xref="taxon:9606"
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76.3%;
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Pred. No. 2.8e
0; Mismatches
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similar to
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Cer
                                                                                                                                                                            Contact: Robert Strausberg, Tel: (301) 496-1550
                                                                                                                                                                                                                              Tumor Gene Index Unpublished (1997)
                                                                                                                                                                                                                                                                                      1 (bases 1 to 413)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
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                                                                                                                                           Email: Robert_Strausberg@nih.gov
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NCI_CGAP_Kid3 pool 1 LLAM 334-3337, 3682-3683, 3798-3803 (IMAGE CloneIDs 1322376-1323911, 1456008-1456775, 1500552-1502855); NCI_CGAP_Kid5 pool 1 LLAM 3338-3342, 145052-1472903, 1492104-1493255); NCI_CGAP_Lu5 pool 1 LLAM 3575-3582, 3851-3854 (IMAGE CloneIDs 1314920-1417991, 1520904-1522439); NCI_CGAP_G4 pool 1 LLAM 3164-3167, 1520904-1522439); NCI_CGAP_G4 pool 1 LLAM 376-3720, 3733-3735 (IMAGE CloneIDs 1414920-1417991, 1520904-1479983, 147552-1476743); NCI_CGAP_F122 pool 1 LLAM 2457-2459, 2758-2759, 3062-3068 (IMAGE CloneIDs 985608-986759, 1101192-1101959, 1217928-1220615); NCI_CGAP_COLD pool 1 LLAM 2647-2653, 2871-2872 (IMAGE CloneIDs 1057416-1061255, 1144584-1145351). Subtraction was performed as previously described (Bonaldo, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery. Genome Research 6 Colone Colone (1996): Normalization and Subtraction: Two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TAG_LIB=NCI_CGAP_Lu5
TAG_TISSUE=lung
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Pred. No. 5.2e-23;
0; Mismatches 46
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TITLE

Sequencing Center

AUTHORS

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BASE COUNT
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AUTHORS
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AI272864/c
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Insert Length: 761 Std Error: 0.00
Seq primer: -40UP from Gibco.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            q143h03.x1
                                                                                                                                                                               Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 459)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NRL1onal Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                Tissue Procurement: Chri
Emmert-Buck, M.D., Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similar to
AI272864
                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                                                                                               Robert_Strausberg@nih.gov
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/lab_host="DH10B"
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/clone_lib="NCI_CGAP_Co8"
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/db_xref="taxon:9606"
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                                                                                                                                     Christopher Moskaluk, M.D., Ph.D.,
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Pred. No. 7.0
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EST.
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                                                              Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 487)
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National Cancer Institute, Cancer Genome Ana
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                                                                                                                                                                                                                                                                                                                       human.
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/db_xref."taxon:9606"
/clone="IMAGE:1875125"
/clone_lib-"NCI_CGAP_CO8"
/tissue_type="adenocarcinoma"
/lab_host-"DH10B"
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/organism="Homo sapiens"
                                 Location/Qualifiers
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Pred. No. 7.7e-23;
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                                                                                                                                                                                                                                                                                                                                                                                      ;, mRNA sequence.
                                                                                                                                                                                                                      Anatomy Project (CGAP)
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                                                                                                                                                                                                                                                                      Hominidae;
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                                                                                                                                                                                                                                                                                      Euteleostomi;
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RESULT 11
AI363868/c
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qy60a10.x1
similar to
                                         cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.B. Consortium/LLNL at:
                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 299)
NCI/NINDS-GAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index
Unpublished (1998)
Tissue Procurement:
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                                                                                                                                                                                                                                                     Robert_Strausberg@nih.gov
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/tissue_type="Pooled human melanocyte, fetal heart,
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Pharmacia) with a modified polylinker; Site_1: Not I;
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77.38;
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Pred. No. 7.7e-23;
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oh86g11.s1
similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            158;
                                                                                                                                                               Mammalia; Eutheria; Primates; Catarrhini; Hom
1 (bases 1 to 546)
NCI-CGAP http://www.ncbi.nlm.nih.gov/nciogap.
National Cancer Institute, Cancer Genome Anat
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
               CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                           Emmert-Buck, M.D., Ph.D.
                                                                                                                             Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.,
                                                                                                                                                  Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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ww-bio.llnl.gov/bbrp/image/image.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
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/clone_lib="NCI_CGAP_Brn25"
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                                                                                                                                                                                                                                                                                                                                                                                                                          546 bp mRNA EST 29-APR-1998 NCI_CGAP_CO8 Homo sapiens cDNA clone IMAGE:1473956 TR:042400 042400 AXIN. ; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                               GI:3055391
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76.0%;
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Pred. No. 7.8e-22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49;
                                                                                                                                                                                                                                            Anatomy Project (CGAP),
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                                                       Sequencing Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gtgggtcgctacagcccacggtcccgc 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AW474251 282 bp mRNA EST 24-FEB-2000 xs23a05.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2770448 similar to TR:070240 070240 AXIL. ;, mRNA sequence.
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                       www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
                                                               cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: MCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                               Tissue Procurement: Chri
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                              Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                       NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
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1 (bases 1 to 282)
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High quality sequence stop: 209
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Location/Qualifiers
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                                                                                                                                                                                                  Robert_Strausberg@nih.gov
Procurement: Christopher Moskaluk, M.D., Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note-*organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from colon adenocarcinoma, and was then primed with a Not I oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "
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/clone_lib="NCI_CGAP_Co8"
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/db_xref="taxon:9606"
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/lab_host="DH10B"
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71.0%;
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Pred. No. 3.5e-20;
0; Mismatches 60;
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AA489644/c
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Best Local Similarity
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                                                                                   Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: polyT not found
Seq primer: -41m13 fwd. ET from Amersham
High quality sequence stop: 389.
                                                                                                                                                                                                                                                                                      Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore K., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wy., T., Waterston, R. and Wilson, R.
Washu-Merck EST Project 1997
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA489644 409 bp mRNA
aa43d02.s1 Soares_NhHMPu_S1
3', mRNA sequence:
AA489644
                                                                                                                                                                                                Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST
                                                                                                                                                                                                                                  Washington University School of Medicine
                                                                                                                                                                                                                                                                         Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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a 72 c
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/clone_lib="NCI_CGAP_Ut2"
/clone_lib="NCI_CGAP_Ut2"
/clone_lib="NCI_CGAP_Ut2"
/tissue_type="moderately-differentiated endometrial
adenocarcinoma, 3 pooled tumors"
/lab_host="DH10B"
/lab_host="DH10B"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Sali;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.85 kb. Life Technologies catalog #:
/clone="IMAGE:823683"
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/db_xref="taxon:9606"
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                 /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                      Location/Qualifiers
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68.7%;
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Pred. No. 4.7e-20;
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RESULT 15
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                                            cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-GGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 537 Std Error: 0.00
Seq primer: -4ml3 fwd. ET from Amersham.
                                                                                                                                                                                                                                                     Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.,
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA937585 444 bp mRNA EST 24-AUG-1998 of71h02.sl NCI_CGAP_CO8 Homo sapiens cDNA clone IMAGE:1435827 similar to TR:O42400 O42400 AXIN. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia; Eutheria; Primates; 1 (bases 1 to 444)
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                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."

108 c 152 g 89 t 1 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pregnant uterus"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GI:3095696
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75.8%;
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Pred. No. 6.7e-19;
0; Mismatches 48; Indels 2
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REFERENCE AUTHORS

JOURNAL TITLE SOURCE

**KEYWORDS** ACCESSION

ERSION

FEATURES

/organism="Homo sapiens"

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ORIGIN
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Best Local Similarity
Matches 139; Conserv
                                            181 gtgg 184
                                                                                       106 ACGATACTGGACGATCACCTGTCCAGGGTCCTCAAGACCCCTGGCTGCCAGTCTCCGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="IMAGE:1435827"
/clone_lib="NCI_CGAP_CO8"
/tissue_type="adenocarcinoma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="DH10B"
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Pred. No. 2.2e-17;
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Title:
Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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153
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(without alignments)
455.200 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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3411 8	3156 8	3072 8	2538 8	2104 8	1863 8	3216 9	3016 9	2825 9	2825 9	153 9	Length DB
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AF009674 Homo sapi	AF009012 Gallus ga	AF078165 Homo sapi	AF205888 Homo sapi	AK025718 Homo sapi	AB052751 Homo sapi	AF017757 Rattus no	AF205889 Mus muscu	AF073788 Mus muscu	A98521 Sequence 6	A98525 Sequence 10	Description

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aagaaggcgagtgacgaatttgcctgcggagcagtttttgaggagatctgggacgacgac
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Birchmeter, W. and Behrens, J.
                                                                                                                                     BIRCHMEIER WALTER (DE); BEHRENS JUERGEN (DE)
Location/Qualifiers
                                                                                                                                                      Patent:
                                                                                                                                                             TUMOR ILLNESSES
                                                                                                                                                                    CONDUCTINE PROTEIN AND A RELATED AGENT FOR DIAGNOSING
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AF006011
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MMU10115
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Pred. No. 7.1e-38;
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Z86090 Human DNA
AL023754 Human DNA
AC009856 Homo sapi
AL357632 Homo sapi
AE004520 Pseudomon
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AF026544 Ralstonia
D88802 Bacillus su
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae;
1 (bases 1 to 2825)
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2 (bases 
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Mus musculus
AF073788
                                                 Behrens,J., Jerchow,B.-A. and Birchmeier,W.
Direct Submission
Submitted (22-JUN-1998) Cellular Biology, Max Delbrueck Center
Molecular Medicine, Robert-Roessle 10, Berlin 13122, Germany
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Patent: WO 9911780-A 6 11-MAR-1999;
BIRCHMEIER WALTER (DE); BEHRENS JUEI
LOCATION/Qualifiers
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                                                                                                                                                                                                                                                                                        1 (bases 1 to 3016)
Zhang, T., Fagotto, F., Hsu, W., Zeng, L., Gilbert, D., Copeland, N.G., Jenkins, N.A., Warburton, D. and Costantini, F.
Properties of mouse Axin2 and human AXIN2: chromosomal location, expression pattern, interaction with Axin and effects on embryoni
                                                                                                             Submitted (16-NOV-1999) Genetics & Development, Columbia University, 701 W168th St. HHSC 1416, New York, NY 10032, Location/Qualifiers
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                                                                                                                                                                                                       Zhang,T.
                                                                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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TKHVHHY IHHHAVPKTKEEIEAEATQRVRCLCPGGTDYCYSKCKSHPKAPEPLPGE
OFCGSRGGTLFKRNAKGTEPGLALSAROGGMSSAAGGPQLPGEEEDRSODVMQWALES
ERQSKSKPHSAQSIRKSYPLESARAAGGERVSRHHLLGASGHSRSVARAHPFTQDPAM
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SDPVRPYHVGSGYLPFAPATSANDSELSSDALTDDSMSWTDSSVDGVPPYBMGSKKQLQ
REMHRSVKANGQVSLPFFPKTHRFKEMTPVEPAAFAAELISRLEKLKLELESRHSLE
ERLQQIREDEEKEGSEQALSSRDGAPVQHPLALLPSGSYEEDPQTILDDHLSRVLKTP
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STKPMPVSNARRNEDGLGEPBGRASPDSPLTRWTKSLHSLLGODGDAYLFTFTFLERE
KCUDTLDFWFACNGERQMULKDTKTLRVAKAJYKRYJENNSVVSKQLKPATKTYIKDG
IKKQQIGSVMFDQAQTEIQAVMEENAVQVFLTSDIYLEYVRSGGENTAYMSNGGLGSL
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                                                                2 (bases 1 to 3216)
2 (bases 1 to 3216)
2 (amanoto, H., Ikeda, S., Murai, H., Kishida, S. and Kikuchi, A. Pramamoto, H.)
2 (amanoto, H.)
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Axil, a member of the Axin family, interacts with both glycogen synthase kinase 3beta and beta-catenin and inhibits axis formation
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
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Rattus norvegicus
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55. .2577
Location/Qualifiers
1. .3216
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/db_xref="GI:6653586"
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Pred. No. 1.1e-37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACAGTGCTCCCCATGTACGAAGGCAGGATCCTG 2577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTGACTCTGGGCCACTTCAAGGAGCAGCTCAGCAAAAAGGGAAATTACAGGTATTACTTC 2484
                                                                                                 Submitted (16-DEC-2000) to the DDBJ/EMBL/GenBank databases. Yoichi Furukawa, Institute of Medical Science, Human Genome Center; 4-6-1 Shirokanedai, Minatto-Ku, Tokyo 108-1639, Japan (E-mail:furukawa@ims.u-tokyo.ac.jp, Tel:81-35449-5373,
                                                                                                                                                                                               Homo sapiens Axin2 mRNA AB052751
                                                                                      Fax:81-35449-5406)
                                                                                                                                                                                      Nakamura, Y., Furukawa, Y. and Takahashi, M.
                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                  AB052751.1
                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                               Homo sapiens cDNA to mRNA.
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DHKEPKRLASVHALQASELIVTYFFCGEEIPYRRMLKAQSLTLGHFKEQLSKKGNYRY
YFKKASDEFACGAVFEEIWDDETVLPMYEGRILGKVERID"
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GCQSPGVGRYSDRSRSDHHHHHHQQCHALLPTGGKLPPEACFULGGKSFLTKQTTK
HVHHHYIHHAVPKTKEELEAEATQRVRCLCPGGTDYYCSKCKSHSKPEPEDLGEGF
CGSRGGTLPKRNTKGTEPGLALPAREGGMSSAAGAPQLPGEEGDRSQDVWQWMLESER
          /organism="Homo sapiens"
/db_xref="taxon:9606"
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SEPVNPYHVGSGYVFAPATSANDSELSSDALTDDSMSMTDSSVDGIPPYRMGSKKQLQ
REMHRSVKANGQVSLPHFPRTHRLPKEMTPVEPAAFAAELISRLEKLKLELESRHSLE
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                                                                  ocation/Qualifiers
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KCVDTLDFWFACNGFRQMNLKDTKTLRVAKAIYKRYIENNSVVSKQLKPATKTYIRDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="Axil"
/protein_id="AAC40089.1"
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/db_xref="taxon:10116"
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/translation="MSSAVLVTLLPDPSSSFREDAPRPPVPGEEGETPPCQPSVGKVQ
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96.1%;
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Pred. No. 1.2e-34;
0; Mismatches 6
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Query Match
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                                                                                                                                                                NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science,
                                                                                                                                                                                                                                                                                                                                 Submitted (29-AUG-2000) to the DDBJ/RMBL/GenBank databases. Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure Analysis, Human Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                oligo capping; fis (full insert sequence). Homo sapiens hepatoma cell_line:HepG2 cDNA
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Homo sapiens cDNA: FLJ22065 fis, clone HEP10566, highly similar to
AF078165 Homo sapiens conductin mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shibahara, T., Tanaka, T. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sugano,S., Suzuki,Y., Ota,T., Obayashi,M., Nishi,T., Isogai,T., Shibahara,T., Tanaka,T. and Nakamura,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kawabata,A., Hikiji,T., Kobatake,N., Inagaki,H., Ikema,Y.,
Okamoto,S., Okitani,R., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T.,
Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.
                                                                                                                                      University of Tokyo (partly supported by Science and Technology
                                                                                                                                                                                                                                                                                                               Fax:81-3-5449-5416)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2000)
2 (bases 1 to 2104)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                    Location/Qualifiers
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/gene="Axin2"
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/db_xref="GI:11967904"
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/product="conductin"
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Pred. No. 1.3e-27;
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Matches 133;
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1 (bases 1 to 2538)

Zhang, T., Fagotto, F., Hsu, W., Zeng, L., Gilbert, D., Copeland, N.G., Jenkins, N.A., Warburton, D. and Costantini, F.

Properties of mouse Axin2 and human AXIN2: chromosomal location, expression pattern, interaction with Axin and effects on embryonic
                                                                                                                                                                                                                                                                                                                                                                                Submitted (16-NOV-1999) Genetics & Development, Columbia University, 701 W168th St. HHSC 1416, New York, NY 10032,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
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KKQQIDSIMFDQAQTEIQSVMEENAYQMFLTSDIYLEYVRSGGENTAYMSNGGLGSLK
VVCGYLPTLNEEEEWTCADFKCKLSPTVVGLSSKTLRATASVRSTETVDSGYRSFKRS
                                    HQTHVCLFQHQAERRWVGEPEGRASPDSPLTRWTKSLHSLLGDQDGAYLFRTFLEREK
CVDTLDFWFACNGFRQMNLKDTKTLRVAKAIYKRYIENNSIVSKQLKPATKTYIRDGI
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/note="cloning vector pME18SFL3"
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/clone="HEP10566"
                                                                      /protein_id="AAF22799.1"
/db_xref="GI:6653584"
/translation="MSSAMLVTCLPDPSSSFREDAPRPPVPGEEGETPPCHHGGQGPG
                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="17"
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                                                                                                                           /codon_start=1
/product="AXIN2"
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Mai.M., Oian.C., Yokomizo, A., Smith, D.I. and Liu, W. Cloning of the human homolog of conductin (AXIN2), a to chromosome 17q23-q24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (15-JUL-1998) Lab Medicine and Pathology, Mayo clinic, 200 First Street SW, Rochester, MN 55905, USA
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Direct Submission
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99168905
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RLQQIREDEEREGSELTLNSREGAPTQHPLSLLPSGSYEEDPQTILODHLSRYLKTPG
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EPKKLAGVHALQASELTVTYFFCGEEITYFRAKLKAQSLTLGHFKEQLSKKGNYRYTFK
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1 724 c 724 g 473 t
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REMHRSYKANGQVSLPHFPRTYHRLFKEMTPVPBAFTAAELISRLEKKKLEESRHSLE
ERLQQIREDEEREGSELTLNSREGAPTQHPLSLLPSGSYEEDPQTILDDHLSRYLKTP
                                                                                                                                                                                                                                                                                                                                                                                 /organism~"Homo sapiens"
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                                                                                                                                                                                                                                                                              /codon_start=1
                                                                                                                                                                                                                                                                                                         /note="AXIN2"
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                                                                                                                                                                                                                                                         /product-"conductin"
                                                                                                                                                                                                                                                                                                                                                         /map="17q23-q24"
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86.9%;
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Pred. No. 1.4e-27;
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Gallus ga
AF009012
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zeng,L., Zhang,T., Perry,W.L. III, Lee,J.J. and Costantini,F. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zeng,L., Fagotto,F., Zhang,T., Hsu,W., Vasicek,T.J., Perry,W.L. 3rd, Lee,J.J., Tilghman,S.M., Gumbiner,B.M. and Costantini,F. The mouse Fused locus encodes Axin, an inhibitor of the Wnt signaling pathway that regulates embryonic axis formation Cell 90 (1), 181-192 (1997)
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KIYSDPSSGSGTGKGLPGYLPTLNEDEEWKCDQDTEPEASRDSAPSSRLTQKLLLETA
TQRATSTRRYSEGREFRHGSWREPVNPYYVNTGYAMAPATSANDSEQQSMSSDADTMS
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RTFLKQEDCADLLDEWFACSGFRKLEPCVSNEEKRLKLAKAIYKKYILDNNGIVSRQI
KPATKSFIKDCVMKLQIDPDMFDQAQTEIQCMIEDNTYPLFLKSDIYLEYTRTGGESP
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SLAPEDHKEPKKLAGVHALQASELVVTYFFCGEEIPYRRMLKAQSLTLGHFKEQLSKK
GNYRYYFKKASDEFACGAVFEEIWEDETVLPMYEGRILGKVERID"
                                                                                                                                                                                                                                                                                mutation due
                                                                                                                                                                       /product="Axin"
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                                                                                                                                                                                             /codon_start=
                                                                                                                                                                                                                                                                                                    /note="Fused
                                                                                                                                                                                                                   function="may
                                                                                                                                                                                                                                         'gene≖"Axin"
                                                                                                                                                                                                                                                                                                                          /gene≖"Axin"
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/db_xref="taxon:9031"
                                                                                                                                                                                                                                                                                                                                                                                                                                 ocation/Qualifiers
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Pred. No. 1.4e-27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       114;
                                                                                                                                                                                                                                                                                                                                                             3rd, Lee,J.J., Tilghman,S.M., Gumbiner,B.M. and Costantini,F. The mouse Fused locus encodes Axin, an inhibitor of the Wnt signaling pathway that regulates embryonic axis formation Cell 90 (1), 181-192 (1997)
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Vasicek, T.J., Tilghm
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2 (bases 1 to 3411)
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                and Zhang,T
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                                                   mutation due
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/gene="AXIN"
/function="may inhibit embryonic axis formation"
                                                                   /note="Fused
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PVAVHPWVSAQLRNVVOPSHPFIQDPTMPPNPAPNPLTQLEEAKRRLEEEEKRAGKLP
LKQRLKPOKRPGSGASQPCENIVVAYYFCGEPIPYRTLVKGRVVTLGQFKELLTKKGN
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                                                                                                                                                                       /chromosome="16"
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                                                                                                                                                                                                         /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YRYYFKKVSDEFDCGVVFEEVREDDTILPIFEEKIIGKVEKID"
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                                                                                                                                     _stage="ubiquitously expressed
                                                                                                                                                                                                                                                                                                                                Tilghman, S.M., Costantini, F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zeng, L., Guan, X.-J., Zhang, T., Costantini, F. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ი
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Pred. No. 2.3e-18;
0; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       858 g
                                                                                                                                                                                                                                                           ) Biological Technology, Millennium 640 Memorial Drive, Cambridge, MA
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                                                   the classical dominant mouse tail kink an iap insertion in the Axin gene"
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                                                                                                                                       development
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Query Match
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                                                                            Submitted (09-SEP-1999) to the DDBJ/EMBL/GenBank databases. Toshio Hirano, Blomedical research center, Osaka Univ. Med. scool, Department of Molecular Oncology; 2-2, Yamadaoka, Suita, Osaka 565-0871, Japan (E-mail:hirano@molonc.med.osaka-u.ac.jp, URL:http://www.med.osaka-u.ac.jp/pub/molonc/www/index.html, Tel:81-6-879-3880, Fax:81-6-879-3889)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shimizu,T., Yamanaka,Y., Ryu,S.L., Hashimoto,H., Yabe,T., Hirata,T., Bae,Y.K., Hibi,M. and Hirano,T. Cooperative roles of Bozozok/Dharma and Nodal-related proteins the formation of the dorsal organizer in zebrafish mech. Dev. 91 (1-2), 293-303 (2000)
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AB032263
                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 3485)
Hirano, T., Hibi, M. and Shimizu, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; L
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Cypriniformes; Cyprinidae; Rasborinae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Danio rerio
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LSETETRSQRKVGGGSAQPCDSIVVAYYFCGEPIPYRTLVRGRAVTLGQFKELLTKKG
SYRYYFKKVSDEFDCGVVFEEVREDEAVLPVFEEKIIGKVEKVD"
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//db_xref="G1:2252820"
//db_xref="G1:225282
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may inhibit embryonic axis formation"
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    Location/Qualifiers
1. .3485
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nRNA for axin2,
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BASE COUNT

SOURCE

ORGANISM

**(EYWORDS** VERSION ACCESSION DEFINITION Snoo AB032263 RESULT 12

REFERENCE

AUTHORS

TITLE

JOURNAL MEDLINE REFERENCE AUTHORS

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FEATURES

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AUTHORS
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                                                                                                                                                                                        Xenopodinae; Xenopus.

1 (bases 1 to 2529)

Hedgepeth, C.M., Deardorff, M.A. and Klein, P.S.
Xenopus axin interacts with glycogen synthase kinase-3 beta
expressed in the anterior midbrain
mech. Dev. 80 (2), 147-151 (1999)
                                                                                                                      2 (bases 1 to 2529)
Hedgepeth, C.M., Dear
Direct Submission
                                                                                                                                                                                                                                                                                                                                     Xenopus laevis
Eukaryota; Metazoa; Chordata
Amphibia; Batrachia; Anura;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xenopus laevis axin AF097313
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AF097313.1
                                                                                    Medical
                                                                                                        Submitted (06-OCT-1998) Medicine,
                                                                                                                                                                                                                                                                                                                                                                                                          African clawed frog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AF097313
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                                                                                    School, 415 Curie
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LQREMQRNMRMIGGVSLPPFPRFRFPREMTFVEDAFAFAQLLA RLERLKREGETMSS
LEERLOGIOEBEERDRSESMSSSASHSLFLLPPGTCEEDPQAILDEHLSRVLKTPGCO
SPGLLRHSPRSRSPEQRPLPRGGLSTRSQSSSMIGYVPAKTFISROSTKHIHHHYIHH
HAGPKSKEQIEVEATORVOCLCHGTSECCTAPYIRSBLGRDCCASPAEVALCHSSTL
SKRLCKSGEEVNMEGLENSLLQLPADSTDRSQNWQMULESDROTKHKPHSTQNVKKS
HSLEFTRTHWGGGGSSGHLRAHGPAHPFVQDPAMPPLPPPNTLAQLEEARRRLEEVS
KPSKQRHSTSSLQRDKSHPVPVQNGSSAFPMDERKDFKKMSGCHSSLGSETVYTYFFFC
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/db_xref="taxon:7955"
297. .2735
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MYEGKILGKVDRMD"
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EREKCYDTLDFWFACNGFROMDLKDTKTHRVAKALIYKRY IENUSIVAKQLLKPATKTFI
RDNIKRQQLDSAMFDQAMEIQTAMEENAXQNFELTSDIYLEYVRTGCENPSHVNRNGL
GGLKLYCGYLPTLNEEEEWSCNDFKAKALATVVGLSAKTLRSPPLRAVEALEKGYRSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene=
297. .
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/product="axin2"
/organism="Xenopus laevis"
/db_xref="taxon:8355"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translation="MNRTLTDPMVSSFREDDPRPPVPGEEGETTCHHPSKLAMMRPKD/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="BAA92440.1"
/db_xref="GI:7229080"
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                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                            Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    GI:3834642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2529 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57.98;
74.28;
                                                                                                                                                   Deardorff, M.A. and Klein, P.S
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Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA
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                                                                                    Blvd.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , DB 8;
?.4e-17;
                                                                                    Philadelphia,
                                                                                    University of Pennsylvania
Philadelphia, PA 19104, USA
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AF017756
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ORIGIN
                                                                                        FEATURES
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                                                                                                                                                                            TITLE
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Best Local :
                                                                                                                                                      JOURNAL
                                                                                                                                                                                                 AUTHORS
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  Sg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2474 TGATTCTGCCTATTTACGAGGAGAAGAT 2501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 tgaccctgggccacttcaaggagcagctcagcaaaaagggaaattacaggtattatttca 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cagtgctccccatgtacgaaggcaggat 149
                                                                                                                             Submitted (08-AUG-1997) Biochemistry, Hiroshima University of Medicine, 1-2-3 Kasumi, Minami-ku, Hiroshima, Hiroshima
                                                                                                                                                                                                                                                            Axin, a negative regulator of the Wnt signaling pathway, forms a complex with GSK-3beta and beta-catenin and promotes GSK-3beta-dependent phosphorylation of beta-catenin EMBO J. 17 (5), 1371-1384 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complete cds.
AF017756
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                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                                                                     Kikuchi, A.
                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 3460)
Ikeda, S., Kishida, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus
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                                                                                                                                                                                                                     (bases 1 to 3460)
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/organism="Rattus norvegicus"
/db_xref="taxon:10116"
199. .2697
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LPGSLGTMQTGHGKHSSKSTAKVDSGLLHHKHVYHHHHHHHKEVKEQLIDESTQRV
GTNIPPWNVESHINYATKSRNYAESMGMAPNPINSLAYSGKVSMLSKRNAKKADLGKSES
ASHEMPVVPEDSERHQKILQWIMEGEKEIIRHKKSNHSSSSAKKQPPTELARPLSIER
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LTDSSVDGIPPYRLRKHYRREMQESANANGRGPLPHIPRTYHMPKDIHVDPEKFAAEL
ISRLEGVLRDREAEQKLEERLKRVRAEEEGDDGDVSSGPSVISHKLPSGPPMHHFNSR
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RTFLQGENCADLLDFWFACSGFRKLEPNDSKVEKRLKAKAIKKYVLDSNGIVSRQI
KTPLQGENCADLLDFWFACSGFRKLEPNDSKVEKRLKAKAIKKYVLDSNGIVSRQI
KPATKSFIKDCVLRQQIDPAMFDQAGMEIQSMAEDNUTYPVFLKSDIYLEYTTIGGESP
KPATKSFIKDCVLRQQIDPAMFDQAGMEIQSMAEDNUTYPVFLKSDIYLEYTIGGESP
KNYSDQSSGSGTGKGPSGYLPTLNEDEEWRCDQGGEHERERECIPSSLFSQKLALDSS
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PQKQRLKPQKKNVSAPSQPCDNIVVAYYFCGEPIPYRTMVKGRVVTLGQFKELLTKKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="axin"
/protein_id="AAC71036.1"
/db_xref="GI:3834643"
                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              translation="MSVKGKGFPLDLGGSFTEDAPRPPVPGEEGELITTDQRPFSHTY"
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73.6%;
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Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                       Yamamoto, H., Murai, H., Koyama, S.
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Pred. No. 2e-16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                 School 734,
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ORIGIN
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCATCCTGCCTGTCTTTGAAGAAAAGATCAT 2672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109;
                                                                                                                                   Zeng, L., Zhang, T., Perry, W.L. III
Direct Submission
Submitted (13-JUN-1997), Genetics
University, 701 W. 168th Street,
Location/Qualifiers
                                                                                                                                                                                                                                                                              Zeng,L., Fagotto,F., Zhang,T., Hsu,W., Vasicek,T.J., Perry,W.L. 3rd, Lee,J.J., Tilghman,S.M., Gumbiner,B.M. and Costantini,F. The mouse Fused locus encodes Axin, an inhibitor of the Wnt signaling pathway that regulates embryonic axis formation Cell 90 (1), 181-192 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
AF009011
                                                                                                                                                                                                                                                                 97373830
                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; 1 (bases 1 to 3761)
                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 house mouse.
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                      /map="between <1. .3761
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KAGGGSAPPCDSIVVAYYFCGEPIPYRTLVRGRAVTLGQFKELLTKKGSYRYYFKKVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EDAEKNQKIMQWIIEGEKEISRHRKAGHGSSGMRKQQAHESSRPLSIERPGAVHPWVS
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FPPRYVDMGCSGLRDAHEENPESILDEHVORVMETPGCQSPGPGHRSPSGHVAKTAV
LGGTASGHGKHAPKLGLKLDSAGLHHBRHVHHHKHHNGAPKEQMEAEARRYQSSES
WGPETHGHAKPRSYSESTGTNPSAGDLAFGGKASAPSKRNTKKAESGKNASAEVPSTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GSESPKVCSDQSSGSGTGKGMSGYLPTLNEDEEWKCDQDADEDDGRDSVPPSRLTQKL
LLETAAPRAPSSRRYNEGRELRYGSWREPYNPYYVNSGYALAPATSANDSEQQSLSSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VNHSFCSGKGTSIKSETSTATPRRSDLDLGYEPEGSASPTPPYLRWAESLHSLLDDQD
GISLFRTFLKQEGCADLLDFWFACSGFRKLEPCDSNEEKRLKLARAIYRKYILDSNGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADTLSLTDSSVDG1PPYR1RKQHRREMQESVQVNGRVPLPH1PRTYRMPKE1RVEPQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VSRQTKPATKSFIKDCVMKQQIDPAMFDQAQTEIQSTMEENTYPSFLKSDIYLEYTRT
                                                          /chromosome="17"
                                                                                 /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="AAC40066.1"
/db_xref="GI:2982198"
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/gene="Axin"
                                                                                                   /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="GSK-3beta interacting
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                                                                                                                                                                                                                          Perry, W.L. III, Lee, J.J. and Costantini, F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 83.8; DB 94; Pred. No. 7.7e-16;
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                                       Hba-ps4 and D17Leh54"
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                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42;
                                                                                                                                                                Development, Columb
York, NY 10032, USA
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note="Fused is the classical dominant mouse"

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Search completed: June Job time: 20991 sec
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ORIGIN
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Best Local Similarity 71.5
Matches 108; Conservative
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ELVSTDSRFVNHLSFCSGCRGTSIKSETSATPRRSDLDLGYEPBEGSASFTPPYLHWAESL
HSLLDDQDGISLFRTFLKQEGCADLLDFWFACSGFRKLEPCDSNEEKRLKLARAIYRK
YILDSNGIVSRQTKPATKSFIKDCVWKQQIDPAMFDQAGTEIQSTMEENTYPSTLKSD
IYLEYTRTGSESFKVCSDQSGSGTGKGMSGYLPTLNEDEEWKCDQDDADEDDGRDPLP
PSRLTQKLLLETAAPRAPSSRRYNEGRELRYGSWREPVNYYVNSGYALAPATSANDS
EQQSLSSDADTLSLTDSSVDGIPPYRIRKQHRREMQESIQVNGRVPJLHIPRTYRMPK
EIRVEPQKFAEELIHRLEAVQRTREAEEKLEERLKRVRMEEEGGEDGEMPSGPMASHKL
PSVPAMHHFPPRYUDMGCSGLRDAHEENPESILDEHYQRVMRTPGCGSFPGGHRSPDS
GHVAKTAVLGGTASGHGKHVPKLGLKLDTAGLHHHRHVHHVHHNSARPKEQMEAEVA.
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NAEVPSTTEDAEKNOKINGWITIGEREKISTSHRKAGHGSSGLRKQVAHESSRPLSIERP
GAVHPWVSAQLRNSVQPSHLFIQDPTMPPNPAPNPLTQLEEARRRLEEEEKRANKLPS
KORYVQAVMQGGRTCVRPACAPVLSOFT GABVETUSTENETUSTONING
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71.5%;
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Database
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Listing first 45 summaries
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N_Geneseq_0401:*
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153
/SIDS2/gcgdata/geneseq/geneseqn/NA1986.DAT:*
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

1 2 3 3 4 4 4 1 1 1 1 1	Result
153 153 121 121 121 88.6 82.3 30.2 29.6 29.6	Score
100.0 100.0 79.1 79.1 57.9 53.7 21.6 19.7 19.3 19.3	% Query Match
2523 2825 401 1205 3411 3761 925 657 363 575	% Query Match Length DB
20 20 20 21 20 21 14 21 21 21	- DB -
X23370 X23369 A77754 A77784 A777843 X09013 X09013 Q12839 Q36133 C41830 C33133 C51167	ID
Human conductin cD Human conductin DN cDNA encoding huma cDNA encoding huma cDNA encoding huma Human axin gene. Murine axin gene. Variable region of MH4H7 MAb heavy ch Arabidopsis thalia Arabidopsis thalia	Description

Tumor-suppressing protein conductin diagnosis of tumors

used for treatment and

WPI; 1999-214706/18. P-PSDB; W93570.

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	Z91253	21	24494	17.3	26.4	45	
Polynucleotide seq	X20550	20	8648	17.3	26.4	44	C
CoA ligase fccF nu	Z91259	21	1377	17.3	26.4	43	
Arabidopsis thalia	C35947	21	1242	17.3	26.4	42	
M. tuberculosis re	219228	20	1166		6	41	C
M. tuberculosis an	Z19440	20	1166		٥.	40	C
Human gene express	Z15585	20	770	17.3	٥.	39	
Arabidopsis thalia	C44660	21	2148	17.4	6.	38	O
. Arabidopsis thalia	Z30413	20	1935	17.4	6.	37	O
Human gene express	Z15741	20	744	17.4	٥.	36	O
	X13181	20	8102	17.5	6.	35	a
	Z16081	20	765	17.5	26.8	34	
Human gene express	Z14749	20	300	17.5	26.8	33	
-	A10595	21	6741	17.6	27	32	
Aspergillus oryzae	F12525	21	1289	17.8	27.2	31	O
Human lung cancer-	C65784	21	559	17.8	27.2	30	O
Human V3 loop HIV	V71742	20	10942	17.9	27.4	. 29	
· . Arabidopsis wax sy	A38860	21	1041	17.9	27.4	28	O
WAX	A49788	21	1041	17.9	27.4	27	C
: Human prostate tum	Z52940	20	1890	18.0	27.6	26	
cDNA encoding Arab	T93777	18	1404	18.0	27.6	25	
thali	C48750	21	1130	18.3	28	24	C
Arabidopsis thalia	C40313	21	1130	18.3	28	23	O
g	A67611	21	457	18.4	28.2	22	G
Arabidopsis thalia	C37835	21	1021	18.6	28.4	21	
Human ORFX ORF125	C74570	21	5503	18.8	28.8	20	
Human secreted pro	C79811	21	1815	18.8	28.8	19	C
	C36225	21	1487	19.1	29.2	18	
Arabidopsis thal	C47412	21	1484	19.1	29.2	17	
Eosinophil &	A52642	21	1397	19.1	29.2	16	
	T19983	16	340	19.1	29.2	15	
	C35517	21	825	19.3	29.6	14	
Arabidopsis thal	C51169	21	811	19.3	29.6	13	
Arabidopsis thalia	C38945	21	627	19.3	29.6	12	

## ALIGNMENTS

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RESULT
X23370
                                                                                                                                                                                         Conductin; tumour; diagnosis; treatment; beta-catenin; anti-tumour; therapy; cytoplasmic degradation; blockade; wnt signalling pathway; Mingless signalling pathway; Adenomatous Polyposis Coll; APC; tumour suppressor; ss.
                                                                                                                                                                                                                                                                               x23370;
                                                                                            02-SEP-1997;
                                                                                                              01-SEP-1998;
                                                                                                                                                   WO9911780-A2
                                                                                                                                                                                                                                                          17-JUN-1999 (first entry)
                                                                                                                                                                                                                                                                                                X23370 standard; cDNA; 2523 BP
                                                     Behrens J, Birchmeier W;
                                                                                                                                 11-MAR-1999
                                                                                                                                                                                        tumour suppressor;
                                                                                                                                                                                                                                        Human conductin cDNA.
                                                                        (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX
                                                                                                                                                                      Homo sapiens
                                                                                            97DE-1038205.
                                                                                                              98WO-DE02621.
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RESULT
X23369
ID X2
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Best Local S
Matches 153
 11-MAR-1999
                     WO9911780-A2
                                                                            misc_feature
                                                                                                                         protein_bind
                                                                                                                                                                                                                 misc_signal
                                                                                                                                                                                                                                                                                                              Conductin; tumour; diagnosis; treatment; beta-catenin; anti-tumour; therapy; cytoplasmic degradation; blockade; Wnt signalling pathway; Wingless signalling pathway; Adenomatous Polyposis Coli; APC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes a novel human conductin protein which has anti-tumour activity. Detecting the presence or amount of conductin, at protein or nucleic acid levels, is used to diagnose tumours, while agents that (re)activate conductin are used for tumour therapy. Conductin binds to beta-catenin and induces its cytoplasmic degradation, resulting in blockade of the Wnt/Wingless signalling pathway in vertebrates. Conductin also binds to Adenomatous Polyposis Coli (APC) fragments and, in conjunction with APC, acts as a tumour suppressor.
                                                                                                                                                                     protein_bind
                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                 Human conductin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2467
                                                                                                                                                                                                                                                                                                       tumour suppressor;
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                                                                                                                                                                                                                                                                                                                                                                                                              X23369;
                                                                                                                                                                                                                                                                                                                                                                                                                                  X23369 standard; cDNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2523 BP; 620 A; 728 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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••
                                                                        /bound_moiety= beta-catenin
/note= "as described in Cla
2561..2713
                                                                                                                                                                                                                 /product= "Conductin"
446..814
                                                                                                                                                                    1241..1402
                                                                                                                        1403..1609
                                                                                                                                   /bound_moiety=
/note= "as des
                                                                                                                                                                                                                                                 Location/Qualifiers
215..2737
                                                                                                             /*tag=
                                                                                                                                                                                          note- "regulator"
                                                                                                                                                                                                                                        /*tag=
                                                                                                                                                                                                                                                                                                         ss.
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                                          "Dishevelled
Claim 22"
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                                                                                                                                                                               described
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                                                                                                                                   described
                                                                                                                                                                                                                                                                                                                                                                                                                                  В₽
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Pred. No. 5.1e-41;
                                                                                                                                             GSK-3beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 723 G;
                                                                                                                                                                             of G-protein
in Claim 19"
                                                    homology region
                                                                                                                                 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2499
                                                                                     Claim
                                                                                                                                   Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 452 T; 0 other;
                                                                                     21 "
                                                                                                                                 20"
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RESULT A7754
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ID 754
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AC A7
XX A7
AC A7
XX HU
XX HU
XX HU
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Best Local
                                              23-DEC-1998;
02-JUL-1999;
22-SEP-1999;
19-NOV-1999;
                                                                                                                                                                                                                                                                                         WO200037643-A2
                                                                                                                                                                                   23-DEC-1999;
                                                                                                                                                                                                                                     29~JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                    Human colon tumour polypeptide; tumour antigen; cancer; vaccine; immunotherapy; diagnosis; progression; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA encoding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention describes a novel human conductin protein which has anti-tumour activity. Detecting the presence or amount of conductin, at protein or nucleic acid levels, is used to diagnose tumours, while agents that (re)activate conductin are used for tumour therapy. Conductin binds to beta-catenin and induces its cytoplasmic degradation, resulting in blockade of the Wnt/Wingless signalling pathway in vertebrates. Conductin also binds to Adenomatcous Polyposis Coli (APC) fragments and, in conjunction with APC, acts as a tumour suppressor.
                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A77754;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 18; Fig 2; 22pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tumor-suppressing protein conductin diagnosis of tumors
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Pred. No. 5.3e-41;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 133; Conserv
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Best Local :
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Wang T,
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WO200037643-A2
                                                                              Human colon tumour polypeptide; tumour antigen; cancer; vaccine;
                                                                                                             cDNA encoding
                                                                                                                                           14-NOV-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                            human colon tumour polypeptide,
                                                             diagnosis; progression;
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86.9%;
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Best Local Similarity
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19-NOV-1999;
02-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                               present sequence represents a cDNA encoding a human colon
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                                                                                                                                                                                                                                                                 Conservative
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99US-0454150.
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Pred. No. 1.5e-30;
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                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                      Nucleic acids encoding mutant and wild type Axin and coligonucleotides derived from them are useful for detecting mutations in the Axin gene and for determining whether a subject is likely to develop cancer (including breast, colorectal, gastrointestinal, esophageal, carcinomas or melanomas). The wild type Axin and homologues of Axin are useful for treating subjects who are likely to develop cancer (thyroid carcinomas). The nucleic acids are also useful for diagnosing cancer and for detecting mutations in cancerous cells. Wild type Axin, its antisense molecule and identified compounds form pharmaceutical compositions in the treatment of cancer. The compositions are also useful for treating cancer by inhibiting tumorigenesis (by inducing degradation of beta-catenin). The nucleic acid encoding Axin acts through negative regulation of the Wnt pathway in the Nieuwkoop Center.
                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                              Matches
                                                                                                                      2529
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                                                                                                                                                                                                                                                  Sequence 3411 BP; 752 A; 1010 C; 1066 G; 582 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Figure 10A-10B; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Newly isolated nucleic acid encoding "axis inhibition"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          beta-catenin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human axin gene
                122 cagtgctccccatgtacgaaggcaggatcct 152
                                                                                        62
                                                                                                                                                 N
                                                                      agaaggcgagtgacgaatttgcctgcggagcagtttttgaggagatctgggacgacgaga 121
                                                                                                                 tcaccctgggccagttcaaggagctgctgaccaaaaagggcagctacagatactacttca 2588
                                                                                                                                tgaccctgggccacttcaaggagcagctcagcaaaaagggaaattacaggtattatttca
                                                       agaaagtgagcgacgagtttgactgtggggtggtgtttgaggaggttcgagaggacgagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1999-120510/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    useful for detecting, diagnosing and treating cancer
                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98WO-US14414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zeng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers 2..2704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product= Axin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag=
                                                                                                                                                                                           57.98;
74.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ŗ
                                                                                                                                                                             0;
                                                                                                                                                                                         Score 88.6; DB 20
Pred. No. 1.1e-19;
                                                                                                                                                                             Mismatches
2679
                                                                                                                                                                                                       DB 20;
                                                                                                                                                                             39;
                                                                                                                                                                           Indels
                                                                                                                                                                                                     Length
                                                                                                                                                                                                        3411;
                                                                                                                                                                          0;
                                                                                                                                                                           Gaps
                                                                                                                                              61
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RESULT

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                                                                                                                                                                                                                                                                 Nucleic acids encoding mutant and wild type Axin and coligonucleotides derived from them are useful for detecting mutations in the Axin gene and for determining whether a subject is likely to develop cancer (including breast, colorectal, gastrointestinal, esophageal, carcinomas or melanomas). The wild type Axin and homologues of Axin are useful for treating subjects who are likely to develop cancer (thyroid carcinomas). The nucleic acids are also useful for diagnosing cancer and for detecting mutations in cancerous cells. Wild type Axin, its antisense in the treatment of cancer. The compositions are also useful for treating cancer by inhibiting tumorigenesis (by inducing degradation of beta-catenin). The nucleic acid encoding Axin acts through
                                                                                                                                                          Matches
                                                                                                                                                                         Query Match
Best Local
                                                                                                   2806
                                        2866 agaaagtgagtgatgagtttgactgtggtgtggtatttgaggaagtacgggaggatgagc 2925
                                                                                                                                                                                                                               Sequence 3761 BP; 890 A; 1012 C; 1088 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 7; Figure 9A-9B; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Newly isolated nucleic acid encoding "axis inhibition" (Axin) - useful for detecting, diagnosing and treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus
                                                                                                                                                                                                                                                        negative regulation of the Wnt pathway in the Nieuwkoop Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Constantini F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W09902179-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 beta-catenin; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gastrointestinal cancer; esophageal cancer; carcinoma; melanoma;
diagnosis; treatment; therapy; thyroid carcinoma; tumorigenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Murine axin gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-JUN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UYCO ) UNIV COLUMBIA NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-JUL-1997;
122 cagtgctccccatgtacgaaggcaggatcct 152
                                                          62 agaaggcgagtgacgaatttgcctgcggagcagtttttgaggagatctggggacgacgaga 121
                                                                                                               2 tgaccctgggccacttcaaggagcagctcagcaaaaagggaaattacaggtattatttca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     musculus.
                                                                                                  tcaccctgggccagttcaaggagctgctaaccaagaaggggagctacagatactacttta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1999-120510/10
                                                                                                                                                          108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cancer; breast cancer; colorectal cancer;
                                                                                                                                                                         Similarity
                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97us-0890865
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                                                                                                                                                                     53.7%;
71.5%;
                                                                                                                                                         0;
                                                                                                                                                                      Score 82.2; DB 20; Pred. No. 1.5e-17;
                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                               other;
                                                                                                                                                          Indels
                                                                                                                                                                                    Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cancer
                                                                                                                                                                                       3761;
                                                                                                                                                         0;
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RESULT
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                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 69; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                      The region encoding the VH region is used to construct a recombinant antibody with a lambda light chain. The antibody recognises an antigenic determinant on the outside core in LPS of P. aeruginosa. See also Q12840.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human antibody gene and corresp. recombinant plasmid or virus - useful in mass -prodn. of human anti Pseudomonas aeruginosa LPS outside core antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1991-234064/32.
P-PSDB; R13182.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q12839;
                Q36133 standard; DNA; 657
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 925 BP; 186 A; 231 C; 270 G; 237 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 2; 16pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-NOV-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-NOV-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JP03151876-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Variable region of u type Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-OCT-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q12839 standard; DNA; 925 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Monoclonal antibody; ss
                                                                                                    728
                                                                                                                                         141
                                                                                                                                                                           833
                                                                                                                                                                                                                                               809
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                                                                                                                                                                                                                                                                                21
                                                   8
                                                                                                                        aggcaggat 149
                                                                                                                                                                        tgcctatggcctggggtcttttgatatctggggccaagggacaatggtcaccgtctcttc
                                                                                                                                                                                                     tgcctgcggagcagtttttgaggagatctgggacgacgacgacagtgctccccatgtacga 140
                                                                                                                                                                                                                                                                 ggagcagctcagcaaaaagggaaattacaggtattatttcaagaaggcgagtgacgaatt 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ccgtcttgcctgtctttgaagaaaagatcat 2956
                                                                                                    aggtaagat 736
                                                                                                                                                                                                                                             gcaactgaacagcctgaaatctgaggacacggctctgtattactgtgtgagagaggaata
                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89JP-0291981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89JP-0291981.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label- VH
/note- "Claim 3"
                                                                                                                                                                                                                                                                                                                                   21.6%;
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                ВР
                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                 Score 33; DB 12; Length 925; Pred. No. 0.17; O; Mismatches 60; Indels
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                                                                                                                                                                                                                                                                                                                   0;
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Best Local S
Matches 65
                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence encodes the heavy chain of a recombinant human monoclonal antibody (MAD) designated MH4H7. This sequence was introduced in to a Namahwa ceill strain which was cultured. The MAD may be used in a drug for the prevention and treatment of diseases caused by microbial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               exon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; heavy chain; recombinant; monoclonal; antibody; MAb; MH4H7; Namalwa; microbial infection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q36133
              C41830 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 657 BP; 150 A; 150 C; 193 G; 164 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 5; Fig 8; 27pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-JUN-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1993-032623/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SUMO ) SUMITOMO CHEM CO
                                                                                                                                                                                                                                               534
                                                                                                      654
                                                                                                                                         141
                                                                                                                                                                        594 tgcctatggcctggggtcttttgatatctggggccaagggacaatggtcaccgtctcttc
                                                                                                                                                                                                                                                                                                                   Local Similarity
nes 65; Conserv
                                                                                                                                                                                                            18
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                                                   9
                                                                                                                                     agg 143
                                                                                                                                                                                        tgcctgcggagcagtttttgaggagatctgggacgacgagacagtgctccccatgtacga 140
                                                                                                                                                                                                                                          gcaactgaacagcctgaaatctgaggacacggctctgtattactgtgtgagaggaata 593
                                                                                                                                                                                                                                                              ggagcagctcagcaaaaagggaaattacaggtattatttcaagaaggcgagtgacgaatt 80
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134..181
/*tag= b
/number= Exon
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/number= Intron
280..657
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/number= Exon
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                                                                                                                                                                                                                                                                                                                                   19.7%;
                  363
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                                                                                                                                                                                                                                                                                                                   Score 30.2; DI
Pred. No. 1.3;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       new human
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Gaps

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1830; COCT-2 cocycle abidop bridis bridis bridis bridis cotoli taboli taboli 103340 10	00	3-AUG-1999 5-AUG-1999	PR		5-0139461. 5-0139462.	SD66 SD66	18-JUN-1999; 18-JUN-1999;	PR
the that not ty)  the that not ty)  the that not ty)  station as years to expression control:  that not the that not ty)  part ty preserver; tendential separch; se.  10.  20.  20.  20.  20.  20.  20.  20	٥٥	0-AUG-1999 3-AUG-1999			5-0139459.	300S	19	PR
It thalians DNA frequent SEQ ID NO: 31289.   PR 18-JUN-1999; 9918 collaboration: Signal transduction pathway:   PR 23-JUN-1999; 9918 collaboration:   PR 23-JUN-1999; 9918 collaboration: Signal transduction pathway:   PR 23-JUN-1999; 9918 collaboration:   PR 23-	0.9	0-AUG-1999			3-0139457.	S066	19	PR
The control of thirst entry   Part	òċ	0-AUG-1999 0-AUG-1999			3-0139456.	S066	9 1	PR
bs thallann DNA fragment SEQ ID No: 32289.    Statistication: stephilan DNA fragment SEQ ID No: 32289.   PR 18-JUN-1999; 9918-012-1016-1999; 9918-	ò	7-AUG-1999	PR		s-0139455.	99US	19	PR
### Thailana DNA frequent SPQ ID NO: 33289.  ### Thailana DNA freq	ė,	-1999	PR		5-0139454.	S066	19	מ מ
the thallang DNA fragment SEQ ID NO: 32289.  The thallang DNA frag	5 6	-1999	ים גיט		3-0130403.	S066	- JUN - 19	PR
Is thallana DNA fragment SRO ID NO: 33289.  PR 18-UNY-1999; 9908: 01261161   PR 18-UNY-1999; 9908:	ò	1999	PR		s-0139452.	99US	JUN-19	PR
Ou (first entry)  PR 18-UNF-1999, 9998-0121610 st thallana DNA fragment SEQ ID NO: 32289.  PR 18-UNF-1999, 9998-0121610 standarfic mapping, genet expression control;  PR 18-UNF-1999, 9998-0121610 stylend transduction pathway;  PR 28-UNF-1999, 9998-012162 st thallana.  PR 28-UNF-199	ò	1999	PR		s-0139119.	SD66	JUN-19	PR
Octivate entry)  Definition assay; genetic mapping; gene expression control;  pathway; promoter; termination sequence; ss.  10.  10.  10.  10.  10.  10.  10.	ġ,	0-AUG-1999		٠	5-0138847	S1156	10 5	ט מ
Oc. (first entry)  PR 18-JNN-1999, 9908-01  Is thallana DAA fragment SEQ ID NO: 32289.  PR 18-JNN-1999, 9908-01  PR 22-JNN-1999, 9908-01  PR 22-JN	غ خ	9-AUG-1999	ט ג ג		5-0130540	S066	61-NDC-8	PR
Cirry   Cirr	ء ذ	6-AUG-1999	PR		3-0137724.	99US	7-JUN-19	PR
Oc. (first entry)  Definition DAA fragment SBQ ID NO: 32289.  St thallana DAA fragment SBQ ID NO: 32289.  PATHONY; pencit control; pence expression control; penthony; pence control; penthony; penthony; pence control; penthony;	ò	6-AUG-1999	PR		3-0137502.	99US	4-JUN-19	PR
Oc. (first entry)  PR 18-UNN 1999; 99US-01261  Is thalland DNA fragment SEQ ID NO: 33289.  PR 18-UNN 1999; 99US-01261  PR 22-UNN 1999; 99US-01261  PR 10-UNL 1999; 99US-01	Ö	5-AUG-1999	PR		5-0137528.	S066	3-JUN-19	PR
Oc (first entry)  PR 18-UNN 1999; 99US-101  Rithallana DNA fragment SEQ ID NO: 33289.  Rethroir, signal transporting gene expression control:  pr 23-UNN 1999; 99US-101  PR 23	ġ,	5-AUG-1999	PR 7		S-0130782. S-0137727	51100	1 - TIN-10	מיק ק
PR 18-UUN1999; 99US-10100   Filtrst entry   PR 18-UUN1999; 99US-10100   PR 18-UUN1999; 99US-10100   PR 18-UUN1999; 99US-101000   PR 18-UUN1999; 99US-10100   PR 23-UUN1999; 99US-101000   PR 23-UUN1999; 99US-1010000   PR 23-UUN1999; 99US-101000   PR 23-UUN1999; 99US-101000   PR	ی د	4 - AUG - 1999 4 - AUG - 1999	ק. ג		5-0136392.	S066	7-MAY-19	PR
Brain   Brai	òò	3-AUG-1999	PR		3-0136021.	99US	5-MAY-19	PR
Recommend to the particle of	ò	-1999	PR		s-0135629.	99US	4-MAY-19	PR
Recommendation   Reco	ġ.	2-AUG-1999	PR		S-0135353.	S066	1-MAY-19	PR
DO (first entry)  10 (first entry)  11	ė,	2-AUG-1999	PR		3-0135124	Silbb	0-MAY-19	ָר ק
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9908-0151930
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99US-0139463. 99US-0139750. 99US-0139753. 99US-0139763. 99US-0139817. 99US-0139899. 99US-0140353.	0000	200	900	90	22	999	200		20	913	01	20	011	200	01	909	90	01.0	01	20	20	9	95	2	25	25	20	έģ	-030		•	thaliana.	promoter;	n assay; genetic mapping; gene expressio tification; signal transduction pathway;
																									•								sequence; ss.	<pre>expression control; pathway;</pre>
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07-OCT 1999
11-OCT 1999
Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                               Arabidopsis thaliana DNA fragment SEQ
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1 Similarity 54.6%;
59; Conservative
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99US-015263

99US-0153778

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99US-0155469

99US-0155659

99US-0156659

99US-0156696

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99US-01611920

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99US-0161193
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Pred. No. 2;
0; Mismatches
                                                 ID NO: 22779.
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                               Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
           Arabidopsis thaliana.
                                                                              Arabidopsis
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                                                                                                                            C51169;
                                                                                                                                                   C51169 standard; DNA; 811 BP
                                                                                                                                                                                                            281
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-0151 -0151 -0151 -0151 -0151 -0151 -0151 -0151 -0151 -0151 -0151			99US-0142055 99US-0142803 99US-0142920 99US-01440853 99US-0144085 99US-0144085 99US-01444085 99US-0144331 99US-0144333 99US-0144333 99US-0144334 99US-0144334 99US-0144339 99US-0144339 99US-0144334 99US-0144339 99US-0144339 99US-0144339 99US-0144339 99US-0144339 99US-0144339 99US-0144339 99US-0144339 99US-0144339	-014
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                                                              Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                                                                                                                           C35517;
 06-SEP-2000
                                                                                                             Arabidopsis thaliana DNA fragment SEQ
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13-OCT-1999;
13-OCT-1999;
14-OCT-1999;
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                                                                                                         Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.
              11-NOV-1994;
                                      01-JUN-1995.
                                                                                     Homo sapiens
                                                                                                                                                             Human gene signature HUMGS01117.
                                                                                                                                                                                                                                     T19983 standard; cDNA to mRNA; 340 BP
                                                              WO9514772-A1
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Best Local Similarity 57.8%;
Matches 52; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying gene signatures in 3'-directed human cDNA library - e.g. for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
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(OKUB/) OKUBO K.
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18.0%; 58.5%;

Score 27.6; DI Pred. No. 2.4; O; Mismatches

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Length 1167; Indels

US-08-261-110A-3  US-08-261-110A-3  US-08-261-110A-3  Sequence 3, Application US  Patent No. 5674992  GENERAL INFORMATION: APPLICANT: CERUTTI, HE  TITLE OF INVENTION: CD  TITLE OF INVENTION: ED  NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESSE: NIXON, HA  STREET: CLINTON SQUA  STREET: CLINTON SQUA  CITY: ROCHESTER  STATE: NEW YORK  COUNTRY: USA  SIP: 14603  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy COMPUTER: IBM PC COM OPERATING SYSTEM: PC SOFTWARE: PATENTION NUMBER: FILING DATE: 16-JUN CLASSIFICATION NUMBER: FILING DATE: 16-JUN APPLICATION NUMBER: FILING DATE: 18-DUG ATTORNEY/AGENT INFORMATINAME: TIMIAN, SUSAN REGISTRATION NUMBER: FILING DATE: 16-JUN REGISTRATION NUMBER: FILING DATE: 16-JUN TELEPHONE: (716) 263-1 INFORMATION FOR SED ID NO SEQUENCE CHARACTERISTIC LENGTH: 1167 base pa TYPE: nucleic acid TIMORESUS: Single TOPOLOGY: Linear MOLECULE TYPE: CDNA	28 25 4 1 29 25 4 1 29 25 4 1 25 1 25 1 25 1 25 1 25 1 25 1 25	
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Sequence 45, Application US/09040984

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GENERAL
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APPLICANT: JAGEND
APPLICANT: CERUTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (716) 263-1600 INFORMATION FOR SEQ ID NO: 1:
                                                                                                                      1232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: TIMIAN, SUSAN J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                         1172
                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: 11
MOLECULE TYPE:
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 28-AUG-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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                                                                                                                                                     73
                                                                                                                                                                                                       13 cacttcaaggagcagctcagcaaaaagggaaattacaggtattatttcaagaaggcgagt 72
                                                                                                                                                                                                                                                                         Match 18.0%;
Local Similarity '58.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1:0
                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 1
CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP STREET: CLINTON SQUARE, P.O. BOX 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                   CENGTH:
                                                                                                                    GATCAACTCCTTTGATGAGCAG 1253
                                                                                                                                                 gacgaatttgcctgcggagcag 94
                                                                                                                                                                                     CTCTTCAAGACGAAATTGAGAAGAAAGTGAGATTGTTGATGTTAGATGGAGAAGTTCATC 123:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (716) 263-1636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-JUN-1994
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28-AUG-1992
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                                                                                                                                                                                        Sequence 2, Application Patent No. 6001631
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 base pairs
TENGTH: nucleic acid
                                                                                                                                                              APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
                                                          CORRESPONDENCE ADDRESS:
                                                                                     TITLE OF INVENTION:
                                                                                                                    APPLICANT:
                                                                                                                                  APPLICANT:
                                                                                                                                                 APPLICANT:
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                                                                        NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                 138 GTAATGCT 131
                                                                                                                                                                                                                                                                                                                             121 acagtgct 128
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                                                                                                                                                                                                                                                                                                                                                                            61 aagaaggcgagtgacgaatttgcctgcggagcagtttttgaggagatctgggacgacgag 120
               STREET:
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                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
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STREET: 6300 Columbia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
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                          ADDRESSEE:
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                                                                                                                                                                                                           2, Application 6001631
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Washington
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             E: Dunner, L.L.P.
1300 I. Street, N.W., Suite 700
                                                                                                                                                            BLANCHE, CAMERON,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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                                                                                                                    FERRERO,
                                                                                                                                                 CROUZET,
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                                                                                                                                  FAMECHON, Alain
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                                        Finnegan, Henderson, Farabow,
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Nucleotide Sequences and Uses Thereof
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                               L.P
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Pred. No. 2.5;
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy

COUNTRY: USA ZIP: 20005-3315

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Best Local Similarity 63.1%;
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FILING DATE: 24-JAN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Elnaudi, Carol P.
REGISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 03806.0394-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (202) 408-4444
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4213 CACGA 4209
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                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: DNA SEQUENCE ENCODING A TUMOR TITLE OF INVENTION: SUPPRESSOR GENE NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/569,721
FILING DATE: 08-DEC-1995
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                                                                                    FILING DATE
                                                                                                                                                                                                                                                 CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
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                                                              CLASSIFICATION:
                                                                                                     APPLICATION NUMBER: US/09/258,257
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Pred. No. 9.1;
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US-09-258-257-1
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Best Local Similarity
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SEQUENCE CHARACTERISTICS:
                                                             TELEFAX: 415-854-8275 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                    COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/258,371
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                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: MOO1, Leslie A.
REGISTRATION NUMBER: 37,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                              SEQUENCE CHARACTERISTICS:
                                                                                             TELEPHONE: 415-854-7400
                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
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STRANDEDNESS:
                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 028722-128
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                               ENGTH:
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      nucleic acid
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                              1902 base pairs
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double
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57.3%;
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                                                                                                                                          37,047
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Pred. No. 10;
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US-08-569-721A-1
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; LOCATION:
US-09-258-371-1
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                                                                Best Local Similarity Matches 47; Conserv
                                                                                              Query Match
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                                                                                                                                                                                                                                                                             TELEFAX: (650) 854-827
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MOOI, Leslie A.
REGISTRATION UNMBER: 37,047
REFERENCE/DOCKET NUMBER: 0287
TELECOMMUNICATION INFORMATION:
1132 CATGGCCAATTAAAAAAATTGTTCATAAAGTAATAATATTACTTGTATTAAAATAAAAA 1073
                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/569,72.
                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic)
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: DNA SEQUENCE ENCODING A TUMOR
TITLE OF INVENTION: SUPPRESSOR GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 1
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FEATURE:
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TOPOLOGY: 11
                                                                                                                                                                        NAME/KEY:
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                 6 cctgggccacttcaaggagcagctcagcaaaaagggaaattacaggtattatttcaagaa 65
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mes 47; Conserv
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                                                                Conservative
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                                                         Score 26; DB 3;
Pred. No. 10;
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RESULT 9
US-09-499-082-1/c
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Best Local Similarity
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Patent No.
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                             1072 AGCTAATGAAATATTTTCCTTC 1051
                                                                                                                                                      1132 CATGGCCAATTAAAAAAATTGTTCATAAAGTAATAATATTACTTGTATTAAAATAAAAA 1073
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: US 0
FILING DATE: 08-DEC-1995
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APPLICANT: Riabowol, Karl
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CORRESPONDENCE ADDRESS:
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                                                                                                                  66 ggcgagtgacgaatttgcctgc 87
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57.3%;
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Pred. No. 10;
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APPLICANT:

Helbing, Caren C. Riabowol, Karl Johnston, Randall N.

CORRESPONDENCE ADDRESS:

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US-09-499-082-1
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                                                                                                                  RESULT 10
US-09-258-371-9/c
                                                                                    Sequence 9, Application US/09258371 Patent No. 5986078
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                  Matches
GENERAL INFORMATION:
APPLICANT: GARKAVESEV, Igor
APPLICANT: Riabowol, Karl
TITLE OF INVENTION: DNA SEQU
TITLE OF INVENTION: SUPPRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: MOOL, Leslie A.
REGISTRATION UNMBER: 37,047
REFERENCE/DOCKET NUMBER: 0287
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-854-7400
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NFORMATION FOR SEQ ID NO: 1:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                  1132 CATGGCCAATTAAAAAAAATTGTTCATAAAGTAATAATATTACTTGTATTAAAAATAAAAA 1073
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APPLICATION NUMBER: US 08/569721
FILING DATE: 08-DEC-1995
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/828,15: FILING DATE: 27-MAR-1997
APPLICATION NUMBER: US 08/751230
FILING DATE: 15-NOV-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
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THERER: 37,047
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57.3%;
   DNA SEQUENCE ENCODING THE TUMOR SUPPRESSOR GENE ING1
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Pred. No.
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US-09-258-371-9
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                                                                                                                                                                                                                                                                         Sequence 9, Application US/08751230 Patent No. 6117633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local Similarity
                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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                                                                                                                                                                                           APPLICANT: Garkavtse
APPLICANT: Riabowol,
TITLE OF INVENTION:
TITLE OF INVENTION:
                              COUNTRY: USA
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                            1231 AGCTAATGAAATATTTTCCTTC 1210
                                                                                                                                                                                                                                                                                                                                                                                                                                           1291 CATGGCCAATTAAAAAAATTGTTCATAAAGTAATAATATTACTTGTATTAAAAATAAAAA 1232
                                                                                                                                                             CORRESPONDENCE ADDRESS:
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NAME: Mooi, Leslie A.
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Alexandria STATE: VA
COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                             STREET: 699 Prin
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                             66 ggcgagtgacgaatttgcctgc 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
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TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: MOOI, Leslie A.
REGISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
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                                                                                                                                               ADDRESSEE:
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                                                                                                                                                                                                                                            Garkavtsev,
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SYSTEM: PC-DOS/MS-DOS
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57.3%;
compatible
PC-DOS/MS-DOS
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Pred. No. 11;
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PRIOR APPLICATION DATA:

CLASSIFICATION: FILING DATE: APPLICATION NUMBER:

15-NOV-1996

US/08/751,230

CURRENT APPLICATION DATA:

PatentIn Release #1.0, Version #1.30

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US-08-751-230-9
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Best Local Similarity
Matches 47; Conserv
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PRIOR APPLICATION NUMBER: US/08/828,158
APPLICATION NUMBER: US/08/828,158
FILING DATE: 27-MAR-1997
APPLICATION NUMBER: US 08/751230
FILING DATE: 15-NOV-1996
                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1231 AGCTAATGAAATATTTTCCTTC 1210
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Garkavtsev, Igor
TITLE OF INVENTION: METHODS OF MODULATING APOPTOSIS
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 ggcgagtgacgaatttgcctgc 87
                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: MOOI, Leslie / REGISTRATION NUMBER:
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                                                                                                         FILING DATE:
                                                                                                                           APPLICATION NUMBER: US/09/499,082
                                                                                                                                                                                                                                                  ZIP: 22313-1404
                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                 CITY: Alexandria
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Pred. No.
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                                                                                                                                                            Version #1.30
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; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-08-846-762-1
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                                                                                                                                                                                                                                                                                                                            SEQ ID NO
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Best Local Similarity
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Best Local Similarity
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APPLICANT: Burrows, Lori
APPLICANT: Charter, Deborah
APPLICANT: de Kievit, Teresa
TITLE OF INVENTION: No. 5994072el Proteins Involved in the Synthesis and Assembly
TITLE OF INVENTION: Of O-Antigen in Pseudomonas Aeruginosa
                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/08/846,762A CURRENT FILING DATE: 1997-04-30
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                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 100
                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 6580-089
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                                             20033 ACCAGGGAACGCGCACCACCGCCGGGGGGGGGGGGTACCAGTAGACCAGCAACGACAGG 19974
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ATTORNEY/AGENT INFORMATION:
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LOCATION:
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                                                                                                            TGGCGCATGGCCAGACGCAAGCCGCCGATCAGCAGCATGCTCAACCACCAGTAGTTGAAC
                                                                                                                                  ttgaccctgggccacttcaaggagcagctcagcaaaaaagggaaaattacaggtattatttc 60
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16..900
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57.3%;
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Pred. No. 11;
                                                                                                                                                                                           Score 26; DB
Pred. No. 28;
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19973 AC 19972

US-08-469-412A-3/c

Sequence 3, Application US/08469412A Patent No. 5856125

ENERAL INFORMATION:

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RESULT 15
US-09-021-715-3/c
; Sequence 3, Application US/09021715
; Patent No. 6194547
; GENERAL INFORMATION:
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Best Local Similarity
Matches 35; Conserv
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NFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOETWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,412A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                2240 TGCCCATGGGCCAGTCCTAGGAGCAGCTGGGGGATGAAGGGGTTGGACCGGT 2190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
LOCATION: 123..698
OTHER INFORMATION: ,
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Garrett-Wackowski,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         OLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADJUKESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (415) 576-0200 •
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UMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POPOLOGY:
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IVENTION: The ERF Genetic Locus and Its Products
EQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Beal Jr., Gregory J. Athanasiou, Meropi A
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                                                                                                                                                                                                                                                      Conservative
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                                Mavrothalassitis, George J.
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Fisher, Robert J.
                  Blair, Donald G
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Pred. No. 18;
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US-09-021-715-3
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Best Local
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TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:
                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/021,715
FILING DATE: 10-Feb-198
CLASSIFICATION: CUBANOWNDATIONNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: The ERF Genetic Locus and Its Products
NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                    SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                              FEATURE:
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                                                                                                                                             1 Similarity
35; Conserv
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                                                                                                                                                                                                                                                                                                       NAME/KEY: CDS
LOCATION: 123..698
                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 2432 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Garrett-Wackowski, Eugenia REGISTRATION NUMBER: 37,330 REFERENCE/DOCKET NUMBER: 015280-229000
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                                                                                                                                             Conservative
7,
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                                                                                                                                                           16.6%;
2001, 00:26:52
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Pred. No. 18;
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                                                                                                                                             Mismatches
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                                                                                                                                             16;
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Search completed: June Job time: 19755 sec

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OM nucleic - nucleic search, using sw
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Maximum DB seq length: 2000000000
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                                              3333309
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Gapop 10.0 , Gapext 1.0
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gb_est3:*
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Result
No.
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   Query
Match
   79.1
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139 BE755017
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140 BE808273
111 AM140896
143 BF076028
3 AA170717
165 BE333754
1 AA028403
4 AA259709
3 AA153185
143 BF039925
144 BF0889872
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gb\_est101:\*
gb\_est102:\*

gb\_est90:

gb\_est85: \*
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AA153185 ms62d10.r
BF889872 289473 MA

AA446378 zw58b07.r Description

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RESULT
AA446378
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ORGANISM
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VERSION
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75.8
67.8
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T., Waterston, R. and Wilson, R.
WashU-Merck EST project 1997
Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. I
                                                                                                                                                                                                                                                                                                                                                                                                         zw58b07.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone
IMAGE:774229 5', mRNA sequence.
                                                                                                                                  Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 490.
                                                                                                                                                                                                                                                                                                              викатуота; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 548)
                                                                                                                                                                                                                                                                                          Hillier, L., Allen, M., Bowles, L., Dubuque, T., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, I
                                                                                                                                                                                                                                                                                                                                                                                               AA446378
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Fax: 314 286 1810
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w &
/note-"Vector: PT7T3D-Pac (Pharmacia) with a modified /note-"Vector: PT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from pooled 8-9 week (total) fetus material with a Not I - oligo(dT) primer [5'
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/db_xref="taxon:9606"
/clone="IMAGE:774229"
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Le,N., Lennon,G., Marra,M., Martin,J., Moore,B.
Steptoe,M., Tan,F., Theising,B., White,Y., Wylie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA355700
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AW445343
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T07178
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AA355700 EST64142
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BE290973 601084133
BE882875 601509279
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AL228087 Tetraodon
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AL304372 Tetraodon
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1M0032J16
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BE755017.1 C
                                                                                                                                                                                               Seq
                                                                                                                                                                                                                                                                                                                                                    USDA, ARS, US Meat Animal PO Box 166, Clay Center, h Tel: 402 762 4366 Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                     Design and use of four | EST discovery in cattle Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 495)
Smith, T.P.L., Casas, E., Stone, R.T.,
Bennett, G.A., Fahrenkrug, S.C., Freki, W.W. and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BE755017
208720 MARC
                                                                                                                                                                                                                                                                                                   Email: smith@email.marc.usda.gov
Single pass sequencing. Bases call
v0.980904.e. Vector identified by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COW
                                                                                                                                                                                                                  BACKWARD: GTTTTCCCAGTCACGACG
Plate: 56 row: K column: 1:
                                                                                                                                                                                                                                                                   PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Smith TPL
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bovidae; Bovinae;
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   Ω
                      /note-"Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from testis, thymus, semitendonosus muscle, longissimus muscle, pancreas, adrenal and endometrium."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the and Eco RI sites of the modified pT7T3 vector. Libra went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo. a 121 c 170 g 116 t
                  adrenal, and
                                                                                 /tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                /organisme"Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 2BOV"
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Pred. No. 5.8e-28;
   164 g
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Freking,B.A., Rohrer,G.A., Laegreid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 tgaccctgggccacttcaaggagcagctcagcaaaaagggaaattacaggtattatttca 61
             tgaccctgggccacttcaaggagcagctcagcaaaaagggaaattacaggtattatttca 61
TGACCTTGGGCCACTTTAAGGAGCAGCTCAGCAAAAAAGGGAAACTACCGGTATTACTTCA 100
                                                       130;
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                                                                                                                                                                                                                                                                                                                                                                                                   EST discovery in cattle (1900) (Inpublished (2000) (Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BE668565
158407 M
                                                                                                                                                                                                                                                                              Plate: 60 row: O column: 14 Seq primer: ATTTAGGTGACACTATAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Design and use of four pooled tissue normalized cDNA libraries for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bovidae; Bovinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bos taurus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W.W. and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 546)
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                                                                                                                                                                                  /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 4BOV"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                 Library made from pooled tissue from day 20 and day 40 embryos."
                                                                                                                                                                                                                                                                                                       GTTTTCCCAGTCACGACG
                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                 76.3%;
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                                                 Score 116.8; DB 130
Pred. No. 1.2e-26;
0; Mismatches 22;
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Pred. No. 1.2e-26;
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                                                                             DB 138;
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Query Match
Best Local Similarity 74.2
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                                                                                                                                                                                                                                                                                                                                                                                        2 tgaccctgggccacttcaaggagcagctcagcaaaaagggaaattacaggtattatttca 61
                                                       cagtgctccccatgtacgaaggcaggatcct 152
                                                                                                                                                                                                                            agaaggcgagtgacgaatttgcctgcggagcagtttttgaggagatctgggacgacgaga 121
                                                                                                                                                                     AGAAAGTGAGCGACGAGTTTGACTGTGGGGTGGTGTTTGAGGAGGTTCGAGAGGACGAGG
CCGTCCTGCCCGTCTTTGAGGAGAAGATCAT 517
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Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM109 row: o column: 14
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National Institutes of Health, Mammalian
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/Clone_lib="NIH_MGC_9"
/Clone_lib="NIH_MGC_9"
/tissue_type="adenocarcinoma cell line"
/tissue_type="adenocarcinoma cell line"
/lab.host="DHIOB (phage-resistant)"
/lab.host="DHIOB (phage-resi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         e: LLCM109 row: o column: 14 quality sequence stop: 673.
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/db_xref="taxon:9606"
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CDNA Library Preparation: M.B. Soares Lab Clone distribution:

Clones will be available through Research Genetics (www.resgen.com)

This clone is also available through the I.M.A.G.E. Consortium at

LLNL (info@lmage.llnl.gov). IMAGE ID- 1791410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UI-R-Y0-acc-b-09-0-\bar{\text{U}}I.rl UI-R-Y0 Rattus norvegicus cDNA clone UI-R-Y0-acc-b-09-0-UI 5', mRNA sequence. BF521997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                451 Eckstein Medical Research Building Iowa City, IA 52242, Tel: 319 335 8250 Fax: 319 335 9565
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nilarity 96.8%;
Conservative
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                                                                                                                                                                                                                                                        //lab.host="bulb" adult
//lab.host="vector: pT7T3D-Pac (Pharmacia) with a modified
//note="vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-YO
library is a subtracted library derived from an
individually-tagged normalized whole-eye (minus the lens).
library is previous libraries (UI-R-AO, UI-R-AI, UI-R-EO,
II-R-EO, II-R-EO, and UI-R-CO). The tag is a string of
pool of all previous libraries (UI-R-AO, UI-R-AI, UI-R-EO,
UI-R-EI, UI-R-CO), and UI-R-CO]. The tag is a string of
3-5 nucleotides present between the Not I site and the
oligo-dT track which allows identification of the library
of origin of a clone within the mixture. The subtracted
library (UI-R-YO) was constructed as follows: PCR
amplified cDNA inserts from previous library clones from
which 3' ESTs had been derived were used as a driver in a
hybridization with the normalized whole-eye library in
the form of single-stranded circles. The remaining
single-stranded circles (subtracted library) was purified
by hydroxyapatite column chromatography, converted to
double-stranded circles and electroporated into DHIOB
bacteria (Life Technologies) to generate the UI-R-YO
library. This procedure has been previously described
(Bonaldo, Lennon and Soares, Genome Research 6: 791-806,
196)"
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/clone_lib="UI-R-Y0"
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/strain="Sprague-Dawley"
/db_xref="taxon:10116"
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                                                                                 Score 88.2; DB 149;
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0; Mismatches 3;
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 36
AAGAAGGCGAGTGACGAATTTGCCTGTGGAGCA 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 319)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 971 Std Error: 0.00 Seq primer: M13RP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: est@watson.wustl.edu
Insert Size: 971
High quality sequence stops:
Source: IMAGE Consortium, LLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Wilson RK
Washington University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R75687.1 GI:850369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                         Similarity
                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      quality sequence stop: 198.
                                                                                                                                                                                     99
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                                                                                                                                                                                                                 double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pn773 vector (Pharmacia). Library went through one round of normalization to a Cot 230. Library constructed by Bento Soares and M.Fatima
                                                                                                                                                                                                                                                                                                         /db_xref="taxon:9606"
/clone="IMAGE:158891"
                                                                                                                                                                                                                                                                                                                                                                                                    /dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Soares breast 2NbHBst"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="GDB:572946"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                       57.3%;
73.5%;
                                                                                       Score 87.6; DB Pred. No. 2e-17;
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                                                                      Mismatches
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                                                                                                          DB 156;
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                                                                        40;
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Matches 106; Conservative
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                                                                487 CCGTCCTGCCCGTCTTGAGG
                                                                                                                                                                                                                   367 TCACCCTGGGCCAGTTCAAGGAGCTGCTGACCAAAAAGGGGCAGCTACAGATACTACTTCA 426
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                                                                                                   122 cagtgctccccatgtacgaag 142
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                                                                                                                                                             62 agaaggcgagtgacgaatttgcctgcggagcagtttttgaggagatctggggacgacgaga 121
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                                                                                                                                         AGAAAGTGAGCGACGAGTTTGACTGTGGGGTGTTTTGAGGAGGTTCGAGAGGACGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cagtgctccccatgtacgaaggcaggatcct 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NH+MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: image.llnl. Plate: LLCM93 row: e column: 09 High quality sequence stop: 600.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 127
                                                                                                                                                                                                                                                                                                                                                                                                              /tissuc_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: ovary; Vector: pOTB7; Site_1: xhoI; Site_2:
ECORI; CDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
27 a 189 C 194 g 91 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:9606"
/clone="IMAGE:3049328"
/clone_lib="NIH_MGC_9"
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75.2%;
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                                                                                                                                                                                                                                                                                                  Score 85; DB 165;
Pred. No. 1.5e-16;
0; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                          Length 601;
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                                                                                                                                                                                                                                        cagtgctccccatgtacgaaggcaggatcct 152
                                                                                                                                                                                                                                                                                                                       agaaggcgagtgacgaatttgcctgcggagcagtttttgaggagatctgggacgacgaga 121
                                                                                                                                                                                                                                                                                              AGAAAGTGAGCGACGAGTTCGAGTGCGGCGTGGTGTTCGAAGAGGTGCGTGAGGACACGG 266
                                                                                                                                                                                                                                                                                                                                                                         TCACCCTGGGCCAGTTCAAGGAGCTGCTGACCAAGAAGGGCAACTACAGGTTCTACTTCA 206
                                                                                                                                                                                                                 CTGTGCTGCCCGTCTTCGAGGAGAAGATCAT 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                            109;
sequence.
AW140896
AW140896.1
EST.
                                                                          AW140896
EST290830 PRGIAS43 5'
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Plate: 68 row: 0 column: 3
Seq primer: ATTTAGGTGACACTATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscorr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ,W.W. and Keele,J.W.
Design and use of four pooled tissue normalized cDNA libraries for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Smith,T.P.L., Casas,E., Stone,R.T.,
Bennett,G.A., Fahrenkrug,S.C., Frek.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bos taurus
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213437 MARC 2BOV Bos taurus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 2BOV"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pCMV SPORT6; Site_1: xbaI; Site_2: xhoI; Library made from pooled tissue from testis, thymus, semitendonosus muscle, longissimus muscle, pancreas, adrenal. and endometrium."
                                                              487 bp mrNA EST 30-OCT-1999
Normalized rat embryo, Bento Soares Rattus sp. cDNA clone
' end similar to GSK-3beta interacting protein rAxin, mrNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            adrenal, and endometrium."
133 c 166 g 74 t
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                GI:6160589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54.8%;
72.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 83.8; DB 14
Pred. No. 3.5e-16;
0; Mismatches 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5', mRNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGAAAGTGAGTGACGAGTTTGACTGTGGTGTGGTATTTGAGGAAATACGGGAAGATGAGG 442
                                                                                                                                                                                                                                                                                                                             BF076794
226536 MARC :
BF076794
 USDA,
PO Bo
                                   EST discovery in cattle Unpublished (2000) Contact: Smith TPL
                                                                                           1 (bases 1 to 503)
Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M.,
Bennett, G.A., Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Laegreid,
W.W. and Keele, J.W.
Design and use of four pooled tissue normalized cDNA libraries for
                                                                                                                                                                                              Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fax: (301)-838-0208

Email: nhlee@tigr.org

For clone availability, additional sequence and expression information related to this EST please check the TIGR Rat Gene Index (http://www.tigr.org/tdb/rgi/rgi.html). To order a clone contact the ATCC (http://www.atcc.org/atcc.html).

Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lee, N.H., Glodek, A., Chandra, I., Mason, T.M., Kerlavage, A.R. and Adams, M.D.
                                                                                                                                                                                                                                                                                                           BF076794.1
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Mammalia; Eutheria;
                                                                                                                                                                                          Bovidae; Bovinae; Bos.
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DA, ARS, US Meat Animal Research Center
Box 166, Clay Center, NE 68933-0166, U
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Rattus sp."
/db_xref="taxon:10118"
/db_nref="taxon:10118"
/clone="RoTANS43"
/clone=lib="Normalized rat embryo, Bento Soares"
/dev_stage="embryo 8, 12, 18 dpc"
/dev_stage="embryo 8, 12, 18 dpc"
/notce="Vector: pT773Pac; Site_1: EcoRI; Site_2: NotI"
125 c 136 g 97 t
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1. .487
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72.2%;
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Rodentia;
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Pred. No. 3.5e-16;
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Sciurognathi; Muridae; Murinae;
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 USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             267 TCACCCTGGGCCAGTTCAAGGAGCTGCTGACCAAGAAGGGCAACTACAGGTTCTACTTCA 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 agaaggcgagtgacgaatttgcctgcggagcagtttttgaggagatctggggacgacgaga 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTGTGCTGCCCGTCTTCGAGGAGAAGATCAT 417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      109;
                                                                                                         Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Single pass sequencing. Bases called and alt_trimmed v0.980904.e. Vector identified by cross_match with the and _minmatch 12 options.
                 Single pass sequencing. Bases c
v0.980904.e. Vector identified
and -minmatch 12 options.
PCR PRimers
                                                                                                                                                                                                   Design and use of four person and use of four person discovery in cattle Unpublished (2000)
                                                                                                                                                                                                                                                    1 (bases 1 to 562)
Smith,T.P.L., Casas,E., Stone,R.T.,
Bennett,G.A., Fahrenkrug,S.C., Frek
,W.W. and Keele,J.W.
                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                     Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                          COM
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Plate: 87 row: N column: 19
Seq primer: ATTTAGGTGACACTATAG.
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FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  225414 MARC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: smith@email.marc.usda.gov
                                                                                        Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                 Bovidae; Bovinae; Bos.
FORWARD: AGGAAACAGCTATGACCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note-"Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from testis, thymus, semitendonosus muscle, longissimus muscle, pancreas, adrenal, and endometrium."

a 146 c 185 g 74 t
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/db_xref="taxon:9913"
/clone_lib="MARC 2BOV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="pooled"
/lab_host="DH10B"
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Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 562 bp
2BOV Bos
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72.2%;
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Pred. No. 3.5e-16;
0; Mismatches 42;
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                                                   called and alt_trimmed by cross_match with the
                                                                                                                                                                                                                                                                          R.T., Heaton, M.P., Freking, B.A., Roh
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Rohrer, G.A., Laegreid
                                                     with the
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                                                                                                                                              Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL;
TMAGE Consortium (info@image.llnl.gov) for further
                                                                                                                                                                                                                                           WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                             The WashU-HHMI Mouse EST Project Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dub
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  o', mRNA sequence.
AA170717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ms70a09.rl Soares mouse
5', mRNA secure
                                                                                                                                                                                                               Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                         Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                     Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                   Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BACKWARD: GTTTTCCCAGTCACGACG
Plate: 85 row: D column: 1
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                                                                          primer: -28M13 rev2 from Amersham
h quality sequence stop: 428.
Location/Qualifiers
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/db_xref="taxon:9913"
/clone_lib="MARC 2BOV"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from testis, thymus, semitendonosus muscle, longissimus muscle, pancreas, adrenal, and endometrium."

171 c 201 g 90 t
              /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
                                      ∕organism="Mus
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72.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 83.8; DB 1
Pred. No. 3.6e-16
0; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3NbMS Mus musculus cDNA clone IMAGE:616888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42;
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REFERENCE
AUTHORS
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BE333754
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGAAAGTGAGTGATGAGTTTGACTGTGGTGTGTTTTGAGGAAGTACGGGAGGATGAGG
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                                                                               Seq primer: -40RP from Gibco
High quality sequence stop: 391.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BE333754 476 bp mRNA EST 14-JUL-2000 us27f06.yl Soares_NMEBA_branchial_arch Mus musculus cDNA clone IMAGE.3168323 5' similar to TR:O15169 O15169 AXIN; mRNA sequence.
                                                                                                                                 MGI:1063783
                                                                                                                                                               CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Washington University Genome Sequencin Clone distribution: NCI-CGAP clone distribution informati found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov/image/html/iresources.shtml
                                                                                                                                                                                                                                                                                                                                                                NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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                                                                                                                                                                                                                                                               cDNA Library Preparation: M. Bento Soares, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   house mouse
                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 476)
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                                                                                                                                                                                                                                                                                  Robert_Strausberg@nih.gov
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/db_xref="taxon:10090"
/clone="IMAGE:3168323"
/clone_lib="Soares_NMEBA_branchial_arch"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="4 weeks"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Soares mouse 3NbMS"
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71.5%;
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Pred. No. 1.1e-15;
0; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                  Genome Anatomy
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Murinae; Mus
                                                                                                                                                                                                                                                                 Fatima Bonaldo
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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cagtgctccccatgtacgaaggcaggatcct 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108;
                                                                                                                                                                                                                                                                                                                                     Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                     Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dub
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA028403 516 bp mRNA EST 16-AUG-1996 m121f04.rl Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone IMAGE:464191 5', mRNA sequence.
                                                                                                                                                                                                                                              WashIngton University School of MedicineP

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 516)
                                                                                                                                                                 Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                      Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                         Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
                                                                                                                                                                                                                    Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              house mouse.
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                                                                                                                                     primer: -28M13 rev2 from Amersham
                                                                                                quality sequence stop: 493.
Location/Qualifiers
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               /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:464191"
clone_lib="Soares mouse embryo NbME13.5 14.5"
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71.5%;
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1.1e-15;
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Best Local Similarity
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 526)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMAGE:733481 5', mRNA sequence.
AA259709
AA259709.1 GI:1896194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA259709 526 bp mRNA EST 18-MAR-va36f09.rl Soares mouse 3NME12 5 Mus musculus cDNA clone
                                                                                                                                   Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
                                                                                                                                                                                                 Tel: 314 286 1800
Fax: 314 286 1810
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WashU-HHMI Mouse EST Project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Lc
                                                                                                                                                                                                                                                                                                                  Unpublished (1996)
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                                                                                                                     MGI:450529
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                                                                                                primer: -28m13 rev2 ET from Amersham
                                                       quality sequence stop: 485.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus'
/strain="C57BL/6J"
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Pred. No. 1.1e-15;
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BASE COUNT
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